

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 15, 2003, 11:49:23 ; Search time 1874.39 Seconds

(without alignments)
8908.057 Million cell updates/sec

Title: US-09-856-320A-1_COPY_272_958

Perfect score: 687

Sequence: 1 atcacaagggttcgagtg.....aggagacgatgaagaacaat 687

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues 45562784

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_esthum:*
3: em_estlu:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_tod:*
26: em_gss_phg:*
27: em_gss_vr1:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	671.4	97.7	1294	11	BC015551 Homo sapi
2	631.6	91.9	678	12	BT763040 603047836
3	627.6	91.4	853	10	BG720793 602692015
4	618	90.0	841	12	BT818697 603037514

5	601.6	87.6	1072	12	BM559782	BM559782 AGENCOURT
6	583.2	84.9	1074	12	BM559617	BM559617 AGENCOURT
7	529.4	77.1	708	10	BG697071	BG697071 602660281
8	514.2	74.8	1295	11	AK009360	AK009360 Mus muscu
9	514.2	74.8	1295	11	AK009720	AK009720 Mus muscu
10	502.2	73.1	1269	11	AK009659	AK009659 Mus muscu
11	470.4	68.5	639	10	BG747134	BG747134 602704354
12	431.8	62.9	973	10	BE867930	BE867930 601443517
13	428.4	62.4	761	12	BM982377	BM982377 UI-CF-EN1
14	379.8	55.3	528	14	BX528424	BX528424 R2PD Mus
15	378	55.0	747	13	BX109836	BX109836 BX109836
16	367	53.4	539	12	BM837078	BM837078 K-EST0113
17	359.8	52.4	467	9	AA073833	AA073833 mJ99h09.y
18	359.8	52.4	467	9	A1893370	A1893370 mJ99h09.y
19	342.8	49.9	368	9	AA112318	AA112318 zt97c06.x
20	340	49.5	673	13	BE684799	BE684799 UI-CF-EN1
21	316.6	46.1	394	10	BE150851	BE150851 RCA-HM027
22	312	45.4	809	10	BE679282	BE679282 602153475
23	305.4	42.5	451	14	W60374	W60374 z6d2p01.r1
24	287	41.8	654	13	BU676834	BU676834 UI-CF-DU1
25	286.4	41.7	526	10	BE898804	BE898804 601681783
26	284.8	41.5	966	14	BY709314	BY709314 BY709314
27	283.6	41.3	579	12	BI046611	BI046611 MR3-FN020
28	269.2	39.2	484	14	CB270157	CB270157 1009064.H
29	262.4	38.2	696	12	BM020073	BM020073 603648624
30	247.6	35.0	1048	11	AK004807	AK004807 Mus muscu
31	241.6	32.6	879	10	BE677072	BE677072 602086616
32	230.6	33.6	644	10	BE219655	BE219655 hv60g10.x
33	225.2	32.8	645	9	AW511566	AW511566 xuf60a02.x
34	224.2	32.6	880	14	CB202840	CB202840 AGENCOURT
35	224.2	32.6	898	14	CB204935	CB204935 AGENCOURT
36	222.6	32.4	582	9	AW243944	AW243944 x091b07.x
37	217.6	31.7	560	10	BF476474	BF476474 naa25d06.
38	213.4	31.1	852	14	CB587168	CB587168 AGENCOURT
39	205.2	29.9	826	14	CB574882	CB574882 AGENCOURT
40	194	28.2	824	13	BU592722	BU592722 AGENCOURT
41	194	28.2	897	13	BU502087	BU502087 AGENCOURT
42	193.8	28.2	585	11	AK009451	AK009451 Mus muscu
43	193.8	28.2	585	11	AK019102	AK019102 Mus muscu
44	193.4	28.2	765	13	BX079152	BX079152 BX079152
45	193.4	28.2	849	13	BX078383	BX078383 BX078383

ALIGNMENTS

RESULT 1
LOCUS BC015551 1294 bp mRNA HTC 29-OCT-2001
DEFINITION Homo sapiens, kallikrein 11, clone IMAGE:3847565, mRNA.
ACCESSION BC015551
VERSION BC015551.1 GI:15930236
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1294)
Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT NIH-MGC Project URL: <http://mhc.ncl.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILMT)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www.shgc.stanford.edu>

Contact: (Dickson, Mark) mcdexpi1.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRK Plate: 20 Row: 1 Column: 12
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA 91: 8574438
This clone has the following problem: frame shifted.

FEATURES

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1. 1294
Location/Qualifiers
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/mol_type="RNA"
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/db_xref="taxon:9606"
/clone="IMAGE:3847565"
/tissue_type="Colon, adenocarcinoma"
/clone_lib="NIH_MGC_65"
/lab_host="DH10B"
/note="Vector: PCMV-SPORT6"
BASE COUNT 317 a 391 c 334 g 252 t
ORIGIN

Query Match 97.7% Score 671.4; DB 11; Length 1294;
Best Local Similarity 99.3%; Pred. No. 5.9e-145;
Matches 666; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

1 ATCATCAAGGGGTTTCAGTGCAGAGCTCTACCTCCAGCCCTGGAGGAGCCCTGTTTCAG 60
278 ATCATCAAGGGGTTTCAGTGCAGAGCTCTACCTCCAGCCCTGGAGGAGCCCTGTTTCAG 337
61 AAGAGCCGGCTACTCTGTGGGGGAGAGCTCATGCCCCAGATGGTCTCTGACAGCAGCC 120
338 AAGAGCCGGCTACTCTGTGGGGGAGAGCTCATGCCCCAGATGGTCTCTGACAGCAGCC 397
121 CACTGCGCTCAAGCC---CCGCTACATAGTTTCAGTGGGGAGAGCAGACACTCCAGAGGA 176
398 CACTGCGCTCAAGCCGGGGGCGCTACTACTGTTACCTGGGGAGAGCAGACTCCAGAGGA 457
177 GAGGGGCTGTGAGCAGACCCGGAGCAGCAGTACTGCTTCCCGCCCGGCTTCAACAA 236
458 GAGGGGCTGTGAGCAGACCCGGAGCAGCAGTACTGCTTCCCGCCCGGCTTCAACAA 517
237 CAGCTCCCCCAAGAGAGCAGCAGCAGTACTGCTGTTGAGATGGCATGCCAGT 296
518 CAGCTCCCCCAAGAGAGCAGCAGCAGTACTGCTGTTGAGATGGCATGCCAGT 577
297 CTTCAATCACTGGGGGCTGTGAGCAGCAGCAGTACTGCTGTTGAGATGGCATGCCAGT 356
578 CTTCAATCACTGGGGGCTGTGAGCAGCAGCAGTACTGCTGTTGAGATGGCATGCCAGT 637
357 CAGCTGCTCATTTTCGGGCTGGGGGAGCAGTCAAGCCCGGATTACGCTGCTTCAAC 416
638 CAGCTGCTCATTTTCGGGCTGGGGGAGCAGTCAAGCCCGGATTACGCTGCTTCAAC 697
417 CTTGGGATCGCCCAACATCATATATTAGACAGAGAGTGTGAGAGCGCTTACCCGG 476
698 CTTGGGATCGCCCAACATCATATATTAGACAGAGAGTGTGAGAGCGCTTACCCGG 757
477 CAACATCAAGAGACACCATGTTGTGAGCAGAGTGTGAGAGAGTGTGAGAGAGTGTGAG 536
758 CAACATCAAGAGACACCATGTTGTGAGCAGAGTGTGAGAGAGTGTGAGAGAGTGTGAG 817
537 GGGTGAAGTCCGGGGGCGCTGTGTGTAAACAGTCTTTCAAGGATTAATCTCTGGGG 596
818 GGGTGAAGTCCGGGGGCGCTGTGTGTAAACAGTCTTTCAAGGATTAATCTCTGGGG 877
597 CCAGGATCGTGTGTGAGTACCCGAAAGCTGTGTCTTACAGAAAGTGTGCAAAATATGT 656
878 CCAGGATCGTGTGTGAGTACCCGAAAGCTGTGTCTTACAGAAAGTGTGCAAAATATGT 937
657 GGAGCTGATCCAGAGAGCATGAGAGCAAT 687

Db 938 GGAGCTGATCCAGAGAGCATGAGAGCAAT 968

RESULT 2
LOCUS B1763040 678 bp mRNA linear EST 25-SEP-2001
DEFINITION 603047836F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5187896 5',
mRNA sequence.
ACCESSION B1763040
VERSION B1763040.1 GI:15754618
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 678)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLML1469 row: h column: 09
High quality sequence stop: 647.
Location/Qualifiers

FEATURES

source
1. 678
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5187896"
/lab_host="DH10B"
/clone_lib="NIH_MGC_116"
/note="Organ: pooled colon, kidney, stomach; Vector:
PCMV-SPORT6; Site: 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs; 62 yo male and 70 yo female. Library is
Oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH-MGC Library."
BASE COUNT 152 a 234 c 172 g 120 t
ORIGIN

Query Match 91.9% Score 631.6; DB 12; Length 678;
Best Local Similarity 99.4%; Pred. No. 7.6e-136;
Matches 634; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

50 CCTGTTGAGAGAGCGGGCTACTCTGTGGGGCAGAGCTCATGCGCCAGATGGCTCC 109
11 CCTGTTGAGAGAGCGGGCTACTCTGTGGGGCAGAGCTCATGCGCCAGATGGCTCC 64
5 TGCAGAGAGCCCAACGCTCAAGCCCGCTCATGTTCACTGCTGGGGCAGCAACCTCC 124
110 TGCAGAGAGCCCAACGCTCAAGCCCGCTCATGTTCACTGCTGGGGCAGCAACCTCC 169
124 TGCAGAGAGCCCAACGCTCAAGCCCGCTCATGTTCACTGCTGGGGCAGCAACCTCC 229
170 AGAAGAGAGGGGCTGTGAGCAGAGCCCGGAGCAGCAGTGTCTTCCCGCCCGGCT 229
125 AGAAGAGAGGGGCTGTGAGCAGAGCCCGGAGCAGCAGTGTCTTCCCGCCCGGCT 184
230 TCACAGAGAGCTCCCAAGAGAGCAGCAGCAGTGTCTTCCCGCCCGGCT 289
185 TCACAGAGAGCTCCCAAGAGAGCAGCAGCAGTGTCTTCCCGCCCGGCT 244

QY 290 CGCCAGTCTCATACCTGGGCTGTGGACCCCTCACCCCTCTCTCACGCTGTCTACTG 349
|||||
Db 245 CGCCAGTCTCATACCTGGGCTGTGGACCCCTCACCCCTCTCTCACGCTGTCTACTG 304
350 CTGGCAGCAGTGTCTCATTTCCGGCTGGGGGACAGCTCCAGGCCAGTTAGGCCGTC 409
|||||
Db 305 CTGGCAGCAGTGTCTCATTTCCGGCTGGGGGACAGCTCCAGGCCAGTTAGGCCGTC 364
410 CTCACACCTTGCATGGGCCCAACATCAACATCATTTGAGCAGCAGAAAGTGTGAGACGCT 469
|||||
Db 365 CTCACACCTTGCATGGGCCCAACATCAACATCATTTGAGCAGCAGAAAGTGTGAGACGCT 424
470 ACCCGGCGACATACAGACACCAATGCTGTGTGCGCAGCTGTCAGAGAGGGGGCAGAGCT 529
425 ACCCGGCGACATACAGACACCAATGCTGTGTGCGCAGCTGTCAGAGAGGGGGCAGAGCT 484
530 CCTGCGAGGAGTACCTGGGGGCGCTGCTGTGTGTAACCAAGTCTTCAAGGCAATTAAT 589
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Db 485 CCTGCGAGGAGTACCTGGGGGCGCTGCTGTGTGTAACCAAGTCTTCAAGGCAATTAAT 544
590 CCTGGGGCCAGGATCCGTGTGCGATCAACCCGAAAGCCTGTGTCTACAGAAAGTCTGCA 649
545 CCTGGGGCCAGGATCCGTGTGCGATCAACCCGAAAGCCTGTGTCTACAGAAAGTCTGCA 604
QY 650 AATATGTGAGTGCATCCAGAGACGATGAAGAACAAT 687
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Db 605 AATATGTGAGTGCATCCAGAGACGATGAAGAACAAT 642

RESULT 3
Bg720793 853 bp mRNA linear EST 08-MAY-2001
LOCUS Bg720793
DEFINITION 602692015F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4824387 5',
mRNA sequence.
ACCESSION Bg720793
VERSION Bg720793.1 GI:139999980
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE NIH-MGC http://mgi.ncl.nih.gov/.

JOURNAL
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki

toshyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM10735 row: n column: 04
High quality sequence stop: 826.
Location/Qualifiers

FEATURES
source
1..853

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4824387"
/lab_host="DH10B"
/clone_id="NIH_MGC_97"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (9tcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTT-3',
size-selected for average insert size 2.2 kb and
normalized to R05 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NHGRI, National

BASE COUNT 180 a 285 c 227 g 161 t
ORIGIN
Institutes of Health). Note: this is a NIH_MGC Library."

Query Match 91.4%; Score 627.6; DB 10; Length 853;
Best Local Similarity 99.1%; Pred. No. 7e-135;
Matches 652; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 1 ATCATCAAGGGGTTGAGTGCAGAGCCCTGACCCAGCCCTGGAGAGAGCCCTGTTGAG 60
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Db 196 ATCATCAAGGGGTTGAGTGCAGAGCCCTGACCTACCTCCAGCCCTGGAGAGAGCCCTGTTGAG 255
61 AAGAGGGGCTACTGCTGTGGGCGAGCGTCATCGCCCAAGATGGCTCTTACAGACAGC 120
256 AAGAGGGGCTACTGCTGTGGGCGAGCGTCATCGCCCAAGATGGCTCTTACAGACAGC 315
QY 121 CACGCGCTCAAGCCCGCTGATATGTTACCTGGGGGCGACAAACCTCCAGAGAGAG 180
|||||
Db 316 CACTGCTCAAGCCCGCTGATATGTTACCTGGGGGCGACAAACCTCCAGAGAGAGAG 375
181 GCGTGTGAGCAGACCCGAGACAGCCAGTGAATCTCCGCCAGCCCGGCTTCAACAAAGC 240
376 GCGTGTGAGCAGACCCGAGACAGCCAGTGAATCTCCGCCAGCCCGGCTTCAACAAAGC 435
QY 241 CTCCCAACAAAGACACACCGCAATGACATGCTGTGTAAGATGGCATCGCCAGTCTCC 300
436 CTCCCAACAAAGACACACCGCAATGACATGCTGTGTAAGATGGCATCGCCAGTCTCC 495
QY 301 ATCACTGGGCTGTGGGCGAGCCCTGACCTCTCTCAGCTGTGTACGTGTGGACACAGC 360
|||||
Db 496 ATCACTGGGCTGTGGGCGAGCCCTGACCTCTCTCAGCTGTGTACGTGTGGACACAGC 555
361 TGCCCTCAATTTCCGGCTGGGGGAGAGACGTCAGCCCGGATTAAGCTGCTCAGACCTTG 420
556 TGCCCTCAATTTCCGGCTGGGGGAGAGACGTCAGCCCGGATTAAGCTGCTCAGACCTTG 615
QY 421 CGATCGCGCAACATCACCATCATTTGAGCAGCAGAGTGTGAAGACGCTTACCCGCGAAC 480
616 CGATCGCGCAACATCACCATCATTTGAGCAGCAGAGTGTGAAGACGCTTACCCGCGAAC 675
Db 481 ATCAAGACACCAATGAGTGTGTGCGACAGCTGTGAGAGAGAGAGAGATCTCTGCAAGGT 540
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QY 676 ATCAAGACACCAATGAGTGTGTGCGACAGCTGTGAGAGAGAGAGAGATCTCTGCAAGGT 734
541 GACTCCGGGGGCGCTGTGTC-TGTAAACAGTCTCTTCAAGCAATATCTCTGGGGCA 599
735 GACTCCGGGGGCGCTGTGTC-TGTAAACAGTCTCTTCAAGCAATATCTCTGGGGCA 794
QY 600 GGATCCGTGTGCGATCACCCGAAAGCCTGTGTGTACAGAGAGTGTGCAAAATATGTG 657
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Db 795 GGATCCGTGTGCGATCACCCGAAAGCCTGTGTGTACAGAGAGTGTGCAAAATATGTG 852

RESULT 4
B1818697 841 bp mRNA linear EST 04-OCT-2001
LOCUS B1818697
DEFINITION 603037514F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:518746 5',
mRNA sequence.

ACCESSION B1818697
VERSION B1818697.1 GI:15930247
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE NIH-MGC http://mgi.ncl.nih.gov/.

JOURNAL
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.

cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: L1AM11445 row: k column: 03
 High quality sequence stop: 784.
 Location/Qualifiers

FEATURES

source

1. 841

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5178746"

/lab_host="DH10B"

/clone_lib="NIH_MGC_115"

/note="Organ: pooled brain, lung, testis; Vector:
 PCMV-SPORE6; Site:1; Notif: site:2; EcoRV (destroyed); RNA
 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 69. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 021. Note: this is a NIH_MGC Library."

BASE COUNT

180 a 288 c 206 g 167 t

ORIGIN

Query Match

Best local Similarity 99.3%; Pred. No. 1.2e-132; Length 841;

Matches 673;

Conservative 0; Mismatches 0; Indels 5; Gaps 5;

QY 15 CGAGTCAAGCCTCACTCCAG-CCCTGGCAGCAGCCCTGTTCGAGAAGACGGGCTAC 73
 DB 1 CGAGTCAAGCCTCACTCCAGTCCAGAGCAGCAGCCCTGTTCGAGAAGACGGGCTAC 60
 QY 74 TCTGTGGGGGAGCGCTCATCGCCCGCAGATGGCTCTGTGACAGAGCCCACTGCTTAAGC 133
 DB 61 TCTGTGGGGGAGCGCTCATCGCCCGCAGATGGCTCTGTGACAGAGCCCACTGCTTAAGC 120
 QY 134 CCCGCTACATAGTTCACCTGCGGAGCAGACACCTCCAGAGAGAGAGGGCTGTGACAGA 193
 DB 121 CCCGCTACATAGTTCACCTGCGGAGCAGACACCTCCAGAGAGAGAGGGCTGTGACAGA 180
 QY 194 CCC-GGACAGCAGTGTCTTCCCAACCCCGGCTTCACACAGCCTCCCAACAAA 252
 DB 181 CCCGCTACAGCAGTGTCTTCCCAACCCCGGCTTCACACAGCCTCCCAACAAA 240
 QY 253 GACACACCGCAATGACATCATGCTGTGAAGATGGCATGCCAGATCTCC-ATCAGCTGGGC 311
 DB 241 GACACACCGCAATGACATCATGCTGTGAAGATGGCATGCCAGATCTCCATCAGCTGGGC 300
 QY 312 TGTGTGACCCCTCACCCTCTCTCTCAAGCTGTGTCACTGTGTGACAGCAGCTGCTCATTTTC 371
 DB 301 TGTGTGACCCCTCACCCTCTCTCTCAAGCTGTGTGTGACAGCAGCTGCTCATTTTC 360
 QY 372 CGGCTGTGGGAGCAGCTCCAGCCCGCAGTTCAGCTGCTCTACACCTTGATGGGCCAA 431
 DB 361 CGGCTGTGGGAGCAGCTCCAGCCCGCAGTTCAGCTGCTCTACACCTTGATGGGCCAA 420
 QY 432 CATTCACCATTTGAGACACAGAGTGTGAGAAAGCTTCACCCCGGCAACATCAACAGAC 491
 DB 421 CATTCACCATTTGAGACACAGAGTGTGAGAAAGCTTCACCCCGGCAACATCAACAGAC 480
 QY 492 CATGTGTGTGCGCAGGTGACAGGA-AGGGGGCAAGAGACTGTGCCAGGTGACTCGGGG 550
 DB 481 CATGTGTGTGCGCAGGTGACAGGAAGGGGGCAAGAGACTGTGCCAGGTGACTCGGGG 540
 QY 551 GGCCTCTGTGTGTAACAGTCTTTCAA-GGCATTATCTCTGGGGCAGGATCCGTGT 609
 DB 541 GGCCTCTGTGTGTAACAGTCTTTCAAATGATGATATCTCTGGGGCAGGATCCGTGT 600
 QY 610 GGGATACACCCGAAGCGCTGTGTCTACAGCAAGTCTGCAATATGTGACTGTGATCCAG 669

DB 601 GCGATACACCCGAAGCGCTGTGTCTACACAGAGTGTGCAAAATATGTGACTGTGATCCAG 660
 QY 670 GAGACGATGAGAAACAAT 687
 DB 661 GAGACGATGAGAAACAAT 678

RESULT 5

BM559782

LOCUS

BM559782

DEFINITION

BM559782 1072 bp mRNA linear EST 20-FEB-2002

5'

ACCESSION

BM559782

VERSION

BM559782.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

REFERENCE

1 (bases 1 to 1072)

AUTHORS

NIH-MGC

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cga@bbs.fda.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.lnl.gov>

Plate: L1AM12765 row: 1 column: 11

High quality sequence stop: 684.

Location/Qualifiers

1. 1072

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5744410"

/tissue_type="medulla"

/lab_host="DH10B"

/clone_lib="NIH_MGC_119"

/note="Organ: brain; Vector: PCMV-SPORE6; Site:1; Notif:
 Site:2; EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.3 kb, insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH_MGC Library."

BASE COUNT

238 a 340 c 307 g 185 t

2 others

ORIGIN

Query Match

Best local Similarity 87.6%; Score 601.6; DB 12; Length 1072;

Matches 637; Conservative 0; Mismatches 21; Indels 4; Gaps 2;

QY 1 ATCATTAAGGGGTTCAGAGTGCAGAGCTCACTCCAGCCCTGGCAGCAGCCCTGTTCCAG 60
 DB 275 ATCATTAAGGGGTTCAGAGTGCAGAGCTCACTCCAGCCCTGGCAGCAGCCCTGTTCCAG 334
 QY 61 AAGACCGGCTACTGTGTGGGGGAGCGTCATCGCCCGCAGATGGCTCTGACAGCAGCC 120
 DB 335 AAGACCGGCTACTGTGTGGGGGAGCGTCATCGCCCGCAGATGGCTCTGACAGCAGCC 394
 QY 121 CACTGCTCAAGCCCGCTACATAGTTCACTGTGGGAGCAGACAACTCCAGAGAGAGAG 180
 DB 395 CACTGCTCAAGCCCGCTACATAGTTCACTGTGGGAGCAGACAACTCCAGAGAGAGAG 454
 QY 181 GCGTGTGACAGACAGCCCGGAGCAGCAGCTGAGTCTTCCCGCCAGCCCGGCTTCAACACAGC 240

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Db      455 GGGTGTGAGCAGACCCGGACAGCCAGTACTGCTTCCCGACCCGGCTTCAACAAACAGC 514
OY      241 CTCCCAACAAAGAACACACCGGACATGATCATGCTGTGAAGATGGCATCGGCACTTCC 300
Db      515 CTCCCAACAAAGAACACACCGGACATGATCATGCTGTGAAGATGGCATCGGCACTTCC 574
OY      301 ATCAGCTGGGCTGTGCGACCCCTCAACCTTCTCTCAGCTGTGTCACCTGTGGACACGAC 360
Db      575 ATCAGCTGGGCTGTGCGACCCCTCAACCTTCTCTCAGCTGTGTCACCTGTGGACACGAC 634
OY      361 TGGCTCATTTCCGGGTGGGGGAGACAGCTCCAGCCCGGACATGAGCTGCTCAGACCTTG 420
Db      635 TGGCTCATTTCCGGGTGGGGGAGACAGCTCCAGCCCGGACATGAGCTGCTCAGACCTTG 694
OY      421 CGATGCGGCAACATCACCATTGATGAGCAGACAGAAAGTGTGAAGAGCCCTACCCCGGAC 480
Db      695 CGATGCGGCAACATCACCATTGATGAGCAGACAGAAAGTGTGAAGAGCCCTACCCCGGAC 754
OY      481 ATCAGAGACACCATGCTGTGTCAGCGCTGACAGAAAGGGGCGAAGGACTCTGCCAGGAT 540
Db      755 ATCAGAGACACCATGCTGTGTCAGCGCTGACAGAAAGGGGCGAAGGACTCTGCCAGGAT 814
OY      541 GACTCCGGGGGCGCTCTGTGTGTGTATACCAAGTCTCTCAAGGCAATATCTCTGGGG-CCA 599
Db      815 GACTCCGGGGGCGCTCTGTGTGTGTATACCAAGTCTCTCAAGGCAATATCTCTGGGGCCA 874
OY      600 GACTCCGGGTGTCGATACACCCGAAAGCCTGTGTGTACAC--GAAAGTGTCAAAATATGT 656
Db      875 GACTCCGGGTGTCGATACACCCGAAAGCCTGTGTGTGTACACCGAAAGTGTGTCAATATGT 934
OY      657 GG 658
Db      935 GG 936

RESULT 6
LOCUS   BM559617 1074 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT 6565456 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5744314
5', mRNA sequence.
ACCESSION BM559617
VERSION   BM559617.1 GI:18803348
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1074)
AUTHORS   NIH-MGC htlp://mgi.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LHAM12765 row: h column: 11
High quality sequence stop: 689.
Location/Qualifiers
1..1074
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5744314"
/tissue_type="medulla"
/lab_host="DH10B"
/clone_id="NIH_MGC_119"
/note="Organ: brain; Vector: pCMV-Sport6; Site_1: NotI;

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Site_2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(univirogen). Research Genetics tracking code 013. Note:
this is a NIH-MGC Library."

BASE COUNT      238 a      339 c      311 g      184 t      2 others
ORIGIN

Query Match      84.9%; Score 583.2; DB 12; Length 1074;
Best Local Similarity 97.8%; Pred. No. 1,4e-124;
Matches 632; Conservative 0; Mismatches 10; Indels 4; Gaps 4;

OY      1 ATCATCAAGGGGTTGAGTGCAGAGCTCACTCCAGCCCTGGACAGGACCCCTGTTTCAG 60
Db      274 ATCATCAAGGGGTTGAGTGCAGAGCTCACTCCAGCCCTGGACAGGACCCCTGTTTCAG 333
OY      61 AAGAGCGGCTACTCTGTGGGCGAGGCTCATCGCCCGAGATGGCTCTGACAGACGCC 120
Db      334 AAGAGCGGCTACTCTGTGGGCGAGGCTCATCGCCCGAGATGGCTCTGACAGACGCC 393
OY      121 CACTGCTCAAGCCCGCTTACATGATGATCACTGGGGGACAGACACCTCCAGAAAGAGAG 180
Db      394 CACTGCTCAAGCCCGCTTACATGATGATCACTGGGGGACAGACACCTCCAGAAAGAGAG 453
OY      181 GGGTGTGAGCAGACCCGGGACAGCCAGCTAGTCTTCCCGACCCCGGCTTCAACAAAGC 240
Db      454 GGGTGTGAGCAGACCCGGGACAGCCAGCTAGTCTTCCCGACCCCGGCTTCAACAAAGC 513
OY      241 CTCCCAACAAAGAACACACCGGACATGATCATGCTGTGAAGATGGCATCGGCACTTCC 300
Db      514 CTCCCAACAAAGAACACACCGGACATGATCATGCTGTGAAGATGGCATCGGCACTTCC 573
OY      301 ATCAGCTGGGCTGTGCGACCCCTCAACCTTCTCTCAGCTGTGTGTCACCTGTGGACAC 360
Db      574 ATCAGCTGGGCTGTGCGACCCCTCAACCTTCTCTCAGCTGTGTGTCACCTGTGGACAC 633
OY      361 TGGCTCATTTCCGGGTGGGGGAGCAGCTCCAGCCCGGATTAAGCTGCTCAGACCTTG 420
Db      634 TGGCTCATTTCCGGGTGGGGGAGCAGCTCCAGCCCGGATTAAGCTGCTCAGACCTTG 693
OY      421 CGATGCGGCAACATCACCATTGATGAGCAGACAGAAAGTGTGAAGAGCCCTACCCGCGAAC 480
Db      694 CGATGCGGCAACATCACCATTGATGAGCAGACAGAAAGTGTGAAGAGCCCTACCCGCGAAC 753
OY      481 ATCAGAGACACCATGCTGTGTCAGCGCTGACAGAAAGGGGCGAAGGACTCTGCCAGGAT 540
Db      754 ATCAGAGACACCATGCTGTGTCAGCGCTGACAGAAAGGGGCGAAGGACTCTGCCAGGAT 813
OY      541 GACTGCC-GGGGGCGCTGTGTCGTAACCACTGCTTCAAGCAATATCTGCT-GGGGC 598
Db      814 GACTGCCGGGGGCGCTGTGTCGTAACCACTGCTTCAAGCAATATCTGCTGCGGGG 873
OY      599 AGGATCCGT-GTGCATCACCAGAA-GCTGTGTGTCTACAGAA 642
Db      874 AGGATCCGTGTGCATCACCAGAAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 919

RESULT 7
LOCUS   BG697071 708 bp mRNA linear EST 07-MAY-2001
DEFINITION 60260281P1 NCI_GCAP_Skn3 Homo sapiens cDNA clone IMAGE:480356 5',
mRNA sequence.
ACCESSION BG697071
VERSION   BG697071.1 GI:13962880
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 708)

```

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM10699 row: a column: 21
High quality sequence stop: 704.
Location/Qualifiers
1. 708
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4803356"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Skn3"
/notes="Organ: skin; Vector: pCMV-SPORT6; Site: 1; Note: Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 147 a 262 c 183 g 116 t
ORIGIN
Query Match 77.1%; Score 529.4; DB 10; Length 708;
Best Local Similarity 99.8%; Pred. NO. 3.4e-112;
Matches 550; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATCATCAAGGGGTTCAGTGCAGACCTCCACCTCGAGCAGCAGCCCTGTTCCAG 60
|||||
178 ATCATCAAGGGGTTCAGTGCAGACCTCCACCTCGAGCAGCAGCCCTGTTCCAG 237
|||||
QY 61 AAGACCGCGCTACTGTGTGGGGGAGCGCTCATCGCCCGCAGATGGCTCTGACAGCAGC 120
|||||
238 AAGACCGCGCTACTGTGTGGGGGAGCGCTCATCGCCCGCAGATGGCTCTGACAGCAGC 297
|||||
QY 121 CACTGCGCTAAGCCCGCTACATAGTTCACTGGGGGAGCAGCAACCTCCAGAGAGAGAG 180
|||||
DB 298 CACTGCGCTAAGCCCGCTACATAGTTCACTGGGGGAGCAGCAACCTCCAGAGAGAGAG 357
|||||
QY 181 GGCTGTGACAGACCCGAGCAGCAGCTGAGTCTTCCCGCCCGCTTCAACAACAGC 240
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DB 358 GGCTGTGACAGACCCGAGCAGCAGCTGAGTCTTCCCGCCCGCTTCAACAACAGC 417
|||||
QY 241 CTCGCCAACAAGACACCGCAATGACATGATGCTGTGAAGATGGCATGCCAGTCTCC 300
|||||
DB 418 CTCGCCAACAAGACACCGCAATGACATGATGCTGTGAAGATGGCATGCCAGTCTCC 477
|||||
QY 301 ATCACTGGGGGTGTGGACCCCGTCACTCTCTCTCAAGCTGTGATCTGTCAGTCCAGCAG 360
|||||
DB 478 ATCACTGGGGGTGTGGACCCCGTCACTCTCTCTCAAGCTGTGATCTGTCAGTCCAGCAG 537
|||||
QY 361 TGGCTCATTTTCGGGTGGGGGAGCAGAGTCCAGGCCCGCTTACGCTGCTCACACTTG 420
|||||
DB 538 TGGCTCATTTTCGGGTGGGGGAGCAGAGTCCAGGCCCGCTTACGCTGCTCACACTTG 597
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QY 421 CGATGGGCCAATCATCATATGAGCAGCAGAGTGTGAGAACCCCTTACCCCGGCAAC 480
|||||
DB 598 CGATGGGCCAATCATCATATGAGCAGCAGAGTGTGAGAACCCCTTACCCCGGCAAC 657
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QY 481 ATCAAGAGACCATGGTGTGTGCGAGCGGAGAGAGAGGGGGAAGAGACGCC 531
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DB 658 ATCAAGAGACCATGGTGTGTGCGAGCGGAGAGAGAGGGGGAAGAGACTAC 708
|||||

RESULT 8
AK009360
LOCUS AK009360 1295 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:231005108 product:protease, serine, 20, full insert sequence.
ACCESSION AK009360
VERSION AK009360.1 GI:12844110
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishie, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Iizawa, M., Ohara, E., Watanabe, Y., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system - 384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamane, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nishikido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Stabelli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Momberti, P., Nordone, P., Ring, B., Ringuwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Welter, C., Whitlaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, J., Kohlsuki, S. and Hayashizaki, Y.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851

TITLE The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I and II Team.
ABSTRACT Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

AUTHORS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hirooka, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,

Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashtanigki, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, K., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE
RIKEN integrated sequence analysis (RISA) system—384-format
sequencing pipeline with 384 multicapillary sequencer

JOURNAL
Genome Res. 10 (11), 1757-1771 (2000)

REFERENCE AUTHORS

TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409 (6821), 685-690 (2001)
MEDLINE	21085660
PUBMED	11217851

AUTHORS

**JOURNAL
REFERENCE
AUTHORS**

TITLE
JOURNAL

COMMENT

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGGAGACGAAGGATCCACAGAGCGCTTTTTTTTTTTTNN 3']. cDNA was prepared by using triazole-based thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was made with the primer adapter of sequence [5' GAGGAGACGATTCGAGACTTAATTAATTAATCCCCCCCCCC 3']. cDNA was cleaved

with *Xho*I and *Sst*I. Cloning sites, 5' end: *Xho*I; 3' end: *Sst*I.
Host: *SOLR*.

Host: SOLR.

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	/db_xref="MGI:1896372"
	/db_xref="Ensembl:ENST00000231004.1"
	/clone="2310040F07"
	/sex="male"
	/tissue_type="tongue"
	/clone_id="RRKEN_full-length enriched mouse cDNA library"
	/dev_stage="adult"
CDS	144..974

CDS

BASE COUNT	311 a	369 c	315 g	300 t
ORIGIN				

Query Match	74.8%;	Score 514.2;	DB 11;	Length 1255;
Best Local Similarity	84.3%;	Pred. No. 1.4e-108;		
Matches 579; Conservative	0;	Mismatches 108;	Indels 0;	Gaps 0;

Qy 1 ATATCAAGGGGTTGAGTGCAGCCCTACTGCCCGCTGGCAGGCGCCCTGTTCG 60
 |||||
Db 285 ATATCAAGGGTTATGAGTGCAGCCCTACTACAGCCATGGCAGGTGGCCCCCTTTCG 344

07 CACTGCGCCAGGCCCGGGTACATGTTCACCTGGGGCAGCACAACTCCGAAGGAGGAG 180
121 |||||
Db 405 CACTGCCGAGCCCCCATTAAGTGATCTCTCCTTTGGAGAACACATCTAGAGAAGACAGAC 464

Oy 181 GCGTGTGAGCAGACCCGGACGCCACTGATGCTTCCCCACCCCGGCTTCACAAACAGC 240
 |||||
Db 465 GGCTGTGAGCAGAGCGCGGATGGCCACTGATGCTTCCCCACCCCGCATTCAACAACAGC 524

QY 241 CTCCCAACAAAGCACCGCAATGACATCATGCTGGGAAGATGGCATTCGCCAGTCTCC 300
Db 535 CTCCCAACAAAGCACCGCAATGACATCATGCTGGGAAGATGGCATTCGCCAGTCTCC 584

Dy 301 ATCAACCTGGGCTGTGCAGACCCTCACCCCTCCTCAGCGTGTGTTCACACTGCTGGACACAGC 360
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Db 585 TTATACCCAGCTGTGCAGCCACTCATCCCTGTCCCCAACACTGTGTGCCGTGCAGGCCACGAC 644
| | | | | | | | | | | | | | | | | |

QY 361 TGGCTCATTTCCGGCTGGGGGACAGCAGCTCCAGCCCCCAGTTACGCCCTGCTACACCCCTTG 420

Db 645 TGGCTCATTTCTGGATGGGGGACACAGCTCCAGCCCCCAGTTGGGCTTGGCTTCAATTCCTTG 704

QY 421 CGATGGCCGCAACATCCACCATCATTTGAGCACCAGAAAGTGTGAGACAGCGCTACCCCGGCAC 480

DB 705 CGATGTGGCAATGTCTCCATCATCGCAACACCAAGAGTGTGAGAGAGCGCTACCCGGGCGAAC 764

481 ATACAGACCACTGTTGTGTGCCAGCGCTGCAGGAAGGGGGCAGAAGACTCTCTCCAGGGT 540
OY
DB 765 ATACAGACCACTGTTGTGTGCCAGCTGTTGGGAAAGAGGGGCAAGGACTCTCTCCAGGGT 824

541 GACTCCGGGGGCTCTGCTCTTAACCAAGTCTTCAAGGCAATTATCTCCTGGGGCCAG 600


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Db      260 ATCATTAAGGGTTATAGTGCAGAGGCTCACTCAACCCATGAGGAGTGCGCCCTTTTCAG
        61 AAGACGCGCTACTTGTGTGGGAGCGCATGCGCCCGAGATGCTCTGACAGCAGCC 120
        320 AAGACACGGCTTCTGTGTGGGAGCGCATGCGCCCGAGATGCTCTGACAGCAGCC 379
QY      121 CACTGCGCTCAAGCCCGCTACATAGTTCACTGGGGAGCACAACCTCCAGAGAGAG 180
        380 CACTGCGCGAGCCCGCTACATAGTTCACTGGGGAGCACAACCTCCAGAGAGAG 439
QY      181 GGTGTGACAGCCCGGAGCGCATGAGTCTTCTCCCGAGCCCGGCTTCAACAGCAGC 240
        440 GGTGTGACAGCGCGGAGCGCATGAGTCTTCTCCCGAGCCCGGCTTCAACAGCAGC 498
QY      241 CTCGCCCAAGAAAGACCGGAGCATGAGTCTGTTGAGATGAGTATGCGCAGCTCC 300
        499 CTCGCCCAAGAAAGACCGGAGCATGAGTCTGTTGAGATGAGTATGCGCAGCTCC 558
QY      301 ATCACTGGGCTGTGGGAGCCCTCAACCTCTCTCAACCTGTCTCACTGTGGCAGC 360
        559 TTTACCCGAGCTGTGGGAGCCCTCAACCTCTCTCAACCTGTCTCACTGTGGCAGC 618
QY      361 TGGCTATTTCCGCGTGGGGAGCAGTCCAGCCCGAGTTAGCGCTGCTCAACCTG 420
        619 TGGCTATTTCCGCGTGGGGAGCAGTCCAGCCCGAGTTAGCGCTGCTCAACCTG 678
QY      421 CGATGCGGCAACATCACTATGAGCAGCAGAGTGTGAGAACGCTTACCCCGGAGC 480
        679 CGATGCGGCAACATCACTATGAGCAGCAGAGTGTGAGAACGCTTACCCCGGAGC 738
QY      481 ATCAACAGACCATGTTGTGTGGGAGCGCATGAGGAGGAGGAGGAGCATCTCCAGG 540
        739 ATCAACAGACCATGTTGTGTGGGAGCGCATGAGGAGGAGGAGGAGCATCTCCAGG 798
QY      541 GACTCGGCGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
        799 GACTCGGCGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 858
QY      601 GATCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
        859 GATCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 918
QY      661 TGGATCCAGAGACGATGAGAAACAT 687
        919 TGGATCCAGAGATGATGAGAAACAT 945
Db

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RESULT 11
BG747134 639 bp mRNA linear EST 15-MAY-2001
DEFINITION 602704354F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:485773 5',
ACCESSION BG747134
VERSION BG747134.1 GI:14057787
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 639)
NIH-MGC <http://mgi.nci.nih.gov/>,
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

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FEATURES
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            /note="Organ: colon; Vector: pORF7, Site_1: XhoI, Site_2:
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            cloned into EcoRI/XhoI sites using the following 5'
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            insert size 1.8kb. Library constructed by Ling Hong in
            the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies)"
BASE COUNT 128 a 241 c 162 g 108 t
ORIGIN
Query Match 68.5%; Score 470.4; DB 10; Length 639;
Best Local Similarity 99.8%; Pred. No. 1.5e-98;
Matches 471; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1 ATCATCAAGGGGTTTCAGATGTCAGAGCTCACTCCAGCCCTGCGAGCGCCCTGTCGAG 60
        168 ATCATCAAGGGGTTTCAGATGTCAGAGCTCACTCCAGCCCTGCGAGCGCCCTGTCGAG 227
QY      61 AAGACGCGCTACTTGTGTGGGAGCGCATGAGTCTTCTCAACCTGTCTCACTGTGGCAGC 120
        228 AAGACGCGCTACTTGTGTGGGAGCGCATGAGTCTTCTCAACCTGTCTCACTGTGGCAGC 287
QY      121 CACTGCGTCAAGCCCGGCTACATAGTTCACTGAGGAGGAGCAGACCACTCCAGAGAGGAG 180
        288 CACTGCGTCAAGCCCGGCTACATAGTTCACTGAGGAGGAGCAGACCACTCCAGAGAGGAG 347
QY      181 GGTGTGAGCAGACCGGAGCAGCAGTGTCTTCCCGAGCCCGGCTTCAACAGCAGC 240
        348 GGTGTGAGCAGACCGGAGCAGCAGTGTCTTCCCGAGCCCGGCTTCAACAGCAGC 407
QY      241 CTCGCCCAAGAAAGACCGGAGCATGAGTCTGTTGAGATGAGTATGCGCAGCTCC 300
        408 CTCGCCCAAGAAAGACCGGAGCATGAGTCTGTTGAGATGAGTATGCGCAGCTCC 467
QY      301 ATCACTGGGCTGTGGGAGCCCTCAACCTCTCTCAACCTGTCTCACTGTGGCAGCAGC 360
        468 ATCACTGGGCTGTGGGAGCCCTCAACCTCTCTCAACCTGTCTCACTGTGGCAGCAGC 527
QY      361 TGGCTATTTCCGCGTGGGGAGCAGCGTCCAGGCCCGAGTTAGCGCTGCTCAACCTTG 420
        528 TGGCTATTTCCGCGTGGGGAGCAGCGTCCAGGCCCGAGTTAGCGCTGCTCAACCTTG 587
QY      421 CGATGCGGCAACATCACTATGAGCAGCAGAAATGTGAGAAAGCCCTTACC 472
        588 CGATGCGGCAACATCACTATGAGCAGCAGAAATGTGAGAAAGCCCTTACC 639
Db

```

RESULT 12
BE867930 973 bp mRNA linear EST 20-OCT-2000
DEFINITION 601443517F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847565 5',
ACCESSION BE867930
VERSION BE867930.1 GI:10316706
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 973)
NIH-MGC <http://mgi.nci.nih.gov/>.

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, Thu Oct 16 09:48:39 2003

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: October 15, 2003, 19:44:50 ; Search time 47.1708 Seconds

(without alignments)
7516.609 Million cell updates/sec

Title: US-09-856-320A-1_COPY_272_958

Perfect score: 1275

Sequence: 1 atcctcaagggttcgagtcg.....agagacagatgaagaacaat 687

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 1661050

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+np_model -DEV=x1p
-O=/cgn2_1/USPTO.spool_P/US0985320/runat_15102003_105639_8524/app_query.fasta_1.2318
-DB=SPTRMBL_23 -QFMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0985320_ECGN_1_159_efunat_15102003_105639_8524 -NCPD=6 -ICPD=3
-NO_MMAP -LARGESQDTRY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

SPTRMBL_23:.*
1: sp_archaea:.*
2: sp_bacteria:.*
3: sp_fungi:.*
4: sp_human:.*
5: sp_invertebrate:.*
6: sp_mammal:.*
7: sp_mhc:.*
8: sp_organelle:.*
9: sp_phase:.*
10: sp_plant:.*
11: sp_podent:.*
12: sp_virus:.*
13: sp_vertebrate:.*
14: sp_unclassified:.*
15: sp_rvirs:.*
16: sp_bacteriap:.*
17: sp_archaeap:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1235.5	96.9	275	4 Q8IXD7	Q8IXD7 homo sapien

2	1062	83.3	249	11	Q9QVNA	Q9QVNA mus musculu
3	1062	83.3	276	11	Q9QVNA	Q9QVNA mus musculu
4	683	53.6	260	4	Q8IWB9	Q8IWB9 homo sapien
5	679	53.3	255	4	Q96RQ0	Q96RQ0 homo sapien
6	678	53.2	254	11	Q8CGR4	Q8CGR4 mus musculu
7	671.5	52.7	276	11	Q8CGR6	Q8CGR6 mus musculu
8	630	49.4	251	11	Q9DBO8	Q9DBO8 mus musculu
9	623.5	48.9	293	11	Q9D140	Q9D140 mus musculu
10	603	47.3	250	11	Q8CGR5	Q8CGR5 mus musculu
11	597.5	46.9	234	11	Q9CV76	Q9CV76 mus musculu
12	590	46.3	246	11	Q921R9	Q921R9 mus musculu
13	588	46.1	245	11	Q9QUR9	Q9QUR9 mus musculu
14	587.5	46.1	235	11	Q63274	Q63274 mus musculu
15	587	46.0	236	11	Q9R0T7	Q9R0T7 mus musculu
16	583.5	45.8	239	11	Q63275	Q63275 mus musculu
17	581.5	45.6	261	11	Q9JW70	Q9JW70 mus musculu
18	574.5	45.1	261	6	Q9N101	Q9N101 mus musculu
19	574.5	45.1	261	6	Q29474	Q29474 canis famli
20	564.5	44.3	269	4	Q8IUT5	Q8IUT5 mus musculu
21	564	44.2	251	11	Q54854	Q54854 homo sapien
22	562.5	44.1	247	11	Q9CPN7	Q9CPN7 mus musculu
23	560.5	44.0	237	13	Q91515	Q91515 fugu rubrip
24	560.5	44.0	244	13	Q80GW3	Q80GW3 mus musculu
25	560	43.9	249	11	Q91VE3	Q91VE3 mus musculu
26	558.5	43.8	245	13	Q42160	Q42160 petromyzon
27	558.5	43.6	261	11	Q8C232	Q8C232 mus musculu
28	556.5	43.6	263	11	Q9JW71	Q9JW71 mus musculu
29	556	43.6	240	13	Q98TH0	Q98TH0 engraulis j
30	556	43.6	246	11	Q88301	Q88301 mus musculu
31	556	43.6	253	11	Q91Y82	Q91Y82 mus musculu
32	555.5	43.6	222	13	Q8AV11	Q8AV11 mus musculu
33	552.5	43.5	263	11	Q9JW69	Q9JW69 mus musculu
34	552.5	43.3	244	6	Q42159	Q42159 petromyzon
35	552.5	43.3	254	6	Q9XSN6	Q9XSN6 sus scrofa
36	551	43.2	247	11	Q9CPN9	Q9CPN9 mus musculu
37	549.5	43.1	247	13	Q42158	Q42158 petromyzon
38	549	43.1	238	13	Q9W706	Q9W706 petromyzon
39	548.5	43.0	247	13	Q42608	Q42608 petromyzon
40	547	42.9	247	11	Q9D7Y7	Q9D7Y7 mus musculu
41	544.5	42.7	242	13	Q92099	Q92099 paratotothe
42	543.5	42.6	261	11	Q88309	Q88309 mus musculu
43	541.5	42.5	242	13	Q9W707	Q9W707 paratichthy
44	541	42.4	247	4	Q8NHM4	Q8NHM4 homo sapien
45	539.5	42.3	242	13	Q93266	Q93266 pseudopleur

ALIGNMENTS

RESULT 1

Q8IXD7 PRELIMINARY; PRT; 275 AA.

AC Q8IXD7;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Variant form hippostasin/KIK11.
GN KIK11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Nakamura T., Mitsui S., Miki T., Yamaguchi N.;
RT "Molecular cloning and expression of a variant form of
RT hippostasin/KIK11 in prostate."
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB078780; BAC54105.1; -
SQ SEQUENCE 275 AA; 30165 MW; 257AA2B28F40E2C4 CRC64;

Alignment Scores: 3.2e-98 Length: 275
Pred. No.: 275

Score: 1235.50 Matches: 229
 Percent Similarity: 90.16% Conservative: 0
 Best Local Similarity: 90.16% Mismatches: 0
 Query Match: 96.90% Indels: 25
 DB: 4 Gaps: 1

US-09-856-320a-1_copy_272_958 (1-687) x Q81XD7 (1-275)

```

OY 1 ATCATCAAGGGGTTTCAGATGCAAGCCTCACTCCAGCCCTGGCAGGAGCCCTGTTTCAG 60
    |||||
Db 22 IleIlelysglyheglucylsyrProHISserGlnProtrpIlnAlaIleuPheGln 41
OY 61 AAGACGGGCTACTCTGTGGGGGAGCGCTCATGCCGCCAGATGGCTCTGACAGAGCC 120
    |||||
Db 42 LysThrArgLeuLeuLeuGlyAlaThrIleuIleAlaProArgTrpLeuLeuThrAlaAla 61
OY 121 CACTGCTCAAGGCC----- 135
    |||||
Db 62 HIScysLeuLysProItrpValSerLeuThrSerProThrHisValSerProAspLeuSer 81
OY 136 -----CGCTACATAGTTCACCTGGGGGACAGACAC 165
    |||||
Db 82 SerSerAsnTyrCysLeuSerHisLeuSerArgTyrIleValHisLeuGlyGlnHisAsn 101
OY 166 CTCACAAAGAGAGAGGGCTGTGAGCAGACCCGAGACAGCAGTACTCTTCCCCACCCC 225
    |||||
Db 102 LeuGlnLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 121
OY 226 GGCTTCAACAAACAGCCCTCCCAACAAGACACACCGAATGACATGCTGCTGAGAGATG 285
    |||||
Db 122 GlyPheAsnAsnSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMet 141
OY 286 GCATCGCCAGCTTCATCAGCTGGGGTGTGAGACCCCTGACCTCTCTCAGCTGTGTC 345
    |||||
Db 142 AlaSerProValSerIleThrItrpAlaValArgProLeuThrLeuSerSerArgCysVal 161
OY 346 ACTGTGGGACAGCTGCTCATTTCCGGTGGGGAGACAGCTGCCAGCCCGGTTAAAGC 405
    |||||
Db 162 ThrAlaGlyThrSerCysLeuIleSerGlyTrpIleSerThrSerSerProGlnLeuArg 181
OY 406 CTGCGCTCACACCTTGGCAGTCCGCAACATCACCATCATGATGAGCAGACAGATGTGAGAC 465
    |||||
Db 182 LeuProHisThrLeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysGlnAsn 201
OY 466 GCTTACCCGGGACATCACAGACACCATGTGTGTGCCAGCTGACGAGAGGGGAGAC 525
    |||||
Db 202 AlaTyrProGlyAsnIleThrAspTrpMetValCysAlaSerValGlnGlnGlyLys 221
OY 526 GACTCGTGCAGGGTGAATCCGGGGGCGCTGCTGTGAACAGTCTCTCAAGGCATTT 585
    |||||
Db 222 AspSerCysGlnIleLysPserGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIle 241
OY 586 ANTCCTGGGGGAGAGATCGTGTGCGATCACACCGAAGCCTGTGTCACAGAAAGTC 645
    |||||
Db 242 IleSerTrpGlyLysProCysAlaIleThrArgLysProGlyValIlyrThrLysVal 261
OY 646 TGCAAATATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 687
    |||||
Db 262 CysLysTyrValAspTrpIleGlnGlnIleThrMetLysAsnAsn 275
  
```

RESULT 2

O9QYN4 PRELIMINARY; PRT; 249 AA.
 AC O9QYN4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE HIPOSTASIN (2310015108RIK protein).
 GN PRSS20 OR 2310015108RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

```

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RA Yamaguchi N., Mitsui S.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RA Mitsui S., Yamaguchi N.;
RT "DNA cloning of a novel brain serine protease, Hippostasin.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino H., Itoh M., Ishii Y.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamaguchi S.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamata N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shinata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,
RA Wuzhuhaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AB016226; BAA88825.1; -
DR EMBL: AK009720; BAB26461.1; -
DR EMBL: AK009360; BAB26241.1; -
DR HSSP: P00763; IDPO.
DR MEROPS: S01.257; -.
DR MGD: MGI:192977; Prss20.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin.1.
DR SMART: SM00020; Tryp_Spc.1.
DR PROSITE: PS00240; TRYPSIN_DOM.1.
DR PROSITE: PS00134; TRYPSIN_HIS.1.
DR PROSITE: PS00135; TRYPSIN_SER.1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 249 AA; 27604 MW; F9FP9CB457D727D5 CRC64;
  
```

Alignment Scores:

Pred. No.: 2,94e-83 Length: 249
 Score: 1062.00 Matches: 186
 Percent Similarity: 91.27% Conservative: 23
 Best Local Similarity: 81.22% Mismatches: 20
 Query Match: 83.29% Indels: 0
 DB: 11 Gaps: 0

US-09-856-320a-1_copy_272_958 (1-687) x Q9QYN4 (1-249)

```

OY 1 ATCATCAAGGGGTTTCAGATGCAAGCCTCACTCCAGCCCTGGCAGGAGCCCTGTTTCAG 60
    |||||
Db 21 IleIlelysglyheglucylsyrProHISserGlnProtrpIlnAlaIleuPheGln 40
OY 61 AAGACGGGCTACTCTGTGGGGGAGCGCTCATGCCGCCAGATGGCTCTGACAGAGCC 120
    |||||
Db 41 LysThrArgLeuLeuGlyAlaThrIleuIleAlaProArgTrpLeuLeuThrAlaAla 60
OY 121 CACTGCTCAAGGCCCGCTACATAGTTCACCTGGGGGACAGACACCACTCCAGAGAGAG 180
    |||||
Db 61 HIScysArgLysProHisTyrValIleLeuLeuGlyGlnHisAsnLeuGlyLysThrAsp 80
OY 181 GGCTGTGAGACAGACCGGAGACAGCAGCAGTCTTCCCCACCCCGGCTTCAACAACAGC 240
  
```


OX NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC040887; AHA0887.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 260 AA; 28090 MW; EF5934EB96295660 CRC64;

Alignment Scores:

Pred. No.:	1 48e-50	Length:	260
Score:	683.00	Matches:	116
Percent Similarity:	70.54%	Conservative:	42
Best Local Similarity:	51.79%	Mismatches:	64
Query Match:	53.57%	Indels:	2
DB:	4	Gaps:	2

US-09-856-320a-1_COPY_272_958 (1-687) x Q81W69 (1-260)

```

OY 1 ATCATCAAGGGGTTGAGTGCAGAGCCTCACTCCAGCCCTGGAGGAGCCCTGTTGAG 60
    ::::: ||| |||||:::|||||:::|||||:::|||||:::|||||:::
Db 33 ValLeuGlYglYHisGlucysGlnProHisSerGlnProTrpGlnAlaLeuPheGln 52
OY 61 AAGACCGGCTACTCTGTGGGGGAGCGCTCATGCCGCCAGATGCTCTGACAGAGCC 120
    :::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 53 GlYGlGlnLeuLeuGlyValLeuValGlyGlyAsnTrpValLeuThrAlaAla 72
OY 121 CACTGCTCAAGCCCGCTACATAGTTCACTGGGGGAGAGCAACCTCCAGAGGAGGAG 180
    ||||| |||||:::|||||:::|||||:::|||||:::|||||:::
Db 73 HisCysLysLysProLysTrpLysThrValArgLeuGlyAspHisSerLeuGlnAsnLysAsp 92
OY 181 GGGTGTGAGCAGACCCGGAGAGCCACTGAGTCTTCCGCCGCCCGGCTTCAACAGAGC 240
    ||||| |||||:::|||||:::|||||:::|||||:::|||||:::
Db 93 GlYProGlnGlnGlnIleProValValGlnSerIleProHisProCysTrpYanSerSer 112
OY 241 CTCGCCCAACAACACCCGCAATGACATATGCTGGTGAAGATGGCATGCCAGTCTCC 300
    ||||| |||||:::|||||:::|||||:::|||||:::|||||:::
Db 113 ---AspValGlnAspHisAsnHisAspLeuMetLeuGlnLeuArgAspGlnAlaSer 131
OY 301 ATCACTGGGCTGTGGACCCCTCACCCCTCTCAAGCTGTGTCACTGTGTGCACACAGC 360
    ::: |||||:::|||||:::|||||:::|||||:::|||||:::
Db 132 LeuGlYSerLysValLysProIleSerLeuAlaAspHisCysThrGlnProGlyGlnLys 151
OY 361 TGGCTCATTTCCGGTGGGGGAGCAGCAGTCCAGCCCGCAGTTACGCTGCTCAACAGC 420
    ::: |||||:::|||||:::|||||:::|||||:::|||||:::
Db 152 CysThrValSerGlyTrpGlyThrValThrSerProArgLysAsnPheProAspThrLeu 171
OY 421 CGATGGCCCAACATCATCATATGAGCAGACAGAAAGTGTGAGAGCGCTTACCCCGCAC 480
    ||||| |||||:::|||||:::|||||:::|||||:::|||||:::
Db 172 AsnCysAlaGlnValLysIlePheProGlnLysLysCysGlnAspAlaTrpProGlyGln 191
OY 481 ATCAACAGACACATGTGTGTGTGCAGCGTGCAGAGAGGGGAGGAGAACTCTCCAGAGT 540
    ||||| |||||:::|||||:::|||||:::|||||:::|||||:::
Db 192 IleThrAspValMetValCysAlaGlySerSerLysGlyAla---AspThrCysGlnGly 210
OY 541 GACTCGGGGGCCCTGTGTGTGTGTACAGAGTCTTCAAGGAGATTAATCTGGGGCAG 600
    ||||| |||||:::|||||:::|||||:::|||||:::|||||:::
Db 211 AspSerGlyGlyProLeuValCysAspGlyAlaLeuGlnGlyIleThrSerTrpGlySer 230
OY 601 GATCCCTGTGCAGTCAACCCGAAAGCTGTGTGTACAGCAAGATCTGCAAAATGTGGAGC 660
    ||||| |||||:::|||||:::|||||:::|||||:::|||||:::
Db 231 AspProGlyGlyArgSerAspLysProGlyValTyrThrAsnIleCysArgTyrLeuAsp 250
OY 661 TGGATCCAGAG 672
    |||||:::|||||:::|||||:::|||||:::|||||:::
Db 251 TrpIleLysLys 254
  
```

RESULT 5
 O96R00 PRELIMINARY; PRT; 255 AA.
 AC O96R00;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)

DT 01-DEC-2001 (TReMBLrel. 19, last sequence update)
 DE 01-MAR-2003 (TReMBLrel. 23, last annotation update)
 DR Protiogen.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21226193; PubMed=11327827;
 RA Takayama T.K., Carter C.A., Deng T.;
 RT "Activation of prostate-specific antigen precursor (pro-PS4) by
 RT Prostin, a novel human prostatic serine protease identified by
 RT degenerate PCR."
 RL Biochemistry 40:1679-1687(2001).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 DR EMBL: AF303046; AAK62813.1; -.
 DR HSSP: P00761; 1ANI.
 DR MEROPS: S01.081; -.
 DR Interpro: IPR001314; Chymotrypsin.
 DR Interpro: IPR001254; Ser_protease_Try.
 DR Pfam: PF00089; trypsin_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; Tryp_SPC; 1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 KW Hydrolase; Protease; serine protease.
 SQ SEQUENCE 255 AA; 27986 MW; 00D5B79E149468F CRC64;

Alignment Scores:

Pred. No.:	3.27e-50	Length:	255
Score:	679.00	Matches:	124
Percent Similarity:	66.53%	Conservative:	35
Best Local Similarity:	51.88%	Mismatches:	66
Query Match:	53.25%	Indels:	14
DB:	4	Gaps:	3

US-09-856-320a-1_COPY_272_958 (1-687) x Q96R00 (1-255)

```

OY 1 ATCATCAAGGGGTTGAGTGCAGAGCCTCACTCCAGCCCTGGAGGAGCCCTGTTGAG 60
    ::::: ||| |||||:::|||||:::|||||:::|||||:::|||||:::
Db 21 LeuLeuGlnLysLysProLysValLysProHisSerGlnProTrpGlnAlaLeuTrpGln 40
OY 61 AAGACCGGCTACTCTGTGGGGGAGCGCTCATGCCGCCAGATGCTCTGACAGAGCC 120
    ::: |||||:::|||||:::|||||:::|||||:::|||||:::
Db 41 ArgGlyArgPheAsnGlyAlaSerLeuIleSerProHisTrpValLeuSerAlaAla 60
OY 121 CACTGCTCAAGCCCGCTACATAGTTCACTGGGGGAGCAGACCACTCCAGAAAGAGAG 180
    ||||| |||||:::|||||:::|||||:::|||||:::|||||:::
Db 61 HisCysGlnSerArgPheMetArgValArgLeuGlyGlnHisAsnLeuArgLysArgAsp 80
OY 181 GGGTGTGAGCAGACCCGGAGAGCCAGTCAAGTCTTCCGCCGCCCGGCTTCAACAGAGC 240
    ||||| |||||:::|||||:::|||||:::|||||:::|||||:::
Db 81 GlYProGlnGlnGlnIleProValValGlnSerIleProHisProArgTrpGlyGln 98
OY 241 CTCGCCCAACAACACCCGCAATGACATATGCTGGTGAAGATGGCATGCCAGTCTCC 300
    ::: |||||:::|||||:::|||||:::|||||:::|||||:::
Db 99 -----AlaArgSerHisArgAsnAspIleMetLeuLeuValGlnProAlaArg 116
OY 301 ATCACTGGGCTGTGGACCCCTCACCCCTCTCAAGCTGTGTCACTGTGTGCACAGC 360
    ||||| |||||:::|||||:::|||||:::|||||:::|||||:::
Db 117 LeuAsnProGlnValArgProAlaValLeuProThrArgCysProHisProGlyGlnAla 136
OY 361 TGGCTCATTTCCGGTGGGGGAGCAGAGTCC-----AGCCGC 396
    |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 137 CysValValSerGlyTrpLysLeuValSerHisAsnGlnProGlyThrAlaLysSerPro 156
OY 397 -----CAGTTAGCCTGCTCAACCTTGCAGTGGCCCAATCAGTCAATGAGCAGC 450
    ||||| |||||:::|||||:::|||||:::|||||:::|||||:::
Db 157 ArgSerGlnValSerLeuProAspThrLeuHisCysAlaAsnIleGlyIleIleSerArg 176
OY 451 CAGAACTGTGAGAGAGCCCTTACCCGGGCAACATCAGACAGACCATGCTGTGTCCAGCGTG 510
    |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
  
```


Db 177 ThSerCysAspLysSerTyrProGlyArgLeuThrAsnThrMetValCysAlaGlyAla 196
 QY 511 CAGGAAGGGGCGAAGACTCTGCCAGGAGTACTCCGGGGCCCTGTGGTGTAAACGAG 570
 Db 197 GluGlyArgGlyAlaGlyLysSerCysGlyLysAspSerGlyGlyProLeuValCysGly 216
 QY 571 TCTCTCAAGGCAATATCTCTGCGGGCCAGGATCCGTGGGATCCAGCCGAAGGCTGT 630
 Db 217 TleuGingLylIleValSerTrpLysAlaProCysAspAsnThrThrLysProGly 236
 QY 631 GTCTACGAAAGTCTGCAATATGTGAGTGTGATCCAGAGACGATGAGAACAT 687
 Db 237 ValTyrThrLysValCysHisTyrLeuGluTrpIleArgGluThrMetLysArgAsn 255

RESULT 6

O8CGR4 PRELIMINARY: PRT: 254 AA.
 AC O8CGR4;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Prostlin.
 GN KLR15.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22325484; PubMed=12437987;
 RA Olsson A.Y., Lundwall A.;
 RT "Organization and evolution of the glandular kallikrein locus in Mus
 musculus.";
 RL Biochem. Biophys. Res. Commun. 299:305-311(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adams M., Mural R.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY152434; AAN78422.1;
 SQ SEQUENCE 254 AA; 28042 MM; AA9E38BEBDD01861 CRC64;

Alignment Scores:

Pred. No.: 3,98e-50 Length: 254
 Score: 678.00 Matches: 124
 Percent Similarity: 66.67% Conservative: 34
 Best Local Similarity: 52.32% Mismatches: 65
 Query Match: 53.18% Indels: 14
 DB: 11 Gaps: 3

US-09-856-320a-1_COPY_272_958 (1-687) x O8CGR4 (1-254)

QY 1 ATCATCAAGGGGTTGAGTGCAGACCTCACTCCAGCCCTGGCAGAGCCCTGTTCGAG 60
 Db 20 ValLeuGluGlyLysValArgProHisSerGlnProTrpGlnValAlaLeuPheGlu 39
 QY 61 AAGACGGGCTACTCTGTGGGCGAGCTCATGCCGCCAGATGGCTGTGACAGACC 120
 Db 40 ArgGlyArgPheAsnGlyAlaPheLeuIleSerProArgTrpValLeuThrAlaAla 59
 QY 121 CAGTCCCTCAAGCCCGCTCATAGTTCACCTGGGAGCAGACACCTCCGAAGAGAGAG 180
 Db 60 HisCysGlnThrArgPheMetArgValArgLeuGlyLysHisAsnLeuArgLysPheAsp 79
 QY 181 GGCTGTGAGCAGACCGGACGACCTAGTCTCCGCCAGCCCGGCTTCACAAACAGC 240
 Db 80 GlyTrpGluGlnLeuArgSerValSerArgLelIleTrpHisProGlyTyrGlu----- 97
 QY 241 CTCGCCCAAGACGACCGGACATGACATCTGTGGTGAAGATGGATGGCCAGTGTCC 300
 Db 98 -----AlaArgTyrThrHisArgHisAspLleMetLeuLeuArgLeuPheLysProAlaArg 115
 QY 301 ATCACTGGGGTGGCAGCCCTGCTCTGACGCTGTGTGACCTGGTGGCAGAGC 360
 Db 301 ATCACTGGGGTGGCAGCCCTGCTCTGACGCTGTGTGACCTGGTGGCAGAGC 360

Db 116 LeuThrAlaTyrValArgProValAlaLeuProArgArgCysProLeuIleGlyLysAsp 135
 QY 361 TGCCTCATTTCCGGCTGGGAGC-----AGCAGCTCCAGCCCC----- 396
 Db 136 CysValValSerGlyTrpGlyLeuLeuSerAspAsnAsnProGlyAlaThrGlySerGln 155
 QY 397 -----CAGTTACGGCTCTCACACCTTGGCGAGCCGCCAACATCAGCATTTGAGCAGC 450
 Db 156 LysSerHisValArgLeuProAspThrLeuHisCysAlaAsnIleSerIleIleSerGlu 175
 QY 451 CAGAAGTGTGAGAACGCTACCCCGGCAACATCAGACAGACACCATGGTGTGGCCAGCTG 510
 Db 176 AlaSerCysAsnLysAspTyrProGlyArgValLeuProThrMetValCysAlaGlyAla 195
 QY 511 CAGGAAGGGGCGAAGACTCTGCCAGGAGTACTCCGGGGCCCTGTGGTGTAAACGAG 570
 Db 196 GluGlyGlyGlyThrAspSerCysGluLysAspSerGlyGlyProLeuValCysGly 215
 QY 571 TCTCTCAAGGCAATATCTCTGCGGGCCAGGATCCGTGGGATCCAGCCGAAGGCTGT 630
 Db 216 TleuGingLylIleValSerTrpLysAlaProCysAspAsnThrThrLysProGly 235
 QY 631 GTCTACGAAAGTCTGCAATATGTGAGTGTGATCCAGAGACGATGAGAACAT 681
 Db 236 ValTyrThrLysValCysHisTyrLeuGluTrpIleArgGluThrMetLysArgAsn 252

RESULT 7

O8CGR6 PRELIMINARY: PRT: 276 AA.
 AC O8CGR6;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Glandular kallikrein KLR13.
 GN KLR13.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22325484; PubMed=12437987;
 RA Olsson A.Y., Lundwall A.;
 RT "Organization and evolution of the glandular kallikrein locus in Mus
 musculus.";
 RL Biochem. Biophys. Res. Commun. 299:305-311(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adams M., Mural R.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY152432; AAN78420.1;
 SQ SEQUENCE 276 AA; 30360 MM; 33E189C67492FDC4 CRC64;

Alignment Scores:

Pred. No.: 1.46e-49 Length: 276
 Score: 671.50 Matches: 119
 Percent Similarity: 69.03% Conservative: 37
 Best Local Similarity: 52.65% Mismatches: 69
 Query Match: 52.67% Indels: 1
 DB: 11 Gaps: 1

US-09-856-320a-1_COPY_272_958 (1-687) x O8CGR6 (1-276)

QY 10 GGCTGTGAGCAGACCGGACGCTCACTCCAGCCCGGAGGAGCCCTGTTCGAGAGACGGG 69
 Db 40 GlyTyrThrCysLeuProHisSerGlnProTrpGlnValAlaLeuLeuIleArgGlyArg 59
 QY 70 CTACTCTGTGGGCGAGCTCATGCGCCGCCAGATGGCTGTGACAGAGCCCACTGGCTC 129
 Db 60 LeuLeuGlyGlyGlyValLeuValHisProLysTrpValLeuThrAlaAlaHisCysArg 79
 QY 130 AAGCCCGGCTAATAGTTCACCTGGGCGCAGACAACTCCAGAAAGAGAGGGCTGTGAG 189
 Db 130 AAGCCCGGCTAATAGTTCACCTGGGCGCAGACAACTCCAGAAAGAGAGGGCTGTGAG 189

Db 80 LysAspClyTyrThrValHisLeuGlyLysHisAlaLeuLysArgValGluAsnGlyGlu 99
 QY 190 CAGACCCGGACAGCCATGAGTCCTTCCACCACCGGCTTCAACAACAGCTCCAC 249
 Db 100 GlnAlaMetGluValValArgSerIleProHisProGluValThrProThrHis 119
 QY 250 AAGACCCAGCCGATCATGATGCTGGTGAAGATGATGATGATGATGATGATGATG 309
 Db 120 LeuAsnHisAspHisAspIleMetLeuGluLeuLysSerProValGlnLeuSerSer 139
 QY 310 GGTGTGGACCCCTCTCTCTCA---CGCTGACCTGCTGCTGCTGCTGCTGCTGCTG 366
 Db 140 HisValArgThrLeuLysLeuSerHisAlaAspCysLeuProThrGlyThrCysArg 159
 QY 367 ATTCGGCTGGGGAGACAGCAGCTCCAGCCAGCTTACGCTGCTGCTGCTGCTGCTG 426
 Db 160 ValSerGlyTyrPglYThrThrThrSerProGlnValAsnTyrProLysThrLeuGlnCys 179
 QY 427 GCCAATCATCATCATGATGACACAGAGAGTGTGAGAACCCCTACCCCGCAACATCACA 486
 Db 180 AlaAsnIleGluLeuArgSerAspGluGluCysArgGlnValTyrProGlyLysIleThr 199
 QY 487 GACACCATGCTGTGTGCGACAGCTGACAGAGGGGGAGAGTCTGCTGCTGCTGCTGCTG 546
 Db 200 AlaAsnMetLeuLysAlaGlyThrLysGluGlyLysAspSerCysGluGlyAspSer 219
 QY 547 GGGGGCCCTCTGCTGTGTAACAGCTCTTCAAGCATTAATGCTGGGGCCAGATCG 606
 Db 220 GlyGlyProLeuLeuLysAsnGlyLysLeuTyrGlyIleLeuSerTyrGlyAspPhe 239
 QY 607 TGTGGCATGACCCGAAAGCTGTGTCTACAGAAAGTGTGCAATATGTGGATGATGATC 666
 Db 240 CysGlyGlnProAsnArgProGlyValTyrThrArgValSerLysTyrLeuArgTyrPle 259
 QY 667 CAGAGACGATGAAGAAC 684
 Db 260 ArgGluIleIleArgAsn 265
 RESULT 8
 Q9DBQ8 PRELIMINARY; PRT; 251 AA.
 AC Q9DBQ8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE 1200016C12RIK protein.
 GN 1200016C12RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamahata I.,
 Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
 Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 Sasakii H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitlaker C., Wilmink L.,
 Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 Hayashizaki Y.,

RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 DR EMBL: AK004807; BAB23579.1; -.
 DR HSSP: P00763; IDPO.
 DR MEROPS: S01.307; -.
 DR MGD: MGI:1921082; 1200016C12RIK.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser_protease_try.
 DR Pfam: PF00089; trypsin_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRYP_SPCL.
 DR PROSITE: PS00240; TRYP_SIN_DOM; 1.
 DR PROSITE: PS00134; TRYP_SIN_HIS; 1.
 KM Hydrolyase; Protease; Serine protease.
 SQ SEQUENCE 251 AA; 28153 MW; F4D667F8C80CA23 CRC64;
 Alignment Scores:
 Pred. No.: 5.51e-46 Length: 251
 Score: 630.00 Matches: 118
 Percent Similarity: 68.75% Conservative: 36
 Best Local Similarity: 52.68% Mismatches: 70
 Query Match: 49.41% Indels: 0
 DB: 11 Gaps: 0
 US-09-856-320a-1_copy_272_958 (1-687) x Q9DBQ8 (1-251)
 QY 16 GAGTGCAGAGCCCTACTCCAGCCCTGAGAGAGCCCTGTGAGAGAGCCGCTACTG 75
 Db 28 GlucyValAlaArgAsnSer***ProTyrGlnAlaGlyLeuSerThrLeuThrArgGlnLeu 47
 QY 76 TGTGGGGAGCCGCTCATCCGCCAGATGGCTCTGACAGACCCAGCTGCTGAGCC 135
 Db 48 CysGlyValAlaThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 67
 QY 136 CGCTACATGATGTCACCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 195
 Db 68 TyrLeuThrValAlaArgLeuGlyGluHisLeuThrThrThrThrThrThrThrThrThrThr 87
 QY 196 CGAGACAGCCAGTGTGAGTCTCTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 255
 Db 88 LeuLeuValAlaThrAspThrPheProHisProGlyPheAsnProAsnLeuSerAlaAsnArg 107
 QY 256 CACCCAGAGATGACATGCTGTGTAAGATGAGCATGCCAGCTGCTGATGACCTGGCTG 315
 Db 108 HisAsnAspAspIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 127
 QY 316 CGAGCCCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 375
 Db 128 GlnProLeuAsnLeuThrGlnSerArgProProValGlyThrGlnCysLeuIlePheGly 147
 QY 376 TGGGGAGAGCATGTCAGAGCCAGCCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 435
 Db 148 TyrGlySerValSerSerSerLysLeuGlnTyrPromethrLeuGlnCysAlaAsnIle 167
 QY 436 ACCATATGTAGAGCAGCAGAGAGTGTGAGAGAGCTTACCCGAGCAGATCAGCAGCAG 495
 Db 168 SerIleLeuAspAsnLysPheCysArgTyrPalaTyrProGlyHisIlePheLysLysIle 187
 QY 496 GTGTGTGCGAGCTGTGAG 555
 Db 188 LeuCysAlaGlyLeuThrPglGlyLysArgGlySerCysGlnLysPheGlyGlyPro 207
 QY 556 CTGTGTGTGTAACGATCTTCAAGGAGTATCTCTGAGGAGAGAGAGAGAGAGAGAGAGAG 615
 Db 208 LeuValCysGluGlyLeuThrLeuAlaGlyIleValPheGlyGlyPheGlyLeuProCysSerArg 227
 QY 616 ACCCGAAGAGCTGTGTGTGACAGAGAGAGTGTGCAAAATATGTGAGTGTGAGTGTGAG 675
 Db 228 ProArgArgProAlaValTyrThrAsnValPheAspTyrLeuGlnTyrPleGlnSerPro 247
 QY 676 ATGAAGAACAT 687
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DB      248 MetgulyasAn 251

RESULT 9
Q9D140  PRELIMINARY;  PRT;  293 AA.
ID      09D140:
AC      09D140:
DT      01-JUN-2001 (TREMBlrel. 17, Created)
DT      01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT      01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE      11100300191K protein.
GN      11100300191K.
OS      Mus musculus (Mouse)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
[1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Embryo;
RX      MEDLINE=21085660; PubMed=11217851;
RA      Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA      Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA      Akawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
RA      Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA      Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA      Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA      Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA      Schiraldi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA      Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA      Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA      Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA      Gustingich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA      Lyons F., Marchionni L., Mashima J., Mazzarelli U., Mombaerts P.,
RA      Noadone P., Ring B., Rohnwald M., Rodriguez I., Sakamoto N.,
RA      Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA      Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA      Mysnhar-Boris A., Yoshida K., Haegawa Y., Kawaji H., Kohlsuki S.,
RA      Hayashizaki Y.;
RT      "Functional annotation of a full-length mouse cDNA collection.";
RL      Nature 409:685-690(2001).
CC      -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR      EMBL; AK003996; BAB3113.1; -.
DR      HSSP; P00763; IDPO.
DR      MEROPS; S01.017; -.
DR      MEROPS; S01.418; -.
DR      MGD; MGI:1915918; 11100300191K.
DR      InterPro; IPR001314; Chymotrypsin.
DR      InterPro; IPR001254; Ser_protease_Try.
DR      Pfam; PF00089; trypsin; 1.
DR      PRINTS; PR00722; CHYMOTRYPSIN.
DR      SMART; SM00020; TRYP_SPE; 1.
DR      PROSITE; PS50240; TRYPSIN_DOM; 1.
DR      PROSITE; PS00134; TRYPSIN_HIS; 1.
DR      PROSITE; PS00135; TRYPSIN_SER; 1.
KW      Hydrolase; Protease; Serine protease
SQ      SEQUENCE 293 AA; 31908 MW; ED1F45D8226FE911 CRC64;

Alignment Scores:
Pred. No.: 2.04e-45 Length: 293
Score: 623.50 Matches: 109
Percent Similarity: 67.53% Conservative: 47
Best Local Similarity: 47.19% Mismatches: 68
Query Match: 48.90% Indels: 7
DB: 11 Gaps: 4

US-09-856-320A-1_COPY_272_958 (1-687) x Q9D140 (1-293)
QY      1 ATATCAAGGGGTGAGTGCAGCTCAGCTCCAGCCCTGGCAGCAGCC---CTGTC 57
DB      68 IlevaIsnglySerAspCysGlnLysAspAlaGlnPrrpGlnGlyAlaLeuLeu 87
QY      58 GAGAAGACGGCTACTGCTGAGGGGCGAGCTCAGCGCCCGCAGATGGCTGCTGACGA 117
DB      88 GlyProAsnLysLeuTYrCysGlyAlaValLeuIleSerProGlnTrpLeuThrAla 107

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QY      118 GCCACGCTTCACAGCCCGCTACATAGTTACCTGGGGGACAGACCTCCAGAG--- 174
DB      108 AlaHisCysArgLysProValIlePheArgIleArgLeuGlnHisIleSerMetSerProVal 127
QY      175 GAGGAGGGCTGTGAGACACACCCGGACAGCCAGCTAGTCTTCCCGCCAGCCGGCTTCAAC 234
DB      128 TyrGlnSerGlyGlnGlnMetPheGlnGlyIleLeuSerIleProHisProGlyTyrIser 147
QY      235 AACAGCTCCCAACAAAGACCCAGTATGACATGACATGCTGAGAGATGGCAGTGGCAG 294
DB      148 -----HisProGlyHisSerAsnSpleMetLeuIleLysMetAsnArgLys 163
QY      295 GTCTCCATCAGCTGGGCTGTGGAGCCCTCAGCCCTCTCTCAGCTGTGTACCTGGC 354
DB      164 IleArgAspSerHisSerValLysProValIleuIleAlaCysAspCysAlaThrIleuGly 183
QY      355 ACCAGCTCCCTCATTTCTCCGGCTGGGGGACAGCAGCTCAGCCCGCACTTACGCCCTCAG 414
DB      184 ThrArgCysMetValSerGlyTyrPoleYThrThrSerSerHisAsnAsnPheProLys 203
QY      415 ACCTTGGCATGGCCACATCATCAGCATATGAGCAGCAGAGTGGAGAGAGCCATGCC 474
DB      204 ValLeuGlnCysLeuAsnIleThrValLeuSerGluArgCysLysAsnSerTyrPro 223
QY      475 GGCACATCATCAGACACCATGATGATGTGTCACAGCCGTGACGAGAGGGGAGAGACTCTGC 534
DB      224 GlyIleuIleAspLysThrMetPheCysAlaGlyAspGluGlu---GlyArgAspSerCys 242
QY      535 CAGGCTGCTCGGGGGGCGCTGTGCTGTGAACAGTCTTTCAGAGCATATCTCTGG 594
DB      243 GlnGlyAspSerGlyGlyProValValCysAsnGlyLysLeuGlnGlyLeuValSerTyr 262
QY      595 GGCCAGATCGGTGGCATCATCAGCCGAAGAGCTGTGCTACAGCAAGATGTCGCAATAT 654
DB      263 GlyAspPheProCysAlaGlnArgAsnArgProGlyValIlyThrAsnLeuGlySerIle 282
QY      655 GTGAGCTGATTCAGAGAGCAGATGAAACAAT 687
DB      283 ValLysTrpIleLysAspThrMetAsnSerAsn 293

RESULT 10
Q8CGR5  PRELIMINARY;  PRT;  250 AA.
ID      Q8CGR5;
AC      Q8CGR5;
DT      01-MAR-2003 (TREMBlrel. 23, Created)
DT      01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT      01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE      Glandular kallikrein KLK14.
GN      KLK14.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
[1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22325484; PubMed=12437987;
RA      Olsson A.Y., Lundwall A.;
RT      "Organization and evolution of the glandular kallikrein locus in Mus
RT      musculus.";
RL      Biochem. Biophys. Res. Commun. 299:305-311(2002).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Adams M., Mural R.;
RL      Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.
DR      EMBL; AY152433; AAN78421.1; -.
SQ      SEQUENCE 250 AA; 27016 MW; F62FEBF2290FEBE8 CRC64;

Alignment Scores:
Pred. No.: 1.18e-43 Length: 250
Score: 603.00 Matches: 109
Percent Similarity: 63.64% Conservative: 38
Best Local Similarity: 47.19% Mismatches: 78

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Query Match:	47.29%	InDels:	6
DB:	11	Gaps:	2

US-09-856-1_320A-1_COPY_272_958 (1-687) x Q8CGR5 (1-250)

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OY      1 ATCATCAAGGGCTGTCAGTCCAAAGCCCTCCACGCCCTGCAGCGACGCCCTGTTCGAC   60
        ||||| ||::: || | :::::::::::::::::::: |||||
Db      24 lletlleglyglttytargcysvalatrganserclnprotreplvalalaleuglnala   43
OY      61 AAGACG-----CGGCTACTCTGTGGGGGACGCTCATGGCCCCAGANTGGCTTGACA   114
        ||| ||||| ||| ||||| ||| ||||| :|||||:|||||:|||||:|||||:
Db      44 glyProglYnlshArghPheucycslglyValleuIenuseraspIntrValIlethr   63
OY      115 GGAGGCCACTGGCTCAAGCCCGGCTCATAGTTTCACCCTGGGCGAGACAACCTCCAGAAG   174
        ||||||| ||| ::||| ||| ||||| :|||||:|||||:|||||:|||||:
Db      64 AlaAlaNIAsyAlatrPrOIleuNIshValAlaleuGlYshIsanIlleVarg   83
OY      175 GAGGAGGCGCTGAGACAGACCCGGACAGCCAGCACATGATCTCTCCCAACCCGGCTTCAC   234
        ||| ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      84 tPgLuAlaIthrGlnGlnValAlaArgValAlaArgGlnValProItshProgInItyrGln   103
OY      235 AACAGCCTCCCAACAAGAACACCCGCAATGACATCATGCTGGTGAAGATGGCATGCCA   294
        ||| ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      104 -----ProglNlaIshAspaNIasAspleuIeuleuIySlauGlnIyLys   119
OY      295 GTCTCCATCATCCTGGGCTGTGGGACCCCTCACCCCTCTCTCCACGCTGTGCATCTGGC   354
        ||| ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      120 ValArgLeuGIYAlgaIValIyShIrIleSerValAlaIaserSerCySalaserProglY   139
OY      355 ACCACTGCTCATTTTTCCGGCTGGGGGACAGCTCCAGGCCCAAGTTACGCTGCCAC   414
        ||| ||| ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      140 ThrProCYshArghValserOlYtrpOlytrIlealaserProIIleaIarqYtrProThr   159
OY      415 ACCTTGCAGTAGGCCAACATCACATCATGTGAGCACAGAAAGTGTGAAGAGCCTACCCC   474
        ||||| ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      160 AlaleuGlnCyValAlaNIleuNIetmetSerGIuAlaAcylshArghAlaIaytrPro   179
OY      475 GGCAACATCACAGACACCATGTGTGTGTGCCAGCGTGCAGGAAGGGGCAAGAGCTCTGC   534
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      180 gLyIleIleIthrSerelYmeValCySAlaGIYValProgluIyglYlysAspSerCyS   199
OY      535 CAGGTGTACTCCGGGGGCCCTGTGGTGTGAACAGTCTTTCANAGCATTTATCTCTGG   594
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      200 GlnGIYAspSerCIyglYproIeuValCySGIyglYlnIeueInIyIeuValIserITrp   219
OY      595 GCCCAGGATCCGTGTGCATCACCCGAAAGCCTGTGTGTACACGAAAGTCTGCATAATAT   654
        ||| ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      220 GlymetGIuArgCySaIameetProglYtrProglYValItyrAlaNIeueIySaantYr   239
OY      655 GTGGACCTGCATCCAGAGACAGCATGAAGAACAAT 687
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      240 HisserTrpIleGIuArgThrmelGlnserAsn 250
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
ID O9CV76 . PRELIMINARY; PRT; 234 AA.
AC O9CV76;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE 231000B01Rik protein (Fragment).
GN 231000B01RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Atzawa K., Izawa M., Nishi K., Kiyosawa H., Konno S., Yamataka I.,

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[illegible]

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Db      146 GlnGlyLeuAsnLeuSerThrValSerAsnGluThrCysArgAlaValAlaPheProGlyArg 165
      481 ATCAGACAGACACCATGCTGTGTCAGAGCTGCAGAGAGGAGGAGAGGAGCTGTCAGAGGT 540
      166 ValThrGluAsnMetLeuCysAlaGly---GlyGluAlaGlyLysAspAlaCysGlnGly 184
      541 GACTCCGGGGGCGCTGTGCTGTGAACAGTCCTTCAAGGCATTATCTCTGGGGCCAG 600
      185 AsperGlyGlyLysProLeuValCysGlyLysValLeuGlnGlyLeuValSerTyrPheSer 204
      601 ---GATCCGTGTGGATACCCGAAAGCTGTGCTTCAAGAGTGTGCAAAATATGTG 657
      205 ValGlyProCysGlyGlnGlyLysGlyLysProGlyValTyrThrLysValCysLysTyrThr 224
      658 GACTGATCCAGAGACGATGATGAGAACAT 687
      225 AsprPheArgIleValIleArgAsn 234

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RESULT 12

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092LR9  PRELIMINARY;      PRT;      246 AA.
AC      092LR9;
DT      01-MAY-1999 (TREMBLrel. 10, Created)
DT      01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Trypsinogen 16.
GN      TRYGN16 OR TRYPSINOGEN.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCB1_taxid=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Balb/c;
RA      Rowen L., Hood L.;
RT      "Comparison between strains Balb/c and 129 in a region of the mouse T
RT      cell receptor beta locus.";
RL      Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Balb/c;
RA      MEDLINE=21103195; PubMed=11160223;
RA      Chen F., Rowen L., Hood L., Rothenberg E.V.;
RT      "Differential transcriptional regulation of individual TCR Vbeta
RT      segments before gene rearrangement.";
RL      J. Immunol. 166:1771-1780(2001).
CC      -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR      EMBL; AF107342; AAC79093.1; -
DR      HSSP; P00763; IDPO.
DR      MEROPS; S01.063; -.
DR      MGD; MGI:2148749; Trypnl6.
DR      InterPro; IPR001254; Ser_protease_Try.
DR      Pfam; PF00089; Trypsin_1.
DR      PRINTS; PR00722; CHYMOTRYPSIN.
DR      SMART; SM00020; TRYP_SPC; 1.
DR      PROSITE; PS50240; TRYPSIN_DOM; 1.
DR      PROSITE; PS00134; TRYPSIN_HIS; 1.
DR      PROSITE; PS00135; TRYPSIN_SER; 1.
KW      Hydrolyase; Protease; Serine protease.
SQ      SEQUENCE 246 AA; 26134 MW; 34E173B18CA2F463 CRC64;

```

Alignment Scores:

```

Pred. No.:      1 55e-42      Length:      246
Score:          590.00      Matches:      114
Percent Similarity: 63.76%      Conservative: 32
Best Local Similarity: 49.78%      Mismatches: 77
Query Match:    46.27%      Indels:      6
DB:            11      Gaps:      3

```

US-09-856-320A-1_COPY_272_958 (1-687) x 092LR9 (1-246)

```

QY      1 ATCATCAAGGGGTTGCAAGTGCAGAGCCCTACATCCAGCCCTGGCAGAGCCCTGTTCCAG 60
      24 IleValGlyGlyTyrThrCysArgGluAsnSerValProTyrGlnValSerLeu---Asn 42
      61 AAGACGGGGCTACTGTGTGGGGCCAGGCTCATGCCCCAGATGGCTCTGCAGACAGCC 120
      43 SerGlyTyrHisPheCysGlyGlySerLeuIleAsnArgGlnTyrValValSerAlaIa 62
      121 CAGTCCCTCAGAGCCCGCTACATAGTCACTGGGGGAGCAACACTCCAGAGAGAG 180
      63 HisCysTyrLysThrArgIleGlnValArgLeuGlyGluHisAsnIleAsnValLeuGlu 82
      181 GGTCTGTGACAGACCCCGGAGCCAGCTAGTCTTCCCCAGCCCGGCTTCAACAAAG 240
      83 GlysangluGlnPheIleAspAlaIaLysIleIleLysHisProAsnPheAsnArgLys 102
      241 CTCGCCAACAAGACACCCGCAAGTACATCATGTGTGTGAAGAGTGCATGCCACTGCC 300
      103 ThrLeuAsn-----AsnAspIleMetLeuIleLysLeuSerSerProValThr 118
      301 ATCAGCTGGGCTGTGCGACCCCTCACCTCTCCCTCAGCTGTGACATGCTGGCAGCAGC 360
      119 LeuAsnAlaArgValAlaThrValAlaLeuProSerSerCysAlaProAlaGlyThrGln 138
      361 TGCTCATATTCGCGCTGGGGCAGCAGCTGCAGCCCGCCAGTTCAGCCTGCTCACACTTG 420
      139 CysLeuIleSerGlyTyrGlyLysAsnThrLeuSerPheGlyValSerGlnProAspLeu 158
      421 CGATGCCCAACATCACCATTATGAGCAGCAGAGAGTGTGAGAACGCTTACCCGCGAAC 480
      159 GlnCysLeuAspAlaProLeuLeuProGlnAlaAspCysGlnAlaSerTyrProGlyLys 178
      481 ATCAGACAGACACCATGCTGTGTCAGAGCTGCAGAGAGGAGGAGAGTCTGCCAGGT 540
      179 IleThrGlyAsnMetValCysAlaGlyPheLeuGlnGlyGlyLysAspSerCysGlnGly 198
      541 GACTCCGGGGGCGCTGTGCTGTGAACAGTCTTCAAGGCATTATCTCTGGGGCCAG 600
      199 AsperGlyGlyProValValCysAsnGlyLeuGlnGlnGlyIleValSerTyrPheLys 218
      601 GATCCGTGTGCGATCACCCGAAAGCTGTGCTTCAAGAGTGTGCAAAATATGTGAG 660
      219 Gly---CysAlaLeuProAspAsnProGlyValTyrThrLysValCysAsnTyrValAsp 237
      661 TGGATCCAGAGACGATGAGAACAT 687
      238 TrpIleGlnAspThrIleAlaIaAsn 246

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RESULT 13

```

090UK9  PRELIMINARY;      PRT;      246 AA.
ID      090UK9;
AC      090UK9;
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      TESP4 (0910001B19RIK protein) (Trypsinogen 9).
GN      TC OR 0910001B19RIK OR TRYPSINOGEN.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCB1_taxid=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Testis;
RA      MEDLINE=99436155; PubMed=10506205;
RA      Ohmura K., Kohno N., Kobayashi Y., Yamagata K., Sato S.,
RA      Kashiwabara S., Baba T.;
RT      "A homologue of pancreatic trypsin is localized in the acrosome of
RT      mammalian sperm and is released during acrosome reaction.";
RL      J. Biol. Chem. 274:29426-29432(1999).
RN      [2]
RP      SEQUENCE FROM N.A.

```



```
Db      63  HiscysTyrIlysSerArgIleGlnValArgLeuGlyIleHisAsnIleAsnValLeuGlu 82
QY      181  GGCTGTAGACGACCCGGACGACCTGAGTCTCCGCCACCCCGGCTTCAACACAGC 240
Db      83  GlyAsnGlnGlnPheValAsnSerAlaLysIleIleLysHisProAsnPheAsnSerArg 102
QY      241  CTCCCAACAAAGAACACCGCATGACATCATCTGTGTGAAGATGGCATGCCATGCTCC 300
Db      103  ThrLeuAsn-----AsnAspIleMetLeuIleLysLeuAlaSerProValThr 118
QY      301  ATCACCTGGGCTGTGGACCCCTCACGCCCTCTCTCAAGCTGTGTCACTGCTGGACACAGC 360
Db      119  LeuAsnAlaArgValAlaThrValAlaLeuProSerSerCysAlaProAlaGlyThrGln 138
QY      361  TGCCTCATTTCCGGCTGGGGGACAGCAGTCCAGCCCCCAGTTACGCTTACACACCTTG 420
Db      139  CysLeuIleSerGlyTrpGlyAsnThrLeuSerPheGlyValAsnAsnProAspLeuLeu 158
QY      421  CGATGGCCCAACATCACCATCATTTGAGCACCAAGTGTGAGAACGCTTACCCGGCAC 480
Db      159  GlnCysLeuAspAlaProLeuLeuProGlnAlaAspCysGlnAlaSerTyrProGlyLys 178
QY      481  ATCACAGACACCATGGTGTGTGTGCCAGCGTGCAGAAAGGGGCAAGACATCTGCCAGGT 540
Db      179  IleThrAsnAsnMetIleCysValGlyPheLeuGlnGlyIleLysAspSerCysGlnGly 198
QY      541  GACTCCGGGGCCCTCTGTGTGTGTAAACAGTCTTCAAGCATTAATCTCTGGGGCCAG 600
Db      199  AspSerGlyGlyProValValCysAsnGlyGlnLeuGlnGlyIleValSerTrpGlyTyr 218
QY      601  GATCCGTGTCCGATCACCCGAAAGCCTGTGTCTACACGAAAGTCTGCAAAATATGTGGAC 660
Db      219  Gly---CysAlaLeuLysAspAsnProGlyValTyrThrLysValCysAsnTyrValAsp 237
QY      661  TGGATCCAGAGACGATGAAGAACAAT 687
Db      238  TrpIleGlnAsnThrIleAlaAlaAsn 246
```

Search completed: October 15, 2003, 20:25:43
Job time : 51.1708 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 15, 2003, 17:34:35 ; Search time 11.0583 Seconds
(without alignments)
5843.068 Million cell updates/sec

Title: US-09-856-320A-1_COPY_272_958
Perfect score: 1275
Sequence: 1 atcacaaggaggttcagagtg.....aggagaagatgaagaacaat 687

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 255726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame_n2p.model -DEV=xlp
-O=/cgn2.1/USPTO_spool_P/US09856320/runat_15102003.105639.8511/app_query.fasta_1.2318
-DB=SwissProt_41 -OEMT=fastan -SUFFIX=rs -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=bl0sum62 -TRANS=human4.0 cdi -LIST=45
-NOALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09856320_ECGN_1_1_32_@runat_15102003.105639.8511 -NCPU=6 -ICPU=3
-NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1258	98.7	250	1	KLKB_HUMAN
2	736	57.7	250	1	KLK9_HUMAN
3	687	53.9	260	1	NRPN_RAT
4	684	53.6	260	1	NRPN_MOUSE
5	682	53.5	256	1	KLK6_HUMAN
6	681	53.4	260	1	KLK8_HUMAN
7	677.5	53.1	277	1	KLK5_HUMAN
8	644.5	50.5	293	1	KLK5_HUMAN
9	621	47.7	251	1	KLKC_HUMAN
10	606	47.5	248	1	KLKC_HUMAN
11	605.5	47.5	261	1	KLK1_RAT
12	600.5	47.1	261	1	KLK7_RAT
13	595.5	46.7	261	1	KLK3_MOUSE
14	594	46.6	248	1	TRK3_CHICK
15	591.5	46.4	263	1	KLKR_PRANA
16	591	46.4	246	1	TRY2_RAT
17	588	46.1	238	1	TRY3_SALSA
18	587	46.0	246	1	TRY1_RAT

19	585.5	45.9	261	1	KLK8_RAT	P36374	rattus norv
20	581.5	45.6	259	1	KLK2_RAT	P36376	rattus norv
21	577.5	45.3	261	1	KLK2_HUMAN	P20151	homo sapien
22	577.5	45.3	261	1	KLK9_MOUSE	P15949	mus musculu
23	577	45.3	231	1	TRYP_PIG	P00761	sus scrofa
24	577	45.3	244	1	KLK6_HUMAN	O92876	homo sapien
25	571	44.8	246	1	TRY2_MOUSE	P07146	mus musculu
26	570.5	44.7	246	1	KLK_PIG	P00752	mus scrofa
27	568	44.5	247	1	TRY2_CANFA	P06872	cattus famil
28	567.5	44.5	259	1	TRY2_RAT	P00759	rattus norv
29	566.5	44.4	261	1	KLK1_MOUSE	P15947	mus musculu
30	564.5	44.3	244	1	KLK6_MOUSE	P36375	rattus norv
31	564.5	44.3	261	1	KLK6_MOUSE	P00755	mus musculu
32	564	44.2	243	1	TRY1_BOVIN	P00760	bos taurus
33	562	44.1	262	1	KLK1_HUMAN	O90627	gallus gall
34	561	44.0	248	1	TRY1_CHICK	O07276	macaca fasc
35	557	43.7	244	1	TRY2_XENLA	P19799	xenopus lae
36	557	43.7	248	1	TRY2_CHICK	O90628	gallus gall
37	556.5	43.6	257	1	KLK1_MACFA	P15946	mus musculu
38	556.5	43.6	261	1	KLK_MOUSE	P19799	xenopus lae
39	556	43.6	243	1	TRY2_XENLA	O29463	bos taurus
40	556	43.6	247	1	TRY2_BOVIN	P08426	rattus norv
41	553	43.4	247	1	TRY3_RAT	P35032	salmo salar
42	552.5	43.3	231	1	TRY2_SALSA	P12788	rattus norv
43	552.5	43.3	247	1	TRY4_RAT	P00757	mus musculu
44	552	43.3	256	1	KLK4_MOUSE	P12323	cavia porce
45	551.5	43.3	239	1	KLK2_CAVPO		

ALIGNMENTS

RESULT 1
ID KLKB_HUMAN STANDARD; PRT; 250 AA.
AC Q9UBX7; O75837; O9N565;
DT 16-OCT-2001 (rel. 40; Created)
DT 16-OCT-2001 (rel. 40; Last sequence update)
DE 15-SEP-2003 (rel. 42; Last annotation update)
DE Kallikrein 11 precursor (EC 3.4.21.-) (Hypotastin) ('trypsin-like
protease').
GN KLK11 OR PRSS20 OR TLSP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxID=9606;
RX [1]
RP TISSUE=Hippocampus; (ISOFORM 1).
RC MEDLINE=98438738; PubMed=9765601;
RA Yoshida S., Taniguchi M., Suemoto T., Oka T., He X.P., Shiosaka S.;
RT "CDNA cloning and expression of a novel serine protease, TLSP.*;
RL Biochim. Biophys. Acta 1399:225-228(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Hippocampus, and Prostate;
RA MEDLINE=20329229; PubMed=10872828;
RT Mitsui S., Yamada T., Okui A., Komitani K., Uemura H., Yamaguchi N.;
RL "A novel isoform of a kallikrein-like protease, TLSP/Hypotastin,
RT (PRSS20), is expressed in the human brain and prostate.*;
RN Biochem. Biophys. Res. Commun. 272:205-211(2000).
RP [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC MEDLINE=20130117; PubMed=10662248;
RA Yousef G.M., Scorilas A., Diamandis E.P.;
RL "Genomic organization, mapping, tissue expression, and hormonal
RT regulation of trypsin-like serine protease (TLSP PRSS20), a new
RT member of the human kallikrein gene family.*;
RL Genomics 63:86-96(2000).
RP [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC MEDLINE=20510030; PubMed=11054574;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuall J.,
RP Moss P., Paepel B., Wang K.;

Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.
 RT Gene 257:119-130(2000).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Lamedin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Barnes J.,
 RA Dangnan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
 RA Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
 RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 RA Olsen A.S., Carrano A.V.,
 RT "Sequence analysis of chromosome 19q13.4."*
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RP [6]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE-Testis;
 RX MEDLINE-22388257; PubMed-12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshylyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
 RA Vallalao D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Gilwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smillie D.E.,
 RA Schnerker A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences."*
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: POSSIBLE MULTIFUNCTIONAL PROTEASE. EFFICIENTLY CLEAVES
 B2-PHE-ARG-4-METHYLCOUMARYL-7-AMIDE, A KALLIKREIN SUBSTRATE, AND
 CC WEAKLY CLEAVES OTHER SUBSTRATES FOR KALLIKREIN AND TRYPSIN.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named Isoforms-2;
 CC Name-1;
 CC IsoId=Q9UBX7-1; Sequence-Displayed;
 CC Name-2;
 CC IsoId=Q9UBX7-2; Sequence-VSP_005402;
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SKIN AND PROSTATE. ISOFORM
 1 IS EXPRESSED PREFERENTIALLY IN BRAIN; ISOFORM 2 IN PROSTATE.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
 CC -----
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 CC EMBL; AB012917; BA33404.1; ALT_INIT.
 DR EMBL; AB013730; BA88713.1; -
 DR EMBL; AB041036; BAA9679.1; -
 DR EMBL; AF164623; AAD47815.1; -
 DR EMBL; AF243527; AAG33364.1; -
 DR EMBL; AC011473; AAG23257.1; -
 DR EMBL; BC022068; AAH22068.1; -
 DR HSSP; P00763; IDPO.
 DR MEROPS; S01.257; -
 DR Genew; HGNC:6359; KLIK1.
 DR MIM; 604434; -
 DR InterPro; IPR001314; Chymotrypsin.

DR InterPro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00089; trypsin.1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYPSIN_SPC.1.
 DR PROSITE; PSS0240; TRYPSIN_DOM.1.
 DR PROSITE; PS00134; TRYPSIN_HIS.1.
 DR PROSITE; PS00135; TRYPSIN_SER.1.
 KW Hydrolyase; Serine protease; Glycoprotein; Signal; Zymogen;
 KW Alternative splicing.
 FT SIGNAL 1
 FT PROPEP 19 21
 FT CHAIN 22 250
 FT ACT_SITE 62 62
 FT ACT_SITE 110 110
 FT ACT_SITE 203 203
 FT DISULFID 28 163
 FT DISULFID 47 63
 FT DISULFID 135 237
 FT DISULFID 142 209
 FT DISULFID 174 188
 FT DISULFID 199 224
 FT CARBOHYD 99 99
 FT CARBOHYD 165 165
 FT CARBOHYD 181 181
 FT CARBOHYD 210 210
 FT VARSPLIC 1
 SQ SEQUENCE 250 AA; 27466 MW; 192D910DBCC07A56 CRC64;
 Alignment Scores:
 Pred. No: 1e-80 Length: 250
 Score: 1258.00 Matches: 229
 Percent Similarity: 100.00% Conservative: 0
 Best local Similarity: 100.00% Mismatches: 0
 Query Match: 98.67% Indels: 0
 DB: 1 Gaps: 0
 US-09-856-320a-1_copy_272_958 (1-687) x KLRB_HUMAN (1-250)
 QY 1 ATCATCAAGAGGAGTTCAGATGCAAGCCCTCACTCCAGCCCTGGAGAGCCCTGTTGCG 60
 |||||
 Db 22 ILELEISGLYHPEGIUCYLSYSPROHISSEGLNPROTRPGLNLALEUPLHGLN 41
 |||||
 QY 61 AAGAGCGGCTACTGTGTGGGGGAGCGCTGACGCCGCCAGATGCTCTGACAGCACC 120
 |||||
 Db 42 LYSTHTRARGLEULEUCYSGLYALATHLEULLEALAPROARGTRLEUPLHGLN 61
 |||||
 QY 121 CACTGCTCAAGCCCGCTCATAGTTCACCTGGGGGAGACACAACTCCGAAGAGAG 180
 |||||
 Db 62 HISCYSLEUYSPROARGTYRILEVALHISLEUGLYGLNHISASNLEUGINTLSGLN 81
 |||||
 QY 181 GGCTGTAGAGAGACCGGAGAGCAGTCACTGCTCCAGCCCGGCTCAACACAGC 240
 |||||
 Db 82 GLYCSEGLDINHTNARGHIALATHGLUSERPHEROHLSPROGLYPHESANASER 101
 |||||
 QY 241 CTCGCCCAAGAACACACCGCAATGACATCATGCTGTGTAAGATGACATGCGCTCC 300
 |||||
 Db 102 LEUPROASNLYSPHISAPHSARGHANAERILEMETLEUVALYSMETLASSERPROVALSER 121
 |||||
 QY 301 ATGACCTGGGCTGTGCACCCCTCACCCCTCTCTCAACGCTGTGTCACCTGTGCACAC 360
 |||||
 Db 122 ILEHTRPALVALAARGPROLEUPLHUSERSERARGYSVALTHRALAGLYTHN 141
 |||||
 QY 361 TGGCTATTTCCGGCGGGGAGACAGTCCAGGCCCAAGTAAAGCTGCTGCTCAACCTTG 420
 |||||
 Db 142 CYSLEULESERGLYTRPGLYSERTHNSETPRGIMLEUARGLEUPROHISTH 161
 |||||
 QY 421 CGATGGCCCAATCATCATGATGAGACACAAAGTGTGAGAAACGCTACCCGGGCAAC 480
 |||||
 Db 162 ARGCYALASNLEHTHRIELLEGLHISGLINLYSCYSGLASNALATYRPROGLYASN 181
 |||||
 QY 481 ATGACAGACACCATGGTGTGTGCCAGCGGTGCAGAAAGGGGAGGAGTCTGCCAGCGT 540

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DB 1182 IIEHRAAPTHMeValaCysAlaSerValGInGluGlyGlyLysAspSerCysGInGly 201
QY 541 GACTCCGGGGGCGCCCTCTGCTGTCTGAACAGCTCTTCAAGCATATCTCTGGGGCCAG 600
DB 202 AapSerGlyGlyProLeuValCysAsnGInSerLeuGInGlyLeuSerTrpGlyGln 221
QY 601 GATCCGTGTGATCATACCCGAAAGCCTGTGTCTACACGAAAGTCTGCAATATGTGAC 660
DB 222 AapProCysAlaIleThrArgLysProGlyValTyrThrLysValCysTyrValAsp 241
QY 661 TGGATCCAGAGACGATGAGAACAT 687
DB 242 TTPILGInGluThrMeLysAsn 250

RESULT 2
KIK9_HUMAN
ID KIK9_HUMAN STANDARD: PRT: 250 AA.
AC 09UK09:
DT 16-OCT-2001 (rel. 40, Created)
DT 16-OCT-2001 (rel. 40, Last sequence update)
DT 28-FEB-2003 (rel. 41, Last annotation update)
DE Kallikrein 9 precursor (EC 3.4.21.-) (Kallikrein-like protein 3) (KIK-
DE L3).
GN KIK9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20118156; PubMed-10652563;
RA Yousef G.M., Luo L.-Y., Diamandis E.P.;
RT "Identification of novel human kallikrein-like genes on chromosome
RT 19q13.3-q13.4."
RL Anticancer Res. 19:2843-2852(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-20247258; PubMed-10783266;
RA Yousef G.M., Diamandis E.P.;
RT "The expanded human kallikrein gene family: locus characterization and
RT molecular cloning of a new member, KIK-L3."
RL Genomics 65:184-194(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-20510030; PubMed-11054574;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
RA Mose P., Paepfer B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region."
RL Gene 257:119-130(2000).
RN [4]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCreedy P.M., Skowronski E., Vismathan V.,
RA Burhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Gares J.,
RA Dangnan L., Erber A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Andeise T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carrano A.V.;
RT "Sequence analysis of chromosome 19q13.4."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- TISSUE SPECIFICITY: SKIN, THYMUS, TRACHEA, CEREBELLUM AND SPINAL
CC CORD.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DB 16 GAGTCAAGCTCTCACTCCAGCCCTGGCAGGAGCCCTGTTCGAGAGACGCGCTACTC 75
QY 16 GAGTCAAGCTCTCACTCCAGCCCTGGCAGGAGCCCTGTTCGAGAGACGCGCTACTC 75
DB 28 GUCysArgProAsnSerGlnProTrpGlnIleGlyLeuPheHisLeuThrArgLeuPhe 47
QY 28 GUCysArgProAsnSerGlnProTrpGlnIleGlyLeuPheHisLeuThrArgLeuPhe 47
DB 76 TGTGGGGGCGAGCTTCATGCCCCAGATGGCTCTGAGAGAGCCGCTCAAGGCC 135
QY 76 TGTGGGGGCGAGCTTCATGCCCCAGATGGCTCTGAGAGAGCCGCTCAAGGCC 135
DB 48 CysGlyAlaThrIleuIleSerAspArgTrpLeuThrAlaHisCysArgLysPro 67
QY 48 CysGlyAlaThrIleuIleSerAspArgTrpLeuThrAlaHisCysArgLysPro 67
DB 136 CGTACATAGTTCACCTGGGGGAGCACAACCTCCAGAAAGAGAGGCTGTGAGCAGAC 195
QY 136 CGTACATAGTTCACCTGGGGGAGCACAACCTCCAGAAAGAGAGGCTGTGAGCAGAC 195
DB 68 TyrLeuThrValArgLeuGlyGlnHisHisLeuTrpLysTrpGlnGlyProGluInleu 87
QY 68 TyrLeuThrValArgLeuGlyGlnHisHisLeuTrpLysTrpGlnGlyProGluInleu 87
DB 196 CGGACAGCAGCTGAGTCTTCCGCCAGCCCGGCTTCACACACAGGCTCCCAACAAAC 255
QY 196 CGGACAGCAGCTGAGTCTTCCGCCAGCCCGGCTTCACACACAGGCTCCCAACAAAC 255
DB 88 PheArgValThrAspPhePheProHisProGlyPheAsnLysAspLeuSerAlaAsnAsp 107
QY 88 PheArgValThrAspPhePheProHisProGlyPheAsnLysAspLeuSerAlaAsnAsp 107
DB 256 CAGCCGATGACATCATCTGCTGAGAGATGAGCAGCAGCAGCTTCATCAGCTGGGCTGTG 315
QY 256 CAGCCGATGACATCATCTGCTGAGAGATGAGCAGCAGCAGCTTCATCAGCTGGGCTGTG 315
DB 108 HisAsnAspAspIleMetLeuIleArgLeuProArgGlnAlaArgLeuSerProAlaVal 127
QY 108 HisAsnAspAspIleMetLeuIleArgLeuProArgGlnAlaArgLeuSerProAlaVal 127
DB 316 CGACCCCTACCTCTCTCTCAAGCTGTGTCTACCTGTGTGAGCAGCAGCTTCATTCGGCG 375
QY 316 CGACCCCTACCTCTCTCTCTCAAGCTGTGTCTACCTGTGTGAGCAGCAGCTTCATTCGGCG 375
DB 128 GlnProLeuAsnLeuSerGlnThrCysValSerProGlyMetGlnCysLeuIleSerCyl 147
QY 128 GlnProLeuAsnLeuSerGlnThrCysValSerProGlyMetGlnCysLeuIleSerCyl 147
DB 376 TGGGGGACAGCTTCAGGCCCCAGTTCAGCTGCTTCACACCTTCGATGCGCAATC 435
QY 376 TGGGGGACAGCTTCAGGCCCCAGTTCAGCTGCTTCACACCTTCGATGCGCAATC 435

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Db 148 TrpGlyAlaValSerSerProLysAlaLeuPheProValThrLeuGlnCysAlaAsnIle 167
 QY 436 ACCATCATGAGCAGCAGAGAGTGTAGACGCTACCCCGCAGCATCACAGACCATG 495
 Db 168 SerIleuGlnAlaValSerCysHisThrAlaIleTrpGlnHisIleSerAspSerMet 187
 QY 496 GTGTGTCCACGCTGACGAGAGGGGCGACGACTCTGCCAGGGTGACTCCGGGGCCCT 555
 Db 188 LeuGlyAlaGlyLeuTrpGlnGlyGlyAlaGlySerCysGlnGlyAspSerGlyGlyPro 207
 QY 556 CTGTGTGTACAGCAGCATATATCTCCGGGGCGAGAGCCGTCGTCGATC 615
 Db 208 LeuValCysAsnGlyThrLeuAlaGlyAlaValSerGlyAlaGlnProCysSerArg 227
 QY 616 ACCCGAAGCCTGTGTCTACACGAGAGTGTGCAATATGTGACGTGATCCAGAGACG 675
 Db 228 ProArgTrpProAlaValIleThrSerValCysHisIleTrpLeuAspTrpIleGlnIle 247
 QY 676 ATGAGAAC 684
 Db 248 MetGlnAsn 250
 RESULT 3
 NRPN_RAT
 ID NRPN_RAT STANDARD; PRT; 260 AA.
 AC 086780;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuropein precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Brain serine
 protease 1).
 GN KUB8 OR PRSS19 OR NRPN OR BSPI.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Elascher; TISSUE=Brain;
 RX MEDLINE=98389725; PubMed=9722524;
 RA Davies B.J., Plöckard B.S., Steel M., Morris R.G.M., Lathe R.;
 RT "Serine proteases in rodent hippocampus";
 RL J. Biol. Chem. 273:23004-23011(1998)
 CC -1- FUNCTION: SUGGESTED TO BE INVOLVED IN KINDLING EPILEPTOGENESIS AND
 HIPPOCAMPAL PLASTICITY. HAS A STRONG PROTEOLYTIC ACTIVITY AGAINST
 CC FIBRONECTIN (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
 CC -1- SUBCELLULAR LOCATION: Secreted (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: RESTRICTED TO HIPPOCAMPUS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: AJ005641; CAA06643.1; -
 CC HSSP: O61955; INPM.
 DR MEROPS: S01.244.1;
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam: PF00089; trypsin_1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; tryp_SPC_1.
 DR PROSITE: PSS0240; TRYPSIN_DOM_1.
 DR PROSITE: PS00134; TRYPSIN_HIS_1.
 DR PROSITE: PS00135; TRYPSIN_SER_1.
 KM Hydrolase; Serine protease; Glycoprotein; Zymogen; signal.
 FT SIGNAL 1 28 POTENTIAL.
 FT PROPEP 29 32 BY SIMILARITY.

FT CHAIN 33 260 NEUROPSIN.
 FT ACT_SITE 73 73 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 120 120 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 212 212 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 39 173 BY SIMILARITY.
 FT DISULFID 58 74 BY SIMILARITY.
 FT DISULFID 145 246 BY SIMILARITY.
 FT DISULFID 152 218 BY SIMILARITY.
 FT DISULFID 184 198 BY SIMILARITY.
 FT DISULFID 208 233 BY SIMILARITY.
 FT CARBOHYD 110 110 N-LINKED (GLCNAC...) (POTENTIAL).
 SO SEQUENCE 260 AA; 28510 MW; 58DF4F062A0BF75 CRC64;
 Alignment Scores:
 Pred. No.: 7.48e-41 Length: 260
 Score: 687.00 Matches: 121
 Percent Similarity: 69.03% Conservative: 35
 Best Local Similarity: 53.54% Mismatches: 68
 Query Match: 53.88% Indels: 2
 DB: 1 Gaps: 2
 US-09-856-320a-1_COPY_272_958 (1-687) x NRPN_RAT (1-260)
 QY 1 ATCATCAAGGGGTTTCGAGTGCAGCCTCCAGCCCTGGAGGAGCCCTGTTTCGAG 60
 Db 33 IlleuGlnGlyGlnGlyCysLysProHisSerGlnProTrpGlnThrAlaLeuPheGln 52
 QY 61 AAGAGCGGCTACTCTGTGGGGGAGAGCATGCGCCCGAGATGGCTGACAGAGCAGC 120
 Db 53 GlyIuArgLeuValGlyGlyGlyGlyValLeuValGlyAspArgTrpValLeuThrAla 72
 QY 121 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGGAGAGCAGCACTCCAGAGAGAG 180
 Db 73 HisCysLysLysAspLysTrpSerValArgLeuGlnAspHisSerLeuGlnLysArgAsp 92
 QY 181 GCGTGTAGAGAGACCCGAGAGCCAGTCCCTCCCGCCAGCCCGCTTCAACAGAGC 240
 Db 93 GluProGlnGlnGlnIleGlnValAlaArgSerIleGlnHisProCysPheAsnSerSer 112
 QY 241 CTCGCCAAGAGAGCCAGCAATGACATGCTGTGGAGAGAGGATGCGCAGTCTGC 300
 Db 113 AsnPro---GluAspHisSerHisAspIleMetLeuIleArgLeuGlnAsnSerAlaAsn 131
 QY 301 ATCACGTGGGCTGTGGAGCCCTTCACCTCTCTCTCAGCTGTGTCTGTGGCAGCAGC 360
 Db 132 LeuGlyAspLysValLysProIleGlnLeuAlaAsnLeuGlyProLysValGlyGlnLys 151
 QY 361 TGCCCTATTCCGGGCTGGGAGAGAGCAGCCCGAGTTAGCCCTGCTCACACCTTG 420
 Db 152 CysIleIleSerGlyTrpGlyThrValThrSerProGlnGlnAsnProAsnThrLeu 171
 QY 421 CGATGCCCAACATCACCATCATTTGAGCAGCAGAGAGTGTGAGAACGCTTACCCGCGAAC 480
 Db 172 AsnGlyAlaGlnValLysIleTrpSerGlnAsnLysGlyLysArgAlaTrpProGlyLys 191
 QY 481 ATCACAGACACCATGTGTGTGCGAGGCTGCAGAGAGGGGCGAGAGCTCTCCAGAGGT 540
 Db 192 IlleThrGlnIleMetValCysAlaGly---SerSerAsnGlyAlaAspThrCysGlnGly 210
 QY 541 GACTCGGGGGGCGCTGTGTGTGATACCATCTCTTCAAGCATATATCTCTGGGGCAG 600
 Db 211 AspSerGlyGlyProLeuValCysAsnGlyValLeuGlnIleThrTrpTrpGlySer 230
 QY 601 GATCCGTTGCGATCAACCCGAGAGCGGTGTGTACAGAGAGTGTGAGAACGCTTGTGAGAG 660
 Db 231 AspProCysGlyLysProGlnLysProGlnLysValThrLysIleCysArgTrpThrAsn 250
 QY 661 TGGATCCAGAGAGAGAGT 678
 Db 251 TrpIleLysLysThrMet 256
 RESULT 4
 NRPN_MOUSE

ID NRPN_MOUSE STANDARD: PRT: 260 AA.
AC Q61955;
DR 15-JUL-1999 (Rel. 38, Created)
DR 15-JUL-1999 (Rel. 38, Last sequence update)
DR 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide precursor (EC 3.4.21.-) (NP) (Kallikrein 8).
GN KIK8 OR PRS19 OR NRPN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-Hippocampus;
RX MEDLINE=95348817; PubMed=7623137;
RA Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T.,
RA Ito J., Nishino H., Aimoto S., Kiyama H., Shiosaka S.;
RT "Expression and activity-dependent changes of a novel limbic-serine
RT protease gene in the hippocampus.";
RL J. Neurosci. 15:5088-5097(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Yoshida S., Hirata A., Inoue N., Shiosaka S.;
RT "Cloning and assignment of mouse neuropeptide gene, prs19 to chromosome
RT 7B4.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF N-TERMINUS, AND CHARACTERIZATION.
RC STRAIN-BALB/C; TISSUE-Brain;
RX MEDLINE=98225202; PubMed=9556608;
RA Shimizu C., Yoshida S., Shibata M., Kato K., Momota Y., Matsumoto K.,
RA Shiosaka S., Midorikawa R., Kamachi T., Kawabe A., Shiosaka S.;
RT "Characterization of recombinant and brain neuropeptide, a
RT plasticity-related serine protease.";
RL J. Biol. Chem. 273:11189-11196(1998).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 33-257.
RC TISSUE-Hippocampus;
RX MEDLINE=99134351; PubMed=9933620;
RA Kishi T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S.,
RA Shiosaka S., Hakoshima T.;
RT "Crystal structure of neuropeptide, a hippocampal protease involved in
RT kindling epileptogenesis.";
RL J. Biol. Chem. 274:4220-4224(1999).
CC -1- FUNCTION: SUGGESTED TO BE INVOLVED IN KINDLING EPILEPTOGENESIS AND
CC HIPPOCAMPAL PLASTICITY. HAS A STRONG PROTEOLYTIC ACTIVITY AGAINST
CC FIBRONECTIN.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-,
CC -1- ENZYME REGULATION: STRONGLY INHIBITED BY DIISOPROPYL
CC FLUOROPHOSPHATE, LEUPEPTIN AND (4-AMIDINOPHENYL)METHANESULFONYL 1-
CC FLUORIDE.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN THE LIMBIC SYSTEM OF
CC MOUSE BRAIN AND IS LOCALIZED AT HIGHEST CONCENTRATION IN PYRAMIDAL
CC NEURONS OF THE HIPPOCAMPAL CA1-3 SUBFIELDS.
CC -1- MASS SPECTROMETRY: MW-26613; METHOD-MALDI; RANGE-29-260.
CC -1- MASS SPECTROMETRY: MW-26229; METHOD-MALDI; RANGE-33-260.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
CC -----
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CC -----
DR EMBL: D30785; BA06451.1; -
DR EMBL: AB032202; BA02435.1; -
DR PIR: I56559; I56559.
DR PDB: INPM; 23-MAR-99.
DR MEROPS: S01.244; -
DR MGD: MGI:892018; KIK8.

DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser-protease_try.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TYP_SPC; 1.
DR PROSITE: PS00240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; 1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
KW Hydrolase; Serine protease; Glycoprotein; zymogen; signal;
KW 3D-structure.
FT SIGNAL 1 28
FT PROPEP 29 32
FT CHAIN 33 260
FT ACT_SITE 73 73
FT ACT_SITE 120 120
FT ACT_SITE 212 212
FT DISULFID 39 173
FT DISULFID 58 74
FT DISULFID 145 246
FT DISULFID 152 218
FT DISULFID 184 198
FT DISULFID 208 233
FT CARBOHYD 110 110
FT STRAND 34 34
FT STRAND 37 38
FT TURN 41 42
FT TURN 45 46
FT STRAND 47 52
FT TURN 53 54
FT STRAND 55 64
FT TURN 65 66
FT STRAND 67 70
FT HELIX 72 74
FT STRAND 80 83
FT STRAND 87 87
FT TURN 88 89
FT STRAND 96 98
FT TURN 100 105
FT TURN 107 108
FT TURN 114 115
FT TURN 118 119
FT STRAND 122 126
FT STRAND 140 141
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FT TURN 236 237
FT STRAND 238 238
FT STRAND 240 244
FT HELIX 245 256
SQ SEQUENCE 260 AA; 28523 MW; B55F6BEB37CD60E CRC64;
Alignment Scores:
Pred. No.: 1.21e-40
Score: 684.00
Percent Similarity: 68.42%
Best Local Similarity: 53.07%
Query Match: 53.65%
DB: 1
Length: 260
Matches: 121
Conservative: 35
Mismatch: 70
Indels: 2
Gaps: 2
N-LINKED (GLCNAC. . .) (POTENTIAL).
POTENTIAL.
NEUROPSIN.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).

US-09-856-3320A-1_COPY_272_958 (1-687) x NRPN_MOUSE (1-260)

OY	1	ATCATCAAGGGGTTGAGTGTGACAGCCTCACTCCACGCTTGGACAGCAGCCTGTTCGAG	60
Db	33	leueuglgluYarglgluYsIleProHISserGlnProtrpIlnAlaIleuPheGln	52
OY	61	AAGAGCGCGCTCTGTGTGGGCGAGACGCTCATCGGCCCCAGATGGCTCCGACAGAGCC	120
Db	53	glYluArglleuIleCyselYglYalIleuValIglYAspArgrtrYalIleuHrAlaIa	72
OY	121	CAGTCTCTCAAGCCCCCGCTACATAGTTCACCTGTGGGCGACACAACTCCAGAAAGAGAG	180
Db	73	HIScYsLYsYsglInLsYsYsSerValArglleuGlyAspHISserLeuGlnSerArgAsp	92
OY	181	GGCTGTGGACAGACCCCGGACAGCACACTGACTGCTTCCCAACCCCGGCTTCAACAACAG	240
Db	93	lnProglInglInglInleGlnValAlaGlnSerIleGlnHISProCYsLYsHISnSer	112
OY	241	CTCCCCAACAAGACCAACCCAGCATGATCATGTGGTAGAGATGGCATGCCAGCTCC	300
Db	113	AsnPro---GluAspHISserHISAspIleMetleuIleArgleuGlnAsnSerAlaSn	131
OY	301	ATCAGCTGGGCTGTGCGAGACCCCTCACTCTCTCACTGCTGTGTACTGCTGGCACCAGC	360
Db	132	leuGlyAspLYsValLYsProValGlnIleuAlaAsnLeuCYsProLYsValGlyGlnLYs	151
OY	361	TGCTTCATTTCCGGCTGGGGGCGACAGTCCACAGCCCACTTACGCTGCTGCTCACACTTG	420
Db	152	CysIleIleSerGlyTYrprLYsThrValTYrSerProglInglUnsnPheProAsnHrLeu	171
OY	421	CGATGGCGCAACATCATACCATCTTAGACACACAGAAAGTGGAGAAACCCCGGCAAC	480
Db	172	AsnCYsAlaGlnValLYsLYsIleTYrSerGlnAsnLYsCYsGlnArgrAlaTYrProglLYs	191
OY	481	ATCACAGACACCAGTGTGTGTGCCAGCGTGCAGAGAGGGGCGAAGAGACTCTGCCAGGT	540
Db	192	IleHrInglInglMetValCYsAlaGly---SerSerAsnGlyAlaAspHrCYsGlnGly	210
OY	541	GACTCTGGGGGGCTCTGTGTGTGTACCAAGCTCTTCAAGGACATTAATCTCTGGGCGAG	600
Db	211	AspSerGlyGlyProleuValCYsAspGlyMetleuGlnGlyIleHrSertrpGlySer	230
OY	601	GATCGGTGGCATATCACCCGGAAGCCTGTGTCTACACAGAAAGTGTGCAAAATATGTGAC	660
Db	231	AspProCYsGlyLYsProglInglYsProglYalTYrThLYsIleCYsArgTYrHrThr	250
OY	661	TGGATCAGAGAGCAGTGAAGAC 684	
Db	251	TrrIleLYsLYsThrMetAspAsn 258	

RESULT 5

KLKF_HUMAN	STANDARD;	PRT;	256 AA.
ID	KLKF_HUMAN		
AC	Q9H2R5; Q15358; Q9H2R3; Q9H2R4; Q9H2R6; Q9HBG9;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DE	28-FEB-2003 (Rel. 41, Last annotation update)		
GN	Kallikrein 15 precursor (EC 3.4.21.-) (Aco protease).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
OX	NCBI_Taxid=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.		
RK	PubMed=11010966;		
RA	Yousef G.M., Scorilas A., Jung K., Ashworth L.K., Diamandis E.P.;		
RT	"Molecular cloning of the human kallikrein 15 gene (KLK15). Up-		
RL	regulation in prostate cancer";		
RL	J. Biol. Chem. 276:53-61(2001).		
RP	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20510030; PubMed=11054574;		

RA	Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McNally J.,
RB	Moss P., Peeter B., Wang K.;
RT	"Sequencing and expression analysis of the serine protease gene
RL	cluster located in chromosome 19q13 region.";
RN	gene 257:119-130(2000).
RP	[3]
RX	PRELIMINARY PARTIAL SEQUENCE FROM N.A.
RC	TISSUE=Brain;
RD	MEDLINE=94289486; PubMed=8018728;
RE	Dhananch M.E., Spiess M.;
RF	"A novel serine proteinase-like sequence from human brain.";
RG	Biochim. Biophys. Acta 1218:225-228(1994).
RH	-1 FUNCTION: Protease whose physiological substrate is not yet known.
RI	-1 SUBCELLULAR LOCATION: Secreted (Probable).
RJ	-1 ALTERNATIVE PRODUCTS:
RK	Event-Alternative splicing; Named isoforms=4;
RL	Name=1;
RM	IsoId=Q9H2R5-1; Sequence=Displayed;
RN	Name=2;
RO	IsoId=Q9H2R5-2; Sequence=VSP_005405;
RP	Name=3;
RQ	IsoId=Q9H2R5-3; Sequence=VSP_005406, VSP_005407;
RS	Name=4;
RT	IsoId=Q9H2R5-4; Sequence=VSP_005404;
RU	-1 TISSUE SPECIFICITY: Highest expression in the thyroid gland. Also
RV	expressed in the prostate, salivary, and adrenal glands and in the
RW	colon testis and kidney.
RX	-1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
RY	-----
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SG	or send an email to license@lsb-sib.ch).
SH	-----
SI	EMBL; AF242195; AACG9469.1; -
SJ	EMBL; AF242195; AACG9470.1; -
SK	EMBL; AF242195; AACG9471.1; -
SL	EMBL; AF242195; AACG9472.1; -
SM	EMBL; AF243527; AACG3354.1; -
SN	EMBL; X75363; CAAS3145.1; ALT_SEQ.
SO	HSSP; P00763; IDPO.
SP	MEOPRS; S01.081;-.
SQ	GO; GO:0005376; C:extracellular; NAS.
SR	GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
SS	InterPro; IPR001314; Chymotrypsin.
ST	InterPro; IPR001254; Ser protease_Try.
SV	Pfam; PF00089; trypsin.1.
SW	PRINTS; PRO0722; CHYMOTRYPSIN.
SX	PROSITE; PS50240; TRYPSIN_DOM.1.
SY	PROSITE; PS00134; TRYPSIN_HIS.1.
SZ	PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.
T0	Hydrolase; Serine protease; Glycoprotein; signal; zymogen;
T1	Alternative splicing.
T2	SIGNAL
T3	PROPEP
T4	CHAIN
T5	ACT_SITE
T6	ACT_SITE
T7	ACT_SITE
T8	CABOHD
T9	CABOHD
T0	VASPLIC
T1	VASPLIC
T2	VASPLIC
T3	VASPLIC
T4	VASPLIC
T5	VASPLIC
T6	VASPLIC
T7	VASPLIC
T8	VASPLIC
T9	VASPLIC
T0	CONFLICT

SQ SEQUENCE 256 AA; 28087 MM; B5EBF8D6022786B5 CRC64;
 Alignment Scores:
 Pred. No.: 1.67e-40 Length: 256
 Score: 682.00 Matches: 124
 Percent Similarity: 66.95% Conservative: 36
 Best Local Similarity: 51.88% Mismatches: 65
 Query Match: 53.49% Indels: 14
 DB: 1 Gaps: 3

US-09-856-320A-1_COPY_272_958 (1-687) x KLF_HUMAN (1-256)

```

OY 1 ATCAATCAAGGGGTTGATGATGCAAGCCCTACATCCAGCCCTGGACAGACCCCTGTTCGAG 60
DB 22 LeuLeuGluGlyAspGluCysAlaAlaProHisSerGlnProTyrGlnValAlaLeuTyrGlu 41
OY 61 AAGAGCGGCTACTCTGTGGGGCGAGCTACGCCAGATGGCTCTGACAGCAGCC 120
DB 42 ArgGlyArgPheAsnCysGlyAlaSerLeuIleSerProHisTyrValLeuSerAlaAla 61
OY 121 CACTGCTCAAGCCCCGCTACATAGTTCACCTGGGGAGCAGACATCCAGAGAGAGAG 180
DB 62 HisCysGlnSerArgPheMetArgValArgLeuGlyGluHisAsnLeuArgLysArgAsp 81
OY 181 GGCCTGTAGCAGACCCGAGCCAGCTGATGCTCCGCCAGCCGCGCTTCACAGACAGC 240
DB 82 GlyProGluGlnLeuArgThrThrSerArgValIleProHisProArgTyrGlu----- 99
OY 241 CTCCCAACAAGACACACCGCATGATGATGCTGAGTGAAGGATGATGATGCTCC 300
DB 100 -----AlaArgSerHisArgAsnAspIleMetLeuLeuArgLeuValGlnProAlaArg 117
OY 301 ATCACTGGCTGTGGAGCCCTCAGCCCTGCTCAGCTGTGTCAGTGTGGCAGCAGC 360
DB 118 LeuAsnProGlnValArgProAlaValLeuProThrArgCysProHisProGlyGluAla 137
OY 361 TGCCCATTCGCGGCTGGGGAGCAGCAGC-----AGCCCC 396
DB 138 CysValValSerGlyTyrGlyLeuValSerHisAsnGluProGlyThrAlaGlySerPro 157
OY 397 -----CAGTTCAGCTGCTCAGACCTTGGAGTGGCGGCAACATCACCATGATGAGCAG 450
DB 158 ArgSerGlnValSerLeuProAspPheThrLeuHisCysAlaAsnIleSerIleLeuSerAsp 177
OY 451 CAGAAAGTGTAGAAAGCCCTACCCGGGAGCATCAGACAGACAGATGCTGTGCGAGCGTG 510
DB 178 ThrSerCysAspLysSerTyrProGlyArgLeuThrAsnThrMetValCysAlaGlyAla 197
OY 511 CAGGAAGGGGGGAGGAGCTCCTGCGAGGTGATCCCGGGGGCCCTGCTGTGAACAG 570
DB 198 GluGlyArgGlyAlaGlySerCysGluGlyAspSerGlyGlyProLeuValCysGlyGly 217
OY 571 TCTCTCAAGGATATATCTCTGGGGGCGAGATCCGTTGGATCAGCAGCAGAGCTGTG 630
DB 218 IleLeuGlnGlyIleValSerTyrGlyAspValProCysAspAsnThrThrLysProGly 237
OY 631 GTCTACACGAAAGTCTGCAATATATGTGACTGTGATCCAGAGAGCAGATGAGAACAT 687
DB 238 ValTyrThrLysValCysHisTyrLeuGlnIleTyrPheArgGluThrMetLysArgAsn 256
  
```

RESULT 6
 KLF_HUMAN
 ID KLF_HUMAN STANDARD: PRT: 260 AA.
 AC 060259; Q9HCB3; Q9UUL9; Q9UQ47;
 DT 15-JUL-1999 (Ref. 38, Created)
 DT 15-JUL-1999 (Ref. 38, Last sequence update)
 DT 28-FEB-2003 (Ref. 41, Last annotation update)
 DE Neurepsin precursor (EC 3.4.21.-) (NP) (Kalikrein 8) (Ovacin) (Serine
 protease TADG-14) (tumor-associated differentially expressed gene-14
 protein).
 GN KLF8 OR PRSS19 OR TADG14 OR NRPN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 ON NCBI_TaxID=9606;
 OX
 RP [1]
 RC SEQUENCE FROM N.A. (ISOFORM 1).
 RX TISSUE-Hippocampus;
 RX MEDLINE=98372070; PubMed=9714609;
 RA Yoshida S., Taniguchi M., Hirata A., Shiosaka S.;
 RT "Sequence analysis and expression of human neurepsin cDNA and gene.";
 RL Gene 213:9-16(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE-Brain;
 RX MEDLINE=99203457; PubMed=10102990;
 RA Mitsui S., Tsuruoka N., Yamashiro K., Nakazato H., Yamaguchi N.;
 RT "A novel form of human neurepsin, a brain-related serine protease, is
 generated by alternative splicing and is expressed preferentially in
 human adult brain.";
 RL Eur. J. Biochem. 260:627-634(1999).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE-Ovary;
 RX MEDLINE=99413504; PubMed=10485494;
 RA Underwood L.J., Tanimoto H., Wang Y., Shigemasa K., Parmley T.H.,
 O'Brien T.J.;
 RT "Cloning of tumor-associated differentially expressed gene-14, a novel
 serine protease overexpressed by ovarian carcinoma.";
 RL Cancer Res. 59:4435-4439(1999).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Gan L., Gelinas R., Gown A.M., Moss P., Smith R., Wang K.;
 RT "Molecular cloning and characterization of a novel serine protease,
 ovacin, a potential molecular marker for ovarian carcinomas.";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=20510030; PubMed=11054574;
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
 Moss P., Paepker B., Wang K.;
 RT "Sequencing and expression analysis of the serine protease gene
 cluster located in chromosome 19q13 region.";
 RL Gene 257:119-130(2000).
 RN [6]
 RP SEQUENCE OF 1-164 FROM N.A. (ISOFORM 1).
 RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
 Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
 Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Barnes J.,
 Dangnan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
 Andreise T., Frankel M., Attix C., Amico-Keller G., Cosfield J.,
 Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
 Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 Olsen A.S., Carraro A.V.;
 RT "Sequence analysis of chromosome 19q13.4.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: SUGGESTED TO BE INVOLVED IN KINDLING EPILEPTOGENESIS AND
 HIPPOCAMPAL PLASTICITY.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms-2;
 CC Name-1;
 CC IsoId-060259-1; Sequence-Displayed;
 CC Name-2;
 CC IsoId-060259-2; Sequence-VSP_005401;
 CC -1- TISSUE SPECIFICITY: ISOFORM 1 IS PREDOMINANTLY EXPRESSED IN THE
 PANCREAS WHILE ISOFORM 2 IS EXPRESSED IN ADULT BRAIN AND
 HIPPOCAMPUS. BOTH FORMS ARE ALSO FOUND IN FETAL BRAIN AND
 PLACENTA. NOT DETECTED IN KIDNEY, SPLEEN, LIVER AND LUNG.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALIKREIN SUBFAMILY.
 CC -----
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CC -----
DR EMBL: AF15024; AAD26425.2; -.
DR EMBL: AC011473; AAG23259.1; -.
DR EMBL: AL050220; CAB43320.1; ALT_INIT.
DR HSSP: P00763; IDPO.
DR MEROPS: S01.306; -.
DR Genew: HGNC:6361; KLK13.
DR MIM: 605505; -.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0006508; P:proteolysis and peptidolysis; NAS.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin; 1.
DR SMART: SM00240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; 1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
KM Hydrolyse: Serine protease; Glycoprotein; Signal.
FT SIGNAL: 1
FT CHAIN: 17 277
FT ACT_SITE: 76 76 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE: 124 124 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE: 218 218 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID: 42 178 BY SIMILARITY.
FT DISULFID: 51 77 BY SIMILARITY.
FT DISULFID: 157 224 BY SIMILARITY.
FT DISULFID: 189 203 BY SIMILARITY.
FT DISULFID: 214 239 BY SIMILARITY.
FT CARBOHYD: 30 30 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD: 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT: 170 180 VNPPTLOCAN -> GMPHPRPEAP (IN REF. 3).
SQ SEQUENCE 277 AA; 30570 MW; BA8A9B8DCFB5D542 CRC64;

Alignment Scores:
Pred. No.: 3.45e-40 Length: 277
Score: 677.50 Matches: 120
Percent Similarity: 71.56% Conservative: 41
Best Local Similarity: 53.33% Mismatches: 63
Query Match: 53.14% Indels: 1
DB: 1 Gaps: 1

US-09-856-320a-1_COPY_272_958 (1-687) x KLRD_HUMAN (1-277)
OY 10 GGGTTCGAGTCAAGCCCTACCTCCAGCCCTGGCAGGCGAGCCCTTTCCAGAGACGGCG 69
DB 39 GLYTYRHCysPheProHisSerGlnProTrpGlnAlaIleuLeuValGlnIleuArg 58
OY 70 CTACTCTGTGGGGGAGCCCTATGCGCCCGAGATGGCTCCGACAGCGCCCATGCTGC 129
DB 59 LeuLeuGlyGlyValLeuValHisProLysTrpValIleuThrAlaIleHisCysLeu 78
OY 130 AAGCCCGCCTACATAGTTCACCTGGGGGAGCGCAACCTCCAGAGGAGGAGGCTGTAG 189
DB 79 LysGlnGlyLeuLysValTYRLeuGlyHisAlaLeuGlyAlaGlyValGlnIleu 98
OY 190 CAGACCCGAGACGCACTAGTCTCCCTCCACCCCGGCTTCAACACAGCCCTCCCAAC 249
DB 99 GlnValArgGlnValAlaValHisSerIleProHisProGlnIleuArgArgSerProThrHis 118
OY 250 AAGACACCGCAATGACATGCTGTGTAAGATGATGATGATGATGATGATGATGATGATG 309
DB 119 LeuHisHisAspHisAspIleMetLeuGlnLeuGlnSerProValGlnLeuThrGly 138
OY 310 GCTGGGAGCCCTCACCCCTCC--TCACGCTGTGTACCTGGTGGGACACAGCTGCCTC 366
DB: 1 Gaps: 1

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DB 139 TYRILEGlnThrLeuProLeuSerHisAsnAsnArgLeuThrProGlyThrThrCysArg 158
OY 367 ATTCGCGCTGGGGCAGACGTCACGCCCGCAGTACGCTCTCACACCTTGGGATGC 426
DB 159 ValSerGlyTrpGlyThrThrThrSerProGlnValAsnTYRProLysThrLeuGlnCys 178
OY 427 GCCAACATCACCATCATTTGATGAGCACGACGAGAGTGTGAAAGCCCTACCCCGGCAACATCA 486
DB 179 AlaAsnIleGlnLeuArgSerAspGlnIleCysArgGlnValTYRProGlyLysIleThr 198
OY 487 CACACCATGCTGTGTGCCACGCTGCAGACGAGGGGGCAGAGACTCTCTGCCAGGTATCC 546
DB 199 AspaSerMetLeuCysAlaGlyThrIleLysGlnGlyLysAspSerCysGlnIleLysPser 218
OY 547 GGGGCGCTCTGTGTGTATACCAAGCTGTCTCAAGGCAATATCTCTGGGGCCAGGATCCG 606
DB 219 GlyGlyProLeuValCysAsnArgThrLeuTYRLeuValIleValSerTrpGlyAspPhePro 238
OY 607 TGTGCGATCACCCGAAAGCTGTGTCTACACGAAAGTCTGCAAAATATGTGATGATGATC 666
DB 239 CysGlyGlnProAspArgProGlyValTYRThrArgValSerArgTYRValLeuTrpIle 258
OY 667 CAGGAGAGGATGAAG 681
DB 259 ArgGlnThrIleArg 263

RESULT 8
KLR5_HUMAN
ID KLR5_HUMAN STANDARD; PRT; 293 AA.
AC Q9Y337; Q9HBG8;
DT 16-OCT-2001 (rel. 40, Created)
DT 16-OCT-2001 (rel. 40, Last sequence update)
DT 15-SEP-2003 (rel. 42, Last annotation update)
DE Kallikrein 5 precursor (EC 3.4.21.-) (Stratum corneum tryptic enzyme)
GN (Kallikrein-like protein 2) (KLK-L2).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Stratum corneum;
RC MEDLINE=99445563; PubMed=10514489;
RA Brattsand M., Egeblad T.;
RT "Purification, molecular cloning, and expression of a human stratum
RT corneum trypsin-like serine protease with possible function in
RT desquamation.";
RL J. Biol. Chem. 274:30033-30040(1999).
RN [2]
RP TISSUE=Stratum corneum;
RC MEDLINE=20118156; PubMed=10652563;
RA Yousef G.M., Luo L.-Y., Diamandis E.P.;
RT "Identification of novel human kallikrein-like genes on chromosome
RT 19q13.3-q13.4.";
RL Anticancer Res. 19:2843-2852(1999).
RN [3]
RP TISSUE=Stratum corneum;
RC MEDLINE=20510030; PubMed=11054574;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McQuaig J.,
RA Moss P., Faerber B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region.";
RL Gene 257:119-130(2000).
RN [4]
RP TISSUE=Ovary;
RC MEDLINE=22388257; PubMed=12477932;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dlatchenko L., Marusina K., Farmer A.A., Rudin G.M., Hong L.,

```

RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carinici P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
RA	Boask S.A., McKernan K.J., Malek J.A., Gurnatratte P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shvachenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Meers R.M.,		
RA	Butterfield V.S.N., Krzywinski M.T., Skalska U., Smallus D.E.,		
RA	Scherch A., Schein J.E., Jones S.J.W., Marra M.A.,		
RT	Generation and initial analysis of more than 15,000 full-length		
RT	human and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
CC	-1- FUNCTION: MAY BE INVOLVED IN DESQUAMATION.		
CC	-1- SUBCELLULAR LOCATION: Secreted.		
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN SKIN, BREAST, BRAIN AND TESTIS.		
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.		
CC			
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CC	-----		
DR	EMBL, AF168768; AAF03101.1; -		
DR	EMBL, AF135028; AAD26429.1; -		
DR	EMBL, AF243527; AAG33358.1; -		
DR	EMBL, BC008036; AAH08036.1; -		
DR	HSSP: P00763; IDPO.		
DR	MEROPS: S01.017; -		
DR	GeneW: HGNC:6366; KLU5.		
DR	MIM: 605643; -		
DR	GO: GO:0005615; C:extracellular space; TAS.		
DR	GO: GO:0008544; P:epidermal differentiation; TAS.		
DR	GO: GO:0006508; P:proteolysis and peptidolysis; NAS.		
DR	InterPro: IPR001314; Chymotrypsin.		
DR	InterPro: IPR001254; Ser_protease_Try.		
DR	Pfam: PF000089; trypsin; 1.		
DR	PRINTS: PR00722; CHYMOTRYPSIN.		
DR	SMART: SMO0020; Tryp_Spc: 1.		
DR	PROSITE: PS50240; TRYPSIN_DOM: 1.		
DR	PROSITE: PS00134; TRYPSIN_HIS: 1.		
DR	PROSITE: PS00135; TRYPSIN_SER: 1.		
KW	Hydrolase; Serine protease; Glycoprotein; signal.		
FT	SIGNAL	1	22
FT	CHAIN	23	293
FT	ACT_SITE	108	108
FT	ACT_SITE	153	153
FT	ACT_SITE	245	245
FT	DISULFID	73	206
FT	DISULFID	93	109
FT	DISULFID	178	279
FT	DISULFID	185	251
FT	DISULFID	217	231
FT	DISULFID	241	266
FT	CARBOHD	69	69
FT	CARBOHD	173	173
FT	CARBOHD	208	208
FT	CARBOHD	252	252
FT	CONFLICT	25	56
SE	SEQUENCE	293 AA; 32020 MW; D92C92F5609E5946 CMC64;	
Alignment Scores:			
Pred. NO.:	6.97e-38	Length:	293
Score:	644.50	Matches:	117
Percent Similarity:	67.97%	Conservative:	40
Best Local Similarity:	50.65%	Mismatches:	67
Query Match:	50.55%	Indels:	7
DB:	1	Gaps:	4

RX MEDLINE=21250997; PubMed=11352573;
RA Hooper J.D., Bul L.T., Rae F.K., Harvey T.J., Myers S.A.,
RA Ashworth L.K., Clements J.A.;
RT "Identification and characterization of KLK14, a novel kallikrein
RT serine protease gene located on human chromosome 19q13.4 and expressed
RT in prostate and skeletal muscle.";
RL Genomics 73:117-122(2001).
[3]
RM SEQUENCE FROM N.A.
RP Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
RA Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Ganes J.,
RA Dargatzis T., Frankheim M., Atlix C., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
RA Ariellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carrano A.V.;
RT "Sequence analysis of chromosome 19q13.4.";
RL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.
[4]
RM TISSUE SPECIFICITY.
RP MEDLINE=20545474; PubMed=10969073;
RA Harvey T.J., Hooper J.D., Myers S.A., Stephenson S.A., Ashworth L.K.,
RA Clements J.A.;
RT "Tissue-specific expression patterns and fine mapping of the human
RT kallikrein (KLK) locus on proximal 19q13.4.";
RL J. Biol. Chem. 275:37397-37406(2000).
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN, BONE MARROW AND
CC FETAL LIVER. ALSO EXPRESSED IN LIVER, PANCREAS, FETAL SPLEEN,
CC PROSTATE AND SKELETAL MUSCLE.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF161221; AAD50773.2; -
DR EMBL: AF283669; AAK48523.1; -
DR EMBL: AF283670; AAK48524.1; -
DR EMBL: AC011473; AAG23260.1; -
DR HSSP: P00763; IDPO.
DR MEROPS: S01.029; -
DR Genew: HGNC:6362; KLK14.
DR MIM: 606135; -
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0006508; P:proteolysis and peptidolysis; NAS.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYP_Spe; 1.
DR PROSITE: PS0240; TRYP_SIN_DOM; 1.
DR PROSITE: PS00134; TRYP_SIN_HIS; 1.
DR PROSITE: PS00135; TRYP_SIN_SER; 1.
KM Hydrolyase: Serine protease; Signal: Zymogen.
FT SIGNAL 18
FT PROPEP 19
FT CHAIN 24
FT ACT_SITE 25
FT ACT_SITE 67
FT ACT_SITE 111
FT ACT_SITE 204
FT DISULFD 31
FT DISULFD 52
FT DISULFD 143
FT DISULFD 175
FT DISULFD 200
FT SEQUENCE 251 AA; 27452 MW; 9087953BAFA7ED25 CRC64;

Alignment Scores:
Pred. No.: 3,046-36 Length: 251
Score: 621.00 Matches: 113
Percent Similarity: 65.22% Conservative: 37
Best Local Similarity: 49.13% Mismatches: 74
Query Match: 48.71% Indels: 6
Gaps: 2
US-09-856-320a-1_copy_272_958 (1-687) x KLKc_HUMAN (1-251)
QY 1 AATCAAGAGGGGTGGAGTGAAGAGGCTGACCTCCGAGCCCTGGACAGGACGCTGTC--- 57
DB 25 IITIEGLYGLYHISThrcysthrArgserSerGlnProTrpGlnAlaIleuLeuAla 44
QY 58 --GAGAGAGCCGCTACTGTGTGGGCGAGCGCTATGCGCCGAGATGGCTGCTGACA 114
DB 45 GLYProArgArgArgPheIleuysGlyGlyAlaIleuLeuSerGlyGlnTrpAlaIleu 64
QY 115 GCAGCCCACTGCTGAGAGCCCGCTATGATGTTCACTGGGGGAGCAGACAGCTCAGAG 174
DB 65 AAlaIleHIScysGlyArgProIleuGlnValAlaIleuGlyHISAsnIleuArg 84
QY 175 GAGGAGGGCTGAGACAGACCCGAGACGCACTGACCTGCTCCGAGCCGCTGCTGAC 234
DB 85 TrpGlnAlaTrpGlnGlnValIleuArgValAlaArgGlnValTrpHisProAsnTrp 104
QY 235 AACAGCCTCCCAACAGACAGCCGATGATGATGATGATGATGATGATGATGATGATG 294
DB 105 -----SerArgThrHisAspAsnAspMetIleuGlnIleuGlnIleuPro 120
QY 295 GTTCATCATCCTGGCTGGCTGGAGCCCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTG 354
DB 121 AAlaArgIleGlyArgAlaValArgProIleuGlnValTrpGlnAlaCysAlaSerPro 140
QY 355 ACGAGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 414
DB 141 ThrSerCysAlaGValSerGlyTrpGlyTrpIleSerProIleAlaArgTrpAla 160
QY 415 ACCTGTCATGAGCCGACATGATGATGATGATGATGATGATGATGATGATGATGATG 474
DB 161 SerIleuGlnCysValAsnIleAsnIleSerProAspGlnValCysGlnIleAlaTrp 180
QY 475 GGCACATCATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 534
DB 181 ArgThrIleThrProGlyMetValCysAlaGlyValProGlnGlyGlyAspSerCys 200
QY 535 CAGGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 594
DB 201 GlnGlyAspSerGlyGlyProIleuValCysArgGlyGlnIleuGlnGlyIleuValSer 220
QY 595 GCGCAGATCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 654
DB 221 GlyMetGlnuArgCysAlaIleuProGlyTrpProGlyValIleTrpAsnIleuCysIle 240
QY 655 GTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 684
DB 241 ArgSerTrpIleGlnGlnIleuTrpMetArgasp 250
RESULT 10
ID KLKc_HUMAN STANDARD: PRT: 248 AA.
AC Q9QKR0; Q9QKR1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kallikrein 12 precursor (EC 3.4.21.-) (kallikrein-like protein 5)
DE (KLK-15)
GN KLK12 OR KLK15.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]


```

Db 205 G1YLYSPHRYCYSGLYSPERG1YGLYPROLEULECYSAANG1YVALLAUG1N 224
QY 580 GGCATATTCCTCTGGGCGCCAGATCCGTGCGCATCCGGAAGCCTGGTGTACAG 639
Db 225 G1YLYHRSERTTGPGLYPHENASPR0CGLYGLU1YPROLYSPROG1YI1ETRYTHR 244
QY 640 AAGCTGCAATATGTGACATCGATCCAGAGACGATGAACAACAT 687
Db 245 LYSLEULELYSPHERNTRPTTRP1LELYSG1VALMELYSGLUASN 260

RESULT 12
KLK7_RAT STANDARD; PRT: 261 AA.
AC P36373;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Glandular kallikrein 7, submandibular/renal precursor (RC 3.4.21.35)
DE (tissue kallikrein) (RCK-7) (RSK-7) (Asterase B) (Proteinase A).
DE KLK7 OR KLK-7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89088074; PubMed=2849988;
RA Chen Y.-P., Chao J., Chao L.;
RT "Molecular cloning and characterization of two rat renal kallikrein
RT genes.";
RL Biochemistry 27:7189-7196(1988).
RN [2]
RP SEQUENCE OF 25-75.
RC TISSUE-Submaxillary gland;
RX MEDLINE=88198057; PubMed=3482210;
RA Kato H., Nakanishi E., Enjyoji K., Hayashi I., Oh-Ishi S., Iwanaga S.;
RT "Characterization of serine proteinases isolated from rat
RT submaxillary gland: with special reference to the degradation of rat
RT kininogens by these enzymes.";
RL J. Biochem. 102:1389-1404(1987).
CC -1- FUNCTION: GLANDULAR KALLIKREINS CLEAVE MET-LYS AND ARG-SER BONDS
CC IN KININOGEN TO RELEASE LYS-BRADYKININ.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage of Arg-I-Xaa bonds in
CC small molecule substrates. Highly selective action to release
CC kallidin (lysyl-bradykinin) from kininogen involves hydrolysis of
CC Met-I-Xaa or Leu-I-Xaa.
CC -1- TISSUE SPECIFICITY: KIDNEY AND SUBMANDIBULAR GLAND.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
CC
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CC
CC EMBL: M19647; AAA41461.1; -.
CC PIR: A31136; A31136.
CC HSSP: P00759; ITON.
CC MEROPS: S01.406; -.
CC InterPro: IPR001254; Ser_protease_Try.
CC Pfam: PF000089; trypsin.1.
CC SMART: SM00020; TRYP_SPC.1.
CC PROSITE: PSS0240; TRYP_SIN_DOM.1.
CC PROSITE: PS00134; TRYP_SIN_HIS.1.
CC PROSITE: PS00135; TRYP_SIN_SER.1.
CC Hydrolyse: Serine protease; Glycoprotein; Multigene family; Zymogen;
CC Signal.
KM
FT SIGNAL.
FT PROPEP 1 18 PROBABLE.
FT PROPEP 19 24 ACTIVATION PEPTIDE (PROBABLE).
FT CHAIN 25 261 GLANDULAR KALLIKREIN 7,

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FT ACT_SITE 65 65 SUBMANDIBULAR/RENAL.
FT ACT_SITE 120 120 CHANGE RELAY SYSTEM.
FT ACT_SITE 213 213 CHANGE RELAY SYSTEM.
FT ACT_SITE 31 173 CHARGE RELAY SYSTEM.
FT DISULFID 50 66 BY SIMILARITY.
FT DISULFID 152 219 BY SIMILARITY.
FT DISULFID 184 198 BY SIMILARITY.
FT DISULFID 209 234 BY SIMILARITY.
FT CARBOHYD 108 108 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 35 35 S -> D (IN REF. 2).
FT CONFLICT 46 46 F -> S (IN REF. 2).
SO SEQUENCE 261 AA; 28972 MW; 4FB06C422F25AF16 CRC64;

Alignment Scores:
Pred. No.: 8,21e-35 Length: 261
Score: 600.50 Matches: 109
Percent Similarity: 62.71% Conservative: 39
Best Local Similarity: 46.19% Mismatches: 81
Query Match: 47.10% Indels: 7
DB: 1 Gaps: 1

US-09-856-320A-1_COPY_272_958 (1-687) x KLK7_RAT (1-261)
QY 1 ATCATCAAGGGGTTTCAGTGCAGAGCTCCAGCCCTGGCAGCAGCCCTGTTTCAG 60
Db 25 VALLIEGLYLYTYR1YLYSCYSGL1YVANSERGLNPR0TRPGL1VAL1AL1EUYR5ER 44
QY 61 AAGAGGGGCTACCTGTGGGGGAGCCGATCGCCCGGAGAGGCTTCGACAGCAGC 120
Db 45 PHERTHYRSTYR1EUCYSGLYGLYVALL1EULE1SPROSERTRPVALL1ETR1AL1A1A 64
QY 121 CACTGCTCAAGCCCGCCCTACATAGTTCACCTGGGCGACAGCAACCTCCAGAGGAGAG 180
Db 65 H1EYSER1SER1ASN1EYR1GLN1VAL1TR1EUL1CYL1R1G1NSH1N1LEU1GLU1ASP1GLU 84
QY 181 GCGCTGACAGACAGCCCGACAGCCAGCTGAGTCTCTCCCGCCAGCCCGGCTTCAACAGC 240
Db 85 PROPH1EAL1AG1N1H1S1ARG1EVAL1SER1GLN1SER1PHE1PRO1H1S1PRO1PHE 104
QY 241 CTC-----CCCAACAAAGACACCGCATGATGATCATCATGCTGTG 279
Db 105 LEU1MET1ARG1ASN1H1STR1ARG1LYSPROG1LYASP1SPH1S1ERN1ASN1LEU1LEU 124
QY 280 AAGATGCAATCGCCAGTCTCCATCATCCTGGGCTGGGAGCCCTACCTCTCTCAGC 339
Db 125 H1S1EUS1ERG1N1PRO1ALA1SP1LET1H1R1ASP1LY1VAL1LYS1VALL1EASP1LEU1PRO1H1GLU 144
QY 340 TGTGTCACTGCTGGCAGCCAGCTGCTCATTTCCGGCTGGGCGACAGCAGTCCAGCCCGCAG 399
Db 145 GLU1PROLYS1VAL1GLY1SER1H1R1CY1LEU1AL1AS1ER1GLY1TRP1LYS1ERT1H1R1LYS1PROLEU1LE 164
QY 400 TTRACGCTGGCTCACCACCTTGCCATGGCGCAACATACATCATGATGACACAGCAAGT 459
Db 165 TRP1GLU1PHE1PRO1ASP1ASP1LEU1GLN1CY1S1VAL1ASN1H1S1EUS1EUS1ERN1GLU1LYS1CY1S 184
QY 460 GAGAACCCCTACCCCGGCAATCATCATCAGACACCATGTTGTGTGGCAGCGTGCAGAGAGG 519
Db 185 I1E1LYS1AL1AR1YR1YS1GLU1LYS1VAL1TH1R1ASP1LEU1MET1EUCYS1AL1AG1LY1LEU1GLU1GLY 204
QY 520 GGCAGAGCATCTGCCAGGCTGACTCGGGGCGCTGTGCTGTGATACAGTCTTCAA 579
Db 205 G1YLYSPHRYCYSGLYSPERG1YGLYPROLEULECYSAANG1YVALLAUG1N 224
QY 580 GGCATATTCCTCTGGGCGCCAGATCCGTGCGCATCCGGAAGCCTGGTGTACAG 639
Db 225 G1YLYHRSERTTGPGLYPHENASPR0CGLYGLU1YPROLYSPROG1YI1ETRYTHR 244
QY 640 AAGCTGCAATATGTGACATCGATCCAGAGACGATGAACAACAT 687
Db 245 LYSLEULELYSPHERNTRPTTRP1LELYSG1VALMELYSGLUASN 260

RESULT 13

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KLK3_MOUSE STANDARD: PRT: 261 AA.
 ID KLK3_MOUSE
 AC P00756;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glutathione S-transferase K3 precursor (EC 3.4.21.35) (Tissue kallikrein)
 DE (mck-3) (7S nerve growth factor gamma chain) (gamma-NGF).
 GN KLK3 OR KLK-3 OR NGF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclerogathi; Muridae; Murinae; Mus.
 OX NCBI-TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=85076169; PubMed=6548955;
 RA Ullrich A., Gray A., Wood W.I., Hayflick J., Seeburg P.H.;
 RT "Isolation of a cDNA clone coding for the gamma-subunit of mouse
 RT nerve growth factor using a high-stringency selection procedure.";
 RL DNA 3:387-392(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=85257431; PubMed=3848399;
 RA Evans B.A., Richards R.I.;
 RT "Genes for the alpha and gamma subunits of mouse nerve growth factor
 RT are contiguous.";
 RL EMBO J. 4:133-138(1985).
 RN [3]
 RP SEQUENCE OF 25-261.
 RA MEDLINE=81264363; PubMed=7263706;
 RA Thomas K.A., Baglan N.C., Bradshaw R.A.;
 RT "The amino acid sequence of the gamma-subunit of mouse submaxillary
 RT gland 7 S nerve growth factor.";
 RL J. Biol. Chem. 256:9156-9166(1981).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (3.15 ANGSTROMS) OF 7S COMPLEX.
 RA STRAIN-Swiss Webster; TISSUE-Submaxillary gland;
 RA MEDLINE=96035451; PubMed=9351801;
 RA Bax B., Blundell T.L., Murray-Rust J., McDonald N.O.;
 RT "Structure of mouse 7S NGF: a complex of nerve growth factor with
 RT four binding proteins.";
 RL Structure 5:1275-1285(1997).
 CC -1- FUNCTION: 7S NGF ALPHA CHAIN STABILIZES THE 7S COMPLEX. THE BETA
 CC DIMER PROMOTES NEURITE GROWTH. THE GAMMA CHAIN IS AN ARGININE-
 CC SPECIFIC PROTEASE; IT MAY ALSO HAVE PLASMINOGEN ACTIVATOR
 CC ACTIVITY, AS WELL AS MITOGENIC ACTIVITY FOR CHICK EMBRYO
 CC FIBROBLASTS.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage of Arg-|-Xaa bonds in
 CC small molecule substrates. Highly selective action to release
 CC kallidin (Lysyl-bradykinin) from kininogen involves hydrolysis of
 CC Met-|-Xaa or Leu-|-Xaa.
 CC -1- SUBUNIT: 7S NERVE GROWTH FACTOR IS COMPOSED OF TWO ALPHA CHAINS,
 CC A BETA DIMER COMPOSED OF IDENTICAL CHAINS, AND TWO GAMMA CHAINS.
 CC -1- MISCELLANEOUS: THIS PRECURSOR IS CLEAVED INTO SEGMENTS TO PRODUCE
 CC THE ACTIVE FORM OF THE GAMMA CHAIN, WHICH OCCURS NATURALLY AS
 CC COMBINATIONS OF EITHER TWO OR THREE SEGMENTS HELD TOGETHER BY
 CC DISULFIDE BONDS: B1 + A OR B1 + C + B2.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUPERFAMILY.
 CC -----
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 CC -----
 CC EMBL; X01389; CAA25645.1; -
 CC EMBL; X01798; CAA25928.1; -
 CC EMBL; X01799; CAA25930.1; -
 CC PIR; A91005; NGSMS.
 CC PDB; 1SGF; 27-MAY-98.
 CC MEROPS; S01.170; -.

DR MGD; MGI:97322; Ngfg.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00089; trypsin; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Serine protease; Glycoprotein; Multigene family; Zymogen;
 KW Signal; Growth factor; 3D-structure.
 FT SIGNAL 1
 FT PROPEP 19 18
 FT CHAIN 25 24
 FT CHAIN 25 261
 FT CHAIN 112 261
 FT ACT_SITE 65 65
 FT ACT_SITE 120 120
 FT ACT_SITE 213 213
 FT DISULFID 31 173
 FT DISULFID 50 66
 FT DISULFID 152 219
 FT DISULFID 184 198
 FT DISULFID 209 234
 FT CARBOHD 102 102
 FT DOMAIN 25 107
 FT DOMAIN 112 261
 FT DOMAIN 165 261
 FT DOMAIN 108 111
 FT CONFLICT 26 26
 FT STRAND 29 30
 FT STRAND 33 35
 FT HELIX 37 38
 FT TURN 39 44
 FT TURN 45 46
 FT TURN 47 56
 FT TURN 57 58
 FT STRAND 59 62
 FT STRAND 62 66
 FT HELIX 72 75
 FT STRAND 79 79
 FT STRAND 80 81
 FT TURN 85 86
 FT TURN 88 97
 FT STRAND 99 100
 FT TURN 103 105
 FT HELIX 118 119
 FT TURN 122 126
 FT TURN 148 149
 FT STRAND 151 156
 FT STRAND 159 159
 FT STRAND 167 167
 FT STRAND 170 170
 FT STRAND 172 179
 FT HELIX 181 187
 FT TURN 194 195
 FT STRAND 196 200
 FT STRAND 207 207
 FT TURN 210 211
 FT TURN 213 214
 FT STRAND 216 219
 FT TURN 220 221
 FT STRAND 222 229
 FT TURN 234 235
 FT TURN 237 238
 FT STRAND 241 245
 FT HELIX 246 249
 FT HELIX 250 258
 FT TURN 259 259

Alignment Scores: 261 AA; 28998 MM; 4870748E174AF7C8 CRC64;

Pred. No.: 1.83e-34 Length: 261
 Score: 595.50 Matches: 105

Percent Similarity: 63.988
 Best Local Similarity: 44.498
 Query Match: 46.718

Conservative: 46
 Mismatches: 78
 Indels: 7
 Caps: 1

US-09-856-320a-1_COPY_272_958 (1-687) x KLR3_MOUSE (1-261)

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QY 1 ATCATCAAGGGGTTTCAGAGCTCAAGCTCACTCCAGCCCTGGAGGAGGAGCCCTGTTCAG 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 25 ILevalGlyglPheylsCysglulysAsnserGlnProthrPhisValAlaValArg 44
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 AAGACGGGCTACTCTGTGGGGGAGGAGCCCTATGCCCCAGATGCGTCTTCAGAGAGCC 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 45 TyrthGlnTyrleucysGlyglValLeuLeuAspProasnTyrValLeuThrAlaAla 64
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGGAGCAGCAACCTCCAGAGAGAG 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 65 HisCysTyrAspAspAsnTyrIysValThrleuGlyIysAsnLeuPheIysAspGlu 84
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 GGCTGTGAGCAGACCCGGCAGCAGCAGCTGCTCCAGCCCGGGCTTCACACAGAGC 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 85 ProserAlaGlnHisArgPheValIserIysAlaIleProHisProGlyPheAsnMetSer 104
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 CTGCCCAACAA-----GACACCGCAATGACATCAGCTGTG 279
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 105 LeuMetCArgIysHisIleArgPheLeuGluTyrAspTyrSerAsnAspLeuMetLeu 124
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 280 AAGATGGCATGCGCAGTCTCATCATCAGCAGCTGGCTGGAGCCCTGCTCTCAGC 339
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 125 ArgIeuSerIysProAlaAspIleThrAspThrValIysProIleThrLeuProthGlu 144
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 340 TGCTGTACTCTGTGGCAGCAGCTGCTCATTCGCGCTGGGGAGCAGCTCCAGCCAG 399
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 145 GluProIysLeuIleIysSerThrCysLeuAlaSerGlyTyrIleSerIleThrProthIys 164
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 400 TTAGCGCTGCTGCACACTGCGATGCGCAGATCCATCCATGTGAGCAGCAAGAGT 459
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 165 PheGlnPheThrAspAspLeuTyrCysValAsnLeuIysLeuProAsnGluAspCys 184
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 460 GAGAACCGCTACCCCGGCAACATCAGACAGCAGCTGTGTGCGCAGCTGAGAGAG 519
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 185 AlAlysAlaHisIleGluIysValThrAspAlaMetLeuIysAlaGlyIleMetAspGly 204
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 520 GGCAAGGACTCTCCGAGGCTGACTCGGGGCGCTGTGCTGTGTAACGACTCTTCA 579
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 205 GlyIysAspThrCysIysGlyAspSerGlyIleProIleIleCysAspGlyValLeuGln 224
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 580 GGCAATATCTCTGGGGCGCAGATCCGTGCGATCAGCCGAAAGCCTGTGTCTACAG 639
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 225 GlyIleThrSerThrProGlyIysThrProGlyGluProAspMetProGlyValTyrThr 244
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 640 AAGAGTGCATAATATGTGACTGATCCAGAGAGCAGTGAAGAACAT 687
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 245 IysLeuAsnIysPheThrSerThrIleIysAspThrMetAlaIysAsn 260
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 14

TRY3_CHICK STANDARD; PRT; 248 AA.

AC 090629;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, last sequence update)
 DT 28-FEB-2003 (Rel. 41, last annotation update)
 DE trypsin IT-P29 precursor (EC 3.4.21.4).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=95251611; PubMed=7733885;
 RA Wang K., Gan L., Lee I., Hood L.E.;

```

RT "Isolation and characterization of the chicken trypsinogen gene
  family.";
RL Blochem. J. 307:471-479(1995).
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-I-Xaa, Lys-I-Xaa.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: HIGH LEVELS ARE SEEN IN THE PANCREAS WHILE
  LOWER LEVELS ARE FOUND IN THE LIVER, SPLEEN AND THYMUS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -----
CC This SWISS-Prot entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL Outstation-
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (See http://www.isb.sib.ch/announce/
  or send an email to license@isb.sib.ch).
CC -----
DR EMBL: U15157; AAA79914.1; -.
DR PIR: S55066; S55066.
DR HSP: P00763; IDPO.
DR MEROPS: S01.151; -.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin_1.
DR SMART: SM00020; trypsin_SPC_1.
DR PROSITE: PS50240; TRYPSIN_DOM_1.
DR PROSITE: PS00134; TRYPSIN_HIS_1.
DR PROSITE: PS00135; TRYPSIN_SER_1.
DR HydroLase: Serine protease; Digestion; Pancreas; Zymogen; Signal;
  KM
KW Multigene family.
FT SIGNAL 1..16
FT PROPEP 17..25
FT CHAIN 26..248
FT ACT_SITE 65..65
FT ACT_SITE 109..109
FT ACT_SITE 202..202
FT DISULFID 32..162
FT DISULFID 50..66
FT DISULFID 134..235
FT DISULFID 141..208
FT DISULFID 173..187
FT DISULFID 198..222
FT SITE 196..196 REQUIRED FOR SPECIFICITY (BY SIMILARITY).
SQ SEQUENCE 248 AA; 26622 MW; ESE16B0762B588E CRC64;

Alignment Scores:
Pred. No.: 2.33e-34 Length: 248
Score: 594.00 Matches: 112
Percent Similarity: 65.048 Conservative: 35
Best Local Similarity: 49.568 Mismatches: 73
Query Match: 46.598 Indels: 6
DB: 1 Gaps: 3

US-09-856-320a-1_COPY_272_958 (1-687) x TRY3_CHICK (1-248)
QY 1 ATCATCAAGGGGTTTCAGAGCTCAAGCTCACTCCAGCCCTGGAGGAGGAGCCCTGTTCAG 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 26 ILevalGlyglYthrCysProGluHisSerValProIyrlnValSerLeu---Asn 44
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 AAGACGGGCTACTCTGTGGGGGAGGAGCCCTATGCCCCAGATGCGTCTTCAGAGAGCC 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 45 serGlyTyrHisIshPheYsglyglYserLeuIlaAsnserGlnTyrValLeuSerAlaAla 64
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGGAGCAGCAACCTCCAGAGAGAGAG 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 65 HisCysTyrIysSerArgIleGlnValArgleuGlyGluTyrAsnIleAspValGlnGlu 84
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 GGCTGTGAGCAGACCCGGCAGCAGCAGCTGCTCCAGCCCGGGCTTCACACAGAGC 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 85 AspserGluValAlaIysSerSerValIleIleArgHisProIysTyrSerIle 104
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 CTGCCCAACAAACACAGCAGATGACATCAGCTGTGTAAGTGGCATCCGAGTCTCC 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 105 ThrLeuAsn-----AsnAspIleMetLeuIleIysLeuAlaSerAlaValGlu 120

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OY 301 ATCAGCTGGCTGTCGACCCCTCAGCTCTCCACGCTGTGTCACGTGGACGAC 360
DB 121 TYSERIALASPILEGIPROILEALALEUPROSERSECYALALYALGLYTHRG 140
OY 361 TGCCCATTTCCGGCTGGGACGACGTCGACCCCGCATTAAGCCCTCCACACCTTG 420
DB 141 CYSLEUILESERGLYTRPGLYASMTHTLSEUSERASNGLYTYRASNTRYPROGLULEU 160
OY 421 CGATCGCCCAACATCCATTCATTTGAGCAGCAGAGATGTGAGAACCCCTACCCGCGAAC 480
DB 161 GINCYSLEUSANALAPROILEUSERSAPGNGIUCYSGINGUALATYTRPROGLYASP 180
OY 481 ATCAGACACACCATGCTGTGTCGACGCTGACGAGAGGGGCGAGAGACTCTCCAGGCT 540
DB 181 ILEHTSERASMETILECYVALGLYPHELEUGIUGIUGLYLYSASPSERCYSGINGLY 200
OY 541 GACATCCGGGGGGCCCTGCTGTACACAGTCTTCAGAGCATATATCTCCGGGGCCAG 600
DB 201 ASPSERGLYGLYPROVALCYASNGIYGLULEUGINGLYILEVALSERTRPGLYILE 220
OY 601 GATCCGTGCGATCAGACCCGGAAGCTGTGTCTACAGAAAGTCTGCAATATGTGAC 660
DB 221 GLY---CYSALALEULYSGLYTYRPROGLYVALTYRTHRLYSVALCYASNTYVALASP 239
OY 661 TGGATCCAGAGACGAGT 678
DB 240 TRPILEGINGIUTHTLLE 245

```

RESULT 15

KIKR_PRANA STANDARD; PRT; 263 AA.

```

AC P32824;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DR 01-NOV-1995 (Rel. 32, Last annotation update)
DE Glandular kallikrein, renal precursor (EC 3.4.21.35) (Tissue
  kallikrein).
OS Proum's natalensis (African soft-furred rat) (Mastomys natalensis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
OC Mastomys.
OC NCBI_TaxID=10112;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RX MEDLINE=94226702; PubMed=7909667;
RA Fahnestock M.;
RT "Characterization of kallikrein cDNAs from the African rodent
  Mastomys.";
RL DNA Cell Biol. 13:293-300(1994).
CC -1- FUNCTION: GLANDULAR KALLIKREINS CLEAVE MET-LYS AND ARG-SER BONDS
CC IN KININOMER TO RELEASE LYS-BRADYKININ.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage of Arg-|-Xaa bonds in
CC small molecule substrates. Highly selective action to release
CC kallidin (Lysyl-bradykinin) from kininogen involves hydrolysis of
CC Met-|-Xaa or Leu-|-Xaa.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL, X17352; CA35232.1; -.
DR PIR, I83227; S15686.
DR HSSP, P00757; 1SGF.
DR MEROPS, S01.160; -.
DR InterPro, IPR001254; Ser_protease_Try.
DR Pfam, PF00089; trypsin; I.

```

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DR SMART; SM00020; TRY_P_SPC; 1.
DR PROSITE; P550240; TRYP_SIN_DOM; 1.
DR PROSITE; P500134; TRYP_SIN_HIS; 1.
DR PROSITE; P500135; TRYP_SIN_SER; 1.
KM Hydrolyse: Serine protease; Glycoprotein; Multigene family; Zymogen;
KW Signal.
FT SIGNAL 1 18 PROBABLE.
FT PROPEP 19 24 ACTIVATION PEPTIDE (PROBABLE).
FT CHAIN 25 263 GLANDULAR KALLIKREIN, RENAL.
FT ACT_SITE 65 65 CHARGE RELAY SYSTEM.
FT ACT_SITE 121 121 CHARGE RELAY SYSTEM.
FT ACT_SITE 215 215 CHARGE RELAY SYSTEM.
FT DISULFID 31 175 BY SIMILARITY.
FT DISULFID 50 66 BY SIMILARITY.
FT DISULFID 153 221 BY SIMILARITY.
FT DISULFID 186 200 BY SIMILARITY.
FT DISULFID 211 236 BY SIMILARITY.
FT CARBOHD 102 102 N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE 263 AA; 29130 MW; ABB8023BB00337D5 CRC64;

```

Alignment Scores:

Pred. No.:	3,49e-34	Length:	263
Score:	591.50	Matches:	106
Percent Similarity:	63.03%	Conservative:	44
Best Local Similarity:	44.54%	Mismatches:	79
Query Match:	46.39%	Indels:	9
DB:	1	Gaps:	2

US-09-856-320a-1_copy_272_958 (1-687) x KIKR_PRANA (1-263)

```

OY 1 ATCATCAAGGGGCTTGCAGTGCAGGCTCCACGCTGCGAGGACGACCCCTGTCGAG 60
DB 25 ILEILEGLYGLYPHEASNCYSGIULYASNSERGINPROTRPHISVALALVALTYLARG 44
OY 61 AAGACGGGCTACCTGTGGGGGCGAGCTATCGGCCCCAATAGGCTCTGACAGACCC 120
DB 45 PHEALATGYTGLINCYSGLYLYVALLEUUSPALAASNTYVALLEUTHALALA 64
OY 121 CACTGCTCAAGCCCGCTCATATGATTCACCTGGGGGAGCAGCAACCTTCAGAGAGGAG 180
DB 65 HISCTGYRANAPRYLTGTGLVALTRPLEUGLYLSANANAPRGPHGLIUSPOLU 84
OY 181 GCGTGTGACAGACCCGAGCAGCAGCTGAGTCCCTCCGCCACCCCGGCTTCAACAGAC 240
DB 85 PROSERALAGINHSINLEUILESERLYSALATLEPROHISPROGLYPHEASNMETSER 104
OY 241 CTCGCCAANAGAACAC-----CGCAATGACATCATGCTG 276
DB 105 LEUENASNLYSASPHISTHTRPROHISPROGLIUSPASYRYSERASNAASPLEUMETHEU 124
OY 277 GTGAAGATGCGATCGCCAGCTCCATCATCTGAGCTGGGCGAGCCCGCTACCGCTCCCA 336
DB 125 VALARGLEULYSYRPROIAGIULIETHRSPALVALIYSRPOIILASPLEUPROTHR 144
OY 337 CGGTGTGCACTGTGCGACAGCAGCTGCTCATTTCCGGCTGGGCGAGCAGCTCC--AGC 393
DB 145 GLIULUPROTHRVALGYSERARGCYALEULASERGLYTRPGLYSERTHTRPROTHR 164
OY 394 CCCAGTTACGCCCTGCCACACACTTGGAGATGGCGCAACATCACATCATATGACACAG 453
DB 165 GIULIUPHEGLIUTYRSEHNISASPLEULINCYSVALIUTYLEULIULENLESEASGLU 184
OY 454 AAGTGTGAGACGCGCTACCGCGGAGCAATCAGACAGACATGATGTTGGCGAGGTGAG 513
DB 185 VALYSALALYSALAHISTHGLIULYSVALTHRSPRTHMETLEUCYVALIGLYMET 204
OY 514 GAAGGGGCAAGAGACTCTGCGACAGGTACTCCGGGGCCCTGTGCTGTACACCACTCT 573
DB 205 ASPGLYGLYLSASPRTHCYVALIGLYASPERGLYGLYPROLEUILECYASPGLYVAL 224
OY 574 CTTCAAGGCATTAATCTCTGGGGCCAGAGATCCGCTGTCGATCACCCGAAGCCGTGCTC 633
DB 225 LEUGINGLYIETHRSETTRPGLYPROTHRPROHISALALEUPROASNAVALPROGLYILE 244

```

QY 634 TACACGAAAGTCTGCAAAATATGTGACTGGATCCAGGAGACGATGAGAACAAAT 687
|||||
:::
Db 245 TTTThrLysLeuIleGIuTYrArgSerTrpIleLysAspValMetAlaAsnAsn 262
|||||
:::
|||

Search completed: October 15, 2003, 20:20:58
Job time : 15.0583 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus.n2p model

Run on: October 15, 2003, 20:04:15 ; Search time 18.8338 Seconds
(without alignments)
7015.902 Million cell updates/sec

Title: US-09-856-320A-1_COPY-272_958
Perfect score: 1275
Sequence: 1 atcctcaaggaggttcagtg.....aggagacgtatgaagacaat 687

Scoring table: BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 566616

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-O/cgn2.1/USPTO.spool.p/US09856320/r/unat.15102003.105640.8549/app.query.fasta_1.2318
-DB=PIR.76 -QFWT=fastan -SUFFIX=prpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-NINITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdi -LIST=45
-DOCAIIGN=200 -THR.SCOR=pcpt -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09856320@cgn.1.1.74@runat.15102003.105640.8549 -NCPV=6 -ICPV=3
-NO_WMAP -LARGEBUFFER -NEG.SCOR=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR.76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	684	53.6	260 2	I56559 neuropsin - mouse
2	605.5	47.5	265 1	KORPT tissue kallikrein
3	600.5	47.1	261 2	A31136 tissue kallikrein
4	595.5	46.7	261 1	NGMSG 7S nerve growth fa
5	594	46.6	248 2	S55066 trypsin (EC 3.4.21
6	591.5	46.4	263 2	S15686 tissue kallikrein
7	591	46.4	246 1	TRRT2 trypsin (EC 3.4.21
8	588	46.1	238 2	S31779 trypsin (EC 3.4.21
9	587	46.0	246 1	TRRT1 trypsin (EC 3.4.21
10	585.5	45.9	261 2	A34079 tissue kallikrein
11	581.5	45.6	259 2	B31136 tissue kallikrein
12	578	45.3	232 1	KOPG tissue kallikrein
13	577.5	45.3	261 2	A29586 tissue kallikrein
14	577.5	45.3	261 2	A29745 tissue kallikrein

15	577	45.3	231 1	TRPCTR trypsin (EC 3.4.21
16	574.5	45.1	261 2	S45303 tissue kallikrein
17	571	44.8	246 2	B25528 trypsin (EC 3.4.21
18	568	44.5	247 1	TRDG trypsin (EC 3.4.21
19	567.5	44.5	259 1	KORPTN tonin (EC 3.4.21.-
20	565.5	44.4	261 2	A25606 tissue kallikrein
21	564.5	44.3	264 2	A44284 tissue kallikrein
22	564.5	44.3	261 1	KOMS1 tissue kallikrein
23	564	44.2	229 1	TRBOTR trypsin (EC 3.4.21
24	562	44.1	262 1	KOHU tissue kallikrein
25	560	43.9	248 2	S55067 trypsin (EC 3.4.21
26	556.5	43.6	257 2	S33772 tissue kallikrein
27	556.5	43.6	261 2	S01971 tissue kallikrein
28	556	43.6	243 2	A35871 trypsin (EC 3.4.21
29	556	43.6	247 2	S13813 trypsin (EC 3.4.21
30	553	43.4	247 2	A27547 trypsin (EC 3.4.21
31	552.5	43.3	231 2	S31778 trypsin (EC 3.4.21
32	552.5	43.3	247 2	S05494 trypsin (EC 3.4.21
33	552	43.3	256 1	NGMSA 7S nerve growth fa
34	551.5	43.3	239 2	A27207 tissue kallikrein
35	551.5	43.3	261 1	A32297 semenogelase (EC 3
36	550	43.1	246 1	TRDGC trypsin (EC 3.4.21
37	548.5	43.0	259 2	A29746 tissue kallikrein
38	548.5	43.0	261 1	S35711 semenogelase (EC 3
39	548.5	43.0	261 2	A41020 tissue kallikrein
40	546	42.8	253 2	A53968 serine proteinase
41	544.5	42.7	242 2	S31775 trypsin (EC 3.4.21
42	544.5	42.7	242 2	S49489 trypsin (EC 3.4.21
43	544.5	42.7	242 2	S31776 trypsin (EC 3.4.21
44	543.5	42.6	261 2	JE0236 tissue kallikrein
45	542.5	42.5	261 1	TRMSMS tissue kallikrein

ALIGNMENTS

RESULT 1
156539
neuropsin - mouse
C:Species: Mus musculus (house mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C:Accession: I56559
R:Chen, Z.L.; Yoshida, S.; Kato, K.; Momota, Y.; Suzuki, J.; Tanaka, T.; Ito, J.; Nis
J. Neurosci. 15, 5088-5097, 1995
A:Title: Expression and activity-dependent changes of a novel limbic-serine protease
A:Reference number: I56559; PMID:95348817; PMID:7623137
A:Accession: I56559
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-260 <RES>
A:Cross-references: GB:D30785; NID:91648847; PIDN:BAA06451.1; PID:91020091
C:Superfamily: trypsin; trypsin homology
F:33-252/Domain: trypsin homology <TRY>

Alignment Scores:

Pred. No.: 4.5e-42
Score: 684.00
Percent Similarity: 68.42%
Best Local Similarity: 53.07%
Query Match: 53.65%
Length: 260
Matches: 121
Conservative: 35
Mismatch: 70
Indels: 2
Gaps: 2

US-09-856-320A-1_COPY_272_958 (1-687) x I56559 (1-260)

QY 1 ATCATCAAGGGGTTGAGTGCATCAAGCCCTGACCCAGCCCTGGAGAGCCCTGTCGAG 60
DB 33 ILELEUGLUGLARGGLUCYSILRPROHSSEGINPOTRPGIALALALEUPHEGIN 52
QY 61 AAGACGGCGTACTCTGTGGGGGAGCGCTCATGGCCCGAGATGGCTCTGCACAGCACC 120
DB 53 GLYGLNARGLEUILRCEGLYGLYVALLLEUVALGILYASPARVTRPVALLLEUTHALALA 72
QY 121 CACTGCCCTCAAGCCCGCTACATAGTTCACCTGGGGGAGACACACCTTCAGAGAAGAGAG 180

```

Db      73 HisCysLysLysGlnLysTyrSerValArgLeuLysPHisSerLeuGlnSerArgasp 92
QY      181 GGCTGTGACGACGCCGCGACGCCATGAGTCTTCCGCCACCCGGCTTCACACAGC 240
        |||||
Db      93 GlnProGlnGlnIleGlnValAlaGlnSerIleGlnIleGlnIleProCysTyrAsnAsnSer 112
QY      241 CTCCCAACAAAGACCCACCGACATGACATCATCTGCTGGTGAAGAGGATGCCAGCTCC 300
        |||
Db      113 AsnPro--GlnAspHisSerHisAspIleMetLeuIleArgLeuGlnAsnSerAlaAsn 131
QY      301 ATCACGTGGGGCTGCGACCCCTCTCACCCTCTCACCCTGTGCTGCTGCTGCTGCTGCTG 360
        |||||
Db      132 LeuLysLysPysValLysProValGlnLeuAlaAsnLeuCysProLysValGlnLys 151
QY      361 TGCTCATATTCGCGCTGGCGACGACGCTCAGCCCGCAGTTCACGCTGCTCAGACCTTG 420
        |||||
Db      152 CysIleIleSerGlyTyrThrValThrSerProGlnGlnAsnProAsnThrLeu 171
QY      421 CGATGGCGGACATCACCATCATGAGACACGAGTGTGAGAACGCTTACCCCGCGCAC 480
        |||||
Db      172 AsnCysAlaGlnValLysIleTyrSerGlnAsnLysCysGlnArgAlaTyrProGlyLys 191
QY      481 ATCAGACACACATGCTGTGTGTGTCGACGCTGACGAGGAGGACGACGCTCCTGCGACGGT 540
        |||||
Db      192 IleThrGlnGlnMetValCysAlaGly--SerSerAsnGlyAlaAspThrCysGlnGly 210
QY      541 GACTCGGGGGCCCTGTGTCTGTATACCATGCTCTTCAGGCAATATTCCTGGGGCGAG 600
        |||||
Db      211 AspSerGlyGlyProLeuValCysAspGlyMetLeuGlnGlyIleThrSerTyrGlySer 230
QY      601 GATCCGTGTGTCGATCACCCCGAACCCGCTGCTTACACGAAAGCTGTCGAATATGTGAC 660
        |||||
Db      231 AspProCysGlyLysProGlnLysProGlyValTyrThrLysIleCysArgTyrThrThr 250
QY      661 TGCATCCAGACGACGATGAGAAC 684
        |||||
Db      251 TrpIleLysLysThrMetAspAsn 258

RESULT 2
KORUP
tissue kallikrein (EC 3.4.21.35) precursor - rat
N:Alternate names: glandular kallikrein; kininogenin; true tissue kallikrein
C:Species: Rattus norvegicus (Norway rat)
C>Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 16-Jun-2000
C:Accession: A00944; A41429; A25137; JX0073; A23863; A33359
R:Swift, G.H.; Dagorn, J.C.; Ashley, P.L.; Cummings, S.W.; Macdonald, R.J.
Proc. Natl. Acad. Sci. U.S.A. 79, 7263-7267, 1982
A:Title: Rat pancreatic kallikrein mRNA: nucleotide sequence and amino acid sequence of
A:Reference number: A00944; MUID:83117659; PMID:6961406
A:Accession: A00944
A:Molecule type: mRNA
A:Residues: 1-265 <SWI>
A:Experimental source: Pancreatic
R:Kato, H.; Nakanishi, E.; Enjoji, K.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.
J. Biochem. 102, 1389-1404, 1987
A:Title: Characterization of serine proteinases isolated from rat submaxillary gland: w
A:Reference number: A41429; MUID:88198057; PMID:3482210
A:Accession: A41429
A>Status: preliminary
A:Molecule type: protein
A:Residues: 29-53, 'X', 55-87 <KAT>
R:Gerard, W.L.; Chao, J.; Chao, L.
Biochim. Biophys. Acta 866, 1-14, 1986
A:Title: Immunological identification of rat tissue kallikrein cDNA and characterization
A:Reference number: A25137; MUID:86131678; PMID:3004582
A:Accession: A25137
A:Molecule type: mRNA
A:Residues: 115-265 <GER>
R:Inoue, H.; Fukui, K.; Miyake, Y.
J. Biochem. 105, 834-840, 1989
A:Title: Identification and structure of the rat true tissue kallikrein gene expressed
A:Reference number: JX0073; MUID:89327211; PMID:2753879
A:Accession: JX0073

```

```

A:Molecule type: DNA
A:Residues: 1-265 <IND>
A:Cross-references: GB:D00448; NID:g220792; PIDN:BA00346.1; PID:g220794
A:Experimental source: Kidney
R:Ashley, P.L.; Macdonald, R.J.
Biochemistry 24, 4512-4520, 1985
A:Title: Kallikrein-related mRNAs of the rat submaxillary gland: nucleotide sequences
A:Reference number: A23863; MUID:86051477; PMID:2998455
A:Accession: A23863
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-265 <ASH>
A:Cross-references: GB:M1563; NID:g205029; PIDN:AAA41464.1; PID:g205030
A:Experimental source: submaxillary gland
R:Wines, D.R.; Brady, J.M.; Pritchett, D.B.; Roberts, J.L.; Macdonald, R.J.
J. Biol. Chem. 264, 7653-7662, 1989
A:Title: Organization and expression of the rat kallikrein gene family.
A:Reference number: A33359; MUID:89214217; PMID:2708383
A:Accession: A33359
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 5-265 <MIN>
A:Cross-references: GB:M23874; GB:J04701; GB:M23875; GB:M23876; NID:g205007; PIDN:AAA
C:Comment: The kallikreins liberate Lysyl-bradykinin, a vasoactive decapeptide, from
C:Comment: The protein presumably assumes the two-chain form by cleavage between resi
C:Comment: Tissue kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to relea
C:Genetics:
A:introns: 20/1; 73/2; 169/1; 214/3
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; pancreas; serine proteinase; zymogen
F:1-17/Domain: signal sequence #status predicted <IG>
F:18-28/Domain: activation peptide #status predicted <AP>
F:29-265/Product: tissue kallikrein, pancreatic #status predicted <MP>
F:29-257/Domain: trypsin homology <TR>
F:35-127, 54-70, 156-223, 188-202, 213-238/Disulfide bonds: #status predicted
F:69,124,217/Active site: His, Asp, Ser #status predicted

Alignment Scores:
Pred. No.: 2,23e-36 Length: 265
Score: 605.50 Matches: 107
Percent Similarity: 63.56% Conservative: 43
Best local Similarity: 45.34% Mismatches: 79
Query Match: 47.49% Indels: 7
DB: 1 Gaps: 1

US-09-856-320A-1_COPY_272_958 (1-687) x KORUP (1-265)
QY      1 ATCATCAAGGGCTTCGATGCAAGCCCTACCTCCACGCTGGCAGCGACCCCTGTCGAG 60
        |||||
Db      29 ValValGlnGlyLysTyrAsnCysGlnMetAsnSerGlnProTyrGlnValAlaValTyrTyr 48
QY      61 AAGACGGGCTACTCTGTGGGGCGAGCTCATGCGCCCGCAGATGGCTCTGACGAGCGC 120
        |||||
Db      49 PheGlnLysLysTyrLeuGlyGlyGlyValLeuIleAspProSerTyrPheIleThrAlaAla 68
QY      121 CACTGCTCAAGCCCGCCCTACATAGTTCACCTGGGCGACGACCACTCTCAGAGAGAGAG 180
        |||||
Db      69 HisCysAlaThrAspAsnTyrGlnValTyrPheGlnGlyArgAsnAsnLeuTyrGlnAspGln 88
QY      181 GCGTGTAGCAGACCCGCGACGACCATGAGTCTCTCCCGACCCCGGCTTCAACACAGC 240
        |||
Db      89 ProPheAlaGlnHisArgLeuValSerGlnSerPheProHisProGlyPheAsnGlnAsp 108
QY      241 CTC-----CCCAACAAGACGACCGCATGACATCATCATGCTGCTG 279
        |||
Db      109 LeuIleTyrPAsnHisThrArgGlnProGlyAspAspTyrSerAsnAspLeuMetLeuLeu 128
QY      280 AAGATGCAATCGCATGCTCATCATCATCTGGCTGGCGACCCCTCAGACCTCTCTCAGCG 339
        |||||
Db      129 HisLeuSerGlnProAlaAspIleThrAspGlyValLysValIleAspLeuProIleGln 148
QY      340 TGTCGTACTGTGGCAGCAGCTGCTCATATTCGCGCTGGGCGACAGCTGCACCCCGCAG 399
        |||||

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Db	149	GIUPRPLYVALIGLYSerThrCysLeuAlaSerGlyTTPGlySerIleThrProAspGly	168
OY	400	TTAGCGCTGGCTCCACACCTTGGGATGGCCCAATCACATCATATATGACCAACGAAGTGT	459
Db	169	LeuGluLeuSerAspAspLeuGlnIleCysValAlaIleAspLeuLeuSerAsnGluCys	188
OY	460	GAGAACGGCTACCCCGGCACATCATCAGACACCATGGTGTGGCCAGCTGCAGAAAGG	519
Db	189	ValGluAlaHisIysGluGluValThrAspLeuMetLeuCysAlaGlyGluMetAspGly	208
OY	520	GGCAAGACACTCTGGCAGAGGTGACTCCGGGGGCGCTCTGGTGTATACCAAGTCTGTCA	579
Db	209	GlyLysAspThrCysLysGlyAspSerGlyLeuProLeuIleCysAsnGlyValLeuGln	228
OY	580	GGCATTAATCTCCCTGGGGCCAGGATCCGTGTGGCATCACCCGAAGCGCTGGTCTTACAG	639
Db	229	GlyIleThrSerTTPGlyPheAsnProCysGlyGluProLysGlyProGlyIleTyrThr	248
OY	640	AAAGCTCAATAATATGGATCGATTCACAGAGAGAGATGAACAACAT	687
Db	249	LysLeuIleLysPheThrProTTPLeuLysGluValMetLysGluAsn	264

RESULT 3

Alignment Scores:

tissue kallikrein (EC 3.4.21.35) 7 precursor, submandibular - rat
N/Alternate names: glandular prokallikrein 7, submandibular; proteinase A
C/Species: Rattus norvegicus (Norway rat)
C/Date: 31-Mar-1990 #sequence, revision 31-Mar-1990 #text, change 22-Jun-1999
C/Accession: A31136, S10698; S10699; D41429; B41429; S09315
R/Chem, Y.P.; Chao, J.; Chao, L.
B/Biochemistry 27, 7189-7196, 1988
A/Title: Molecular cloning and characterization of two rat renal kallikrein genes.
A/Reference number: A31136, MUID:69088074; PMID:2849988
A/Accession: A31136
A/Molecule type: DNA
A/Residues: 1-261 <CHED>
A/Cross-references: GB:M19647; GB:J02837; NID:g204999; PIDN:AAA41461.1; PID:g205000
R/Elmoujahed, A.; Gutman, N.; Brillard, M.; Gauthier, F.
FEBS Lett. 265, 137-140, 1990
A/Title: Substrate specificity of two kallikrein family gene products isolated from the
A/Reference number: S10698; MUID:90306305; PMID:2194829
A/Accession: S10698
A/Molecule type: protein
A/Residues: 25-36 <ELM>
A/Accession: S10699
A/Molecule type: protein
A/Residues: 112-139 <EL2>
R/Kato, H.; Nakamishi, E.; Enjyoji, K.; Hayashi, I.; Oh-Ishii, S.; Iwanaga, S.
J Biol Chem. 102, 1389-1404, 1987
A/Title: Characterization of serine proteinases isolated from rat submaxillary gland: with
A/Reference number: A41429; MUID:88198057; PMID:3482210
A/Accession: D41429
A/Molecule type: protein
A/Residues: 112-133 <KAW>
A/Accession: B41429
A/Molecule type: protein
A/Residues: 25-34,'D',36-45,'S',47-67,'X',69-75 <KA2>
R/Brady, J.M.; MacDonald, R.J.
Arch. Biochem. Biophys. 278, 342-349, 1990
A/Title: The expression of two kallikrein gene family members in the rat kidney.
A/Reference number: S09315; MUID:90225801; PMID:2183721
A/Accession: S09315
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 43-45,'S',47-114,'A',116-261 <BRA>
C/Superfamily: trypsin; trypsin homology
C/Keywds: hydrolase; serine proteinase
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-261/Product: tissue prokallikrein 7, submandibular #status predicted <MAT>
F:25-253/Domain: trypsin homology <TRY>
F:65,120,213/Active site: His, Asp, Ser #status predicted

Pred. No.:	5.15e-36	length:	261
Score:	600.50	Matches:	109
Percent Similarity:	62.71%	Conservative:	39
Best local Similarity:	46.19%	Mismatches:	81
Query Match:	47.10%	Indels:	7
DB:	2	Gaps:	1

US-09-856-320A-1_COPY_272_958 (1-687) x A31136 (1-261,

[illegible]

RESULT 4

7S nerve growth factor gamma chain (EC 3.4.21.-) precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 18-Dec-1981 #sequence, revision 17-May-1985 #text change 18-Jun-1999
C/Accession: A91005; A90949; A93510; A92541; A00942; A21053; A22705
R/Evans, B.A.; Richards, R.I.
EMBO J. 4, 133-138, 1985
A/Tittle: Genes for the alpha and gamma subunits of mouse nerve growth factor are contiguous
A/Reference number: A91005; MUID:5257431; PMID:3848399
A/Accession: A91005
A/Molecule type: DNA
A/Residues: 1-261 <EYAA>
R/Dillrich, A.; Gray, A.; Wood, W.I.; Hayflick, J.; Seeburg, P.H.
DNA 3, 387-392, 1984
A/Tittle: Isolation of a cDNA clone coding for the gamma-subunit of mouse nerve growth factor

A:Reference number: A90949; MUID:85076169; PMID:6548955
A:Accession: A90949
A:Molecule type: mRNA
A:Residues: 1-261 <UDL>
A:Cross-references: GB:X01389; NID:953373; PIDN:CAA25645.1; PID:953374
R:Howles, P.N.; Dickinson, D.P.; DiCaprio, L.L.; Woodworth-Gutal, M.; Gross, K.W.
Nucleic Acids Res. 12, 2791-2805, 1984
A:Title: Use of a cDNA recombinant for the gamma-subunit of mouse nerve growth factor to
A:Reference number: A93510; MUID:84169573; PMID:6200835
A:Accession: A93510
A:Molecule type: mRNA
A:Residues: 127-202, 'E', 204-261 <HOW>
A:Cross-references: GB:X00472; NID:954260; PIDN:CAA25154.1; PID:954261
R:Experimental source: Inbred strain DBA/2J
R:Thomas, K.A.; Baglan, N.C.; Bradshaw, R.A.
J. Biol. Chem. 256, 9156-9166, 1981
A:Title: The amino acid sequence of the gamma-subunit of mouse submaxillary gland 7 S ne
A:Reference number: A92341; MUID:81264363; PMID:7263706
A:Accession: A92341
A:Molecule type: protein
A:Residues: 25-107, 112-261 <THO>
A:Experimental source: outbred strain Swiss Webster
C:Comment: 7S nerve growth factor is composed of two alpha chains, a beta dimer composed
C:Comment: The active form of the gamma chain occurs naturally as combinations of either
C:Genetics:
A:Map position: 7
A:Introns: 16/1; 69/2; 165/1; 210/3
C:Superfamily: trypsin; trypsin homology
C:Keywords: glycoprotein; growth factor; hydrolase; serine proteinase; submandibular gla
F:1-18/Domain: signal sequence #status predicted <SIG>
F:25-253/Domain: trypsin homology <TRY>
F:25-107/Domain: segment B1 <GB1>
F:25-107, 112-261/Product: nerve growth factor gamma chain (active form) #status experime
F:112-261/Domain: segment A <GAA>
F:112-164/Domain: segment C <GCC>
F:165-261/Domain: segment B2 <GB2>
F:31-173, 50-66, 152-219, 184-198, 209-234/Disulfide bonds: #status predicted
F:65, 120, 213/Active site: His, Asp, Ser #status predicted
F:102/Binding site: carbohydrate (Asn) (covalent) #status experimental

Alignment Scores:
Pred. No.: 1.19e-35 Length: 261
Score: 595.50 Matches: 105
Percent Similarity: 63.98% Conservative: 46
Best Local Similarity: 44.49% Mismatches: 78
Query Match: 46.71% Indels: 7
DB: 1 Gaps: 1

US-09-856-320a-1_COPY_272_958 (1-687) x NGMSG (1-261)

QY 1 ATCATCAAGGGGTTGCGAGTCGCAAGCCCTACCTCCAGCCCTGGCAGGAGCCCTGTTGAG 60
DB 25 ILeValIcIyIyIrrhPheYsGslYsAsnSerClnProrPrlhSValAlaValTyrArg 44

QY 61 AAGACGGGCTACTCTGTGGGCGAGCGTCATCGCCCGCCAGATGGCGCTGACAGCAGCC 120
DB 45 TyrThcIcInIyrrhPheYsGslYsValIleuLeuAspProGlnhProrPrlhSValAlaValTyrArg 64

QY 121 CACTGCTCAAGCCCGCTACATAGTTACCTGGGGGAGCAGCAACCTCCAGAGGAGAG 180
DB 65 HisCysTyrAspAsnTyrLysValITrPleuGlyYsAsnSlnLeuPheLysAspGlu 84

QY 181 GGGTGTGAGCAGACCGGAGCAGCAGTCTCTCCCGCCAGCCCGGCTTCAACACAGC 240
DB 85 ProSerAlaGlnhIstIleArgPheValSerLysAlaIleProhIstProGlyPheAsnMetSer 104

QY 241 CTCGCCAACAA-----GACACCGCAATGACATGACATGCGTGG 279
DB 105 LeuMetArgLysHisIleArgPheLeuGlyTyrAspTyrSerAsnSpleuMetLeuLeu 124

QY 280 AAGATGGAGCAGTCCTCATACCTAGCTGGGCTGGGAGCCCTCAACCTCTCTCAGC 339
DB 125 ArgLeuSerLysProAlaAspIleThrAspThrValLysProIleThrLeuProThrGlu 144

QY 340 TGTGTACTGCTGGACACACCTGCTCATTTCCGGCTGGGGCAGACAGCTCCAGCCCCAG 399
DB 145 GluProLysLeuGlySerThrCysLeuAlaSerCylYrrpGlySerIleThrProThrLys 164

QY 400 TTACGCGCTGCTCACCCTTGGCATGGCGCCCAATCCATCATATTGAGCAGCAGAGTGT 459
DB 165 PhehInIethrAspAspIleTyrCysValAlaSlnLeuYsLeuProAsnGluAspCys 184

QY 460 GAGAACGCTACCCCGGCAACATCATGACACCATGCTGGTGTGGTGGCAGCGAGGAAGG 519
DB 185 AlAlaYsAlaHisIleGlyLysValIThrAspAlaMetLeuYsAlaGlyLumetAspGly 204

QY 520 GGCAGAGCCTCTGCCAGGTGATCCGGGGGCGCTGTGCTTAACAGTCTTCAAA 579
DB 205 GlyLysAspThrCysLysGlyAspSerGlyLysProLeuIleCysAspGlyValLeuGln 224

QY 580 GGCATTTTCCTCGGGGCGCAGATCCGTGTGCCATCACCCGAAAGCTGGTGTCTACAG 639
DB 225 GlyIleThrSerThrPrlhSlnThrProCysGlyGluProAspMetProGlyValTyrThr 244

QY 640 AAGTCTGCAAAATATGTGACTGATCCAGAGCAGATGAACAAT 687
DB 245 LysLeuSlnhSphrThrSerThrPrlleLysAspThrMetAlaLysAsn 260

RESULT 5
S55066
trypsin (EC 3.4.21.4) II precursor, pancreatic (clone 2-P29) - chicken
N:Alternate names: trypsinogen II
C:Species: Gallus gallus (chicken)
C:Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 22-Jun-1999
A:Accession: S55066; S72347
R:Wang, K.; Gan, L.; Lee, I.; Hood, L.
Biochem. J. 307, 471-479, 1995
A:Title: Isolation and characterization of the chicken trypsinogen gene family.
A:Reference number: S55065; MUID:95251611; PMID:7733885
A:Accession: S55066
A:Molecule type: mRNA
A:Residues: 1-248 <MAN1>
A:Cross-references: EMBL:U01517; NID:9603906; PIDN:AAA79914.1; PID:9603907
A:Experimental source: Clone 2-P29
A:Accession: S72347
A:Molecule type: DNA
A:Residues: 1-248 <MAN2>
A:Cross-references: EMBL:U01517; NID:9603906; PIDN:AAA79914.1; PID:9603907
A:Experimental source: Clone 2-P29
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F:1-25/Domain: signal sequence #status predicted <SIG>
F:17-25/Domain: activation peptide #status predicted <AP>
F:26-248/Product: trypsin II #status predicted <MAT>
F:26-241/Domain: trypsin homology <TRY>
F:65, 109, 202/Active site: His, Asp, Ser #status predicted

Alignment Scores:
Pred. No.: 1.53e-35 Length: 248
Score: 594.00 Matches: 112
Percent Similarity: 65.04% Conservative: 35
Best Local Similarity: 49.56% Mismatches: 73
Query Match: 46.59% Indels: 6
DB: 2 Gaps: 3

US-09-856-320a-1_COPY_272_958 (1-687) x S55066 (1-248)

QY 1 ATCATCAAGGGGTTGCGAGTCGCAAGCCCTACCTCCAGCCCGGAGCAGCAGCCCTGTTGAG 60
DB 26 ILeValIcIyIyrrhPheYsGslYsValIleuLeuAspProGlnhProrPrlhSValAlaValTyrArg 44

QY 61 AAGACGGGCTACTCTGTGGGCGAGCGTCATCGCCCGCCAGATGGCGCTGACAGCAGCC 120
DB 45 SerGlyTyrhIstIleArgPheLeuGlyTyrAspTyrSerAsnSpleuMetLeuLeu 124

QY 121 CACTGCTCAAGCCCGCTACATAGTTACCTGGGGGAGCAGCAACCTCCAGAGGAGAG 180

```

Db      65 HISCSTYRYSSEATRIIEGInValArgLeuGlyGlyTyrAsnIleSprValIngu 84
QY      181 GGCTGTGAGACAGCCGAGACAGCCAGTCCCTCCCGCCGGCTTAAACAAGC 240
Db      85 ASPserGIuValArgSerSerValIleIleArgHisProLysTyrSerSerIle 104
QY      241 CTCGCCAACAAGACCCAGCCATGATCATGCTGGTGAAGATGGATGCCAGCTGCC 300
Db      105 ThrIeuAn-----AsnAspIleMetIleuIleLysIleuAlaSerAlaValGlu 120
QY      301 ATCAGCTGGGCTGTGGACCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCAGC 360
Db      121 TyrSerAlaAspIleGlnProIleAlaLeuProSerSerCysAlaLysAlaGlyThrGlu 140
QY      361 TGCCATATTCCTGGCTGGGAGAGACAGCTCCAGCCCGAGTACGCTCCACACCTTG 420
Db      141 CysLeuIleSerGIYTrpGIYAsnThrIeuSerAsnGIYTyraSntYrProGluIeuLeu 160
QY      421 CGATGCCCAACATCACCATCATTCAGACACCAAGATGTGAGAACCCGTACCCGGCAGC 480
Db      161 GInCysIleuAsnAlaProIleIeuSerAspGlnGlySglnGlnAlaLysProGlyAsp 180
QY      481 ATCAGACAGACCATGGTGTGCCAGCTGCAGAGGAGGGGAGAGACTCCCTCCAGGCT 540
Db      181 IleThrSerAsnMetIleCysValGlyPheIeuGlnGlyGlyLysAspSerCysGlnGly 200
QY      541 GACTCCGGGGGCGCTGTGCTGTATACCATGCTCTTCAAGCATATTCCTGGGGGCGCAG 600
Db      201 AspSerGIYGIYProValIValCysAsnGlyGluIeuGlnGlyIleValSerTrpIYle 220
QY      601 GATCCGTGTGGATCACCAGCCGAAAGCTGTGTCTATACAGAAAGTGTGCAATATGTGGAC 660
Db      221 Gly---CysAlaLeuLysGIYTrpGIYValIYThrLysValCysAsnTyIValAsp 239
QY      661 TGGATCCGAGACGATG 678
Db      240 TrpIleGlnGluThrIle 245

```

RESULT 6

```

S15686
tissue kallikrein (EC 3.4.21.35) precursor, renal - multimammate rat (Mastomys natalensis)
C:Species: Mastomys natalensis
C>Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C:Accession: 183227; S15686
R:Fannestock, M.
DNA Cell Biol. 13, 293-300, 1994
A:Title: Characterization of kallikrein cDNAs from the African rodent Mastomys.
A:Reference number: 160208; MUID:94226702; PMID:7909667
A:Accession: 183227
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-263 <RES>
A:Cross-references: EMBL:X17352; NID:g55526; PIDN:CAA35232.1; PID:g55527
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:23-255/Domain: trypsin homology <TRY>
F:65,121,215/Active site: His, Asp, Ser #status predicted

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Alignment Scores:

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Pred. No.:      2,31e-35      Length:      263
Score:          591.50      Matches:      106
Percent Similarity: 63.03%      Conservative: 44
Best Local Similarity: 44.54%      Mismatches: 79
Query Match:     46.39%      Indels:      9
DB:              2          Gaps:      2

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US-09-856-320a-1_COPY_272_958 (1-687) x S15686 (1-263)

```

QY      1 ATCATCAAGGGGTTCGATGTCAGCTTCATCCAGCCCTGGAGAGCCCTGTTCGAG 60
Db      25 IletIleGIYGIYpHeAsnGlySglnLysAsnSerGIYProTrpHisValAlaValTyArg 44

```

```

QY      61 AAGACCGGCTACTGTGTGGGGGAGCCGCTACGCCCCAGATGGCTCTGACAGCAGCC 120
Db      45 PheAlaArgTyrgInGlySglnGlyValIleuLeuAsnAlaAsnTrpValIleuThrAlaAla 64
QY      121 CAGCTGCTCAAGCCCGGCTAGTATGACCTGGGGGAGAGCAACATCCAGAAAGAGAG 180
Db      65 HISCSTYRYSAspRysTrpGIYValIleTrpLeuGIYLysAsnAsnArgPheIleuSprGlu 84
QY      181 GGCTGTGAGACAGCCGAGACAGCCAGTACGCTCCCTCCCGCCGGCTTAAACAAGC 240
Db      85 ProSerAlaGlnHisGlnIleuLeuSerLysAlaIleProHisProGIYpHeAsnMetSer 104
QY      241 CTCGCCAACAAGACCCAGCCATGATCATGCTGGTGAAGATGGATGCCAGCTGCC 300
Db      105 LeuIeuAnLysAspRisthrProHisProGluAspRysTySerAsnIleuMetIleu 124
QY      277 GTGAAGATGGCATGGCCAGTCCATCCATCCCTGGCTGGGAGAGAGCTCC--AGC 336
Db      125 ValArgLeuLysLysProAlaGluIleThrAspValValLysProIleAspLeuProThr 144
QY      337 CGCTGTGCTACGTGTGGAGCAGAGCTGCTCATATTCGGCTGGGAGAGAGCTCC--AGC 393
Db      145 GluGluProThrIValGlySerArgCysLeuAlaSerGIYTrpGIYSerThrProThr 164
QY      394 CCCAGTTAACGCTGCTCCACAGCTTGGAGTCCGCAACATCACCATTCATTCAGACAGCAG 453
Db      165 GluGluPheGluTySerThrIAspLeuGlnGlyValTyLeuGlnIleuLeuSerAsnGlu 184
QY      454 AAGCTGAGAACGCTTACCCTCCGAGACATCAGACACCATTCAGTGTGTCAGAGCTGAG 513
Db      185 ValCysAlaLysAlaHisThrGluLysValIleThrAspThrMetLeuCysAlaGlyIleuMet 204
QY      514 GAAGGGGAGAGAGACTCCCTCCAGGGTACTCCGGGGGCGCTGTGTTAACAGACT 573
Db      205 AspGIYGIYLysAspThrCysValGlyAspSerGIYGIYProLeuIleCysAspIYal 224
QY      574 CTTCAGGATTCATCTCTGGGGCCAGAGATCCGTGTGCGATGCCGGAAGCCGTGGTC 633
Db      225 LeuGlnGlyIleThrSerTrpGIYProThrProCysAlaLeuProAsnValProGIYle 244
QY      634 TACAGAAAGTGTGCAATATGTGAGCTGGATCCGAGAGATGAGAGCAACAAT 687
Db      245 TythrLysLeuIleGluTyArgSerTrpIleLysAspValMetAlaAsnAsn 262

```

RESULT 7

```

TRRT2
trypsin (EC 3.4.21.4) II precursor - rat
N:Alternate names: trypsinogen II
C:Species: Rattus norvegicus (Norway rat)
C>Date: 05-Apr-1983 #sequence_revision 30-Sep-1987 #text_change 18-Jul-1997
C:Accession: A22657; A00949
R:Craik, C.S.; Choo, O.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.
J. Biol. Chem. 259, 14255-14264, 1984
A:Title: Structure of two related rat pancreatic trypsin genes.
A:Reference number: A22657; MUID:85054880; PMID:6094547
A:Accession: A22657
A:Molecule type: DNA
A:Residues: 1-246 <CRA>
R:MacDonald, R.J.; Stary, S.J.; Swift, G.H.
J. Biol. Chem. 257, 9724-9732, 1982
A:Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences
A:Reference number: A00948; MUID:82265624; PMID:6896710
A:Accession: A00949
A:Molecule type: mRNA
A:Residues: 9-246 <MAC>
C:Comment: The trypsin II mRNA is present in much lower quantities than the trypsin I
C:Genetics:
A:Introns: 14/1; 67/2
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-23/Domain: activation peptide #status predicted <APY>
F:24-246/Product: trypsin II #status predicted <ENZ>

```


trypsin (EC 3.4.21.4) I precursor - rat
 M.Alternate names: trypsinogen I
 C.Species: Rattus norvegicus (Norway rat)
 C.Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 24-Sep-1999
 C.Accession: B22657; A00948
 R.Craik, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.
 J. Biol. Chem. 259, 14255-14264, 1984
 A.Title: Structure of two related rat pancreatic trypsin genes.
 A.Reference number: A22657; MUID:85054880; PMID:6094547
 A.Accession: B22657
 A.Molecule type: DNA
 A.Residues: 1-246 <CRA>
 A.Cross-references: GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508
 A.Note: The authors translated the codon ATC for residue 6 as Leu and GAC for residue 17
 R.MacDonald, R.J.; Stary, S.J.; Swift, G.H.
 J. Biol. Chem. 257, 9724-9732, 1982
 A.Title: Two similar but nonallelic rat pancreatic trypsin genes. Nucleotide sequences of
 A.Reference number: A00948; MUID:82265624; PMID:6896710
 A.Accession: A00948
 A.Molecule type: mRNA
 A.Residues: 1-246 <MAC>
 A.Cross-references: GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508
 C.Genetics:
 A.Introns: 14/1; 67/2; 152/1; 197/3
 C.Superfamily: trypsin; trypsin homology
 C.Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:16-23/Domain: activation peptide #status predicted <APTP>
 F:24-246/Product: trypsin I #status predicted <ENZ>
 F:24-239/Domain: trypsin I #status predicted <TRY>
 F:30-160-48-64-132-233-139-206-171-185/Disulfide bonds: #status predicted
 F:63-107-200/Active site: His, Asp, Ser #status predicted
 F:75-77-80-85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Alignment Scores:
 Pred. No.: 4,94e-35 Length: 246
 Score: 587.00 Matches: 111
 Percent Similarity: 63.32% Conservative: 34
 Best Local Similarity: 48.47% Mismatches: 78
 Query Match: 46.04% Indels: 6
 DB: 1 Gaps: 3

US-09-856-320a-1_COPY_272_958 (1-687) x TRRT1 (1-246)

```

OY 1 ATCATCAAGGGGTTGAGTGCAGAGCCATCCAGCCCTGGAGAGAGCCCTGTTGAG 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 24 IlevaIglYglYTYrThnCysProglUnhISerValProTYglNValSerIeu---Asn 42
OY 61 AAGACGGGGTACTGTGTGGGGGAGGCTATCGCCCGGAGATGGCTCTGACAGCAGC 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 43 SerGIYrThnISpHeCysglYglYSerIeuIleAsnAspGIInTrYValISerAlaIa 62
OY 121 CACGTGCTCAAGCCCGGTGACTATGATGACCTGGGGGAGCAACCTCCAGAGAGAG 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 63 HISCSTYrLysSerArIleelNValArgLeuGlYglUnhISAsnIleISnValIeuGl 82
OY 181 GCGTGTGAGCAGACCCGAGACAGCCAGTGCCTTCCCGCCGGCTTCAACAACAGC 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 83 GlYAspGIInTrYpHeIleAsnAlaIalYsIleIleYlSISProAsnTYSerSerTrp 102
OY 241 CTCGCCAACAAGACACCCGAGATGACATGCTGCTGGTGAAGATGGATCGCATCTCC 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 103 ThrIeuAsn-----AsnAspIleMetIleuIleYlSISerSerProValIys 118
OY 301 ATCACTGGGCTGTCAGCCCTGACCCCTGCTCCAGCTGTGCTGCTGTCGACAGC 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 119 LeuAsnAlaIArgValAlaIProValAlaIeuproSerAlaCysAlaProAlaIYrGl 138
OY 361 TGCCCTCATTTCCGGCTGGGGGAGCAGCTGACAGCCCGCCAGTACGCGCTGCACACTTG 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 139 CysIeuIleSerGIYrTrpGIYAsnThrIeuSerAsnGlYValAsnAsnProAspIeu 158
OY 421 CGATCGCGCAACATCATCATTTGAGCAGCAGAAAGTGTGAGACGCTTACCCGGCAGC 480
  
```

trypsin (EC 3.4.21.35) P1 precursor - rat
 tissue kallikrein (EC 3.4.21.35) P1 precursor - rat
 M.Alternate names: kallikrein-related proteinase k8
 C.Species: Rattus norvegicus (Norway rat)
 C.Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 22-Jun-1999
 C.Accession: A34079; S10700
 R.Brady, J.M.; Wines, D.R.; MacDonald, R.J.
 Biochemistry 28, 5203-5210, 1989
 A.Title: Expression of two kallikrein gene family members in the rat prostate.
 A.Reference number: A34079; MUID:89352606; PMID:2765531
 A.Accession: A34079
 A.Molecule type: preliminary
 A.Status: preliminary
 A.Molecule type: DNA; mRNA
 A.Residues: 1-261 <BRA>
 A.Cross-references: GB:M27215; GB:M27216; GB:M27217; NID:g206638; PIDN:AAA42036.1; PI
 A.Experimental source: prostate
 R.Elmojaded, A.; Gutman, N.; Brillard, M.; Gauthier, F.
 FEBS Lett. 265, 137-140, 1990
 A.Title: Substrate specificity of two kallikrein family gene products isolated from t
 F:112-261/Product: tissue kallikrein P1 heavy chain #status experimental <MAT2>
 F:65-120-213/Active site: His, Asp, Ser #status predicted

Alignment Scores:
 Pred. No.: 6,31e-35 Length: 261
 Score: 585.50 Matches: 105
 Percent Similarity: 61.86% Conservative: 41
 Best Local Similarity: 44.49% Mismatches: 83
 Query Match: 45.92% Indels: 7
 DB: 2 Gaps: 1

US-09-856-320a-1_COPY_272_958 (1-687) x A34079 (1-261)

```

OY 1 ATCATCAAGGGGTTGAGTGCAGAGCCATCCAGCCCTGGAGAGAGCCCTGTTGAG 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 25 IleIleGlYglYrPhAsnCySglYglYValIeuIleISProSerTrYValIleThAlaIa 44
OY 61 AAGACGGGGTACTGTGTGGGGGAGGCTATCGCCCGGAGATGGCTCTGACAGCAGC 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 45 PhAsnGIInTrYpHeIleAsnAlaIalYsIleIleYlSISProSerTrYValIleThAlaIa 64
OY 121 CACGTGCTCAAGCCCGGTGACTATGATGACCTGGGGGAGCAACCTCCAGAGAGAG 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 65 HISCSTYrSerValISnTYrGlNValTrpLeuGlYArgAsnAsnIleuGlUnhISpIu 84
  
```

QY	181	GGCTGTGAGCAGACCCGCGACAGCCACCTAGTCTCTCCACCCGCGCTTCAACACAGC	240
		:::::	
Db	85	ProhehlaaGlnHisArgLeuValSerGlnSerPheProHisProGluPheHisLeuAar	104
QY	241	CTC-----CCCAACAAGACACCGCAATGCATCATGCTGTGG	279
		:::	
Db	105	IleIleIysAsnHisIsthrArgLysProGluAaenApyrSerHisAspLeuMetLeuLeu	124
QY	280	AAGATGGCATGGCCAGTCCATCATCCCTGGGTGGCGACCCCTCAACCTCTCTCCACGC	339
		::: ::::: ::::: ::: :::	
Db	125	HisLeuIysThrProIleAspIleThrAspGluValIleAspLeuProThrGlu	144
QY	340	TGTGTCACTGCTGGCACCACAGCTGCTCATTTCCGGCTGGGGCAGCACAGTCCAGCCCA	399
		::: :::	
Db	145	GluProIysValGlySerThrCysLeuThrSerGlyTyrGlySerIleThrProLeuIys	164
QY	400	TTACGCCCTCCACACCTTCGATCGACCCACATCACCATATTGAGCAGACAGAGTGT	459
		::: :::::	
Db	165	TrpGluPheProAspAspLeuGlnIncysValAsnIleHisLeuLeuSerIasnGluCys	184
QY	460	GAGAACGCTTACCCCGGCACATCACAGACACCATGTGTGTGCCAGCGTGCAGGAAGG	519
		::	
Db	185	IleIysAlaTyrAsnAspIleValIleThrAspValIleMetLeuCyAlaGlyIleMetAspGly	204
QY	520	GGCAGAGCATCTGTGCACAGGTGATCCGGGGGGCCCTGTGTGTGTAACCAAGTCTGTCAA	579
		:::::	
Db	205	GlyIysAspIleCysGlyAspSerIleGlyProLeuIleCysAspIleValLeuGln	224
QY	580	GGCATTTATCTCCGTGGGGCCAGAGTCCGTGTGCATCACCCGAAGCGCTGTGTCTACAG	639
Db	225	GlyIleThrSerTyrGlySerMetProCysGlyIleProAsnIlyProSerValTyrThr	244
QY	640	AAGGCTCAAAATATGTGATCGATGATCCAGACAGACAGATGAAGAACAAT	687
		::: :::::	
Db	245	LysLeuIleIysPheThrSerTyrMetLysIysValIleMetLysGluIasn	260

```

RESULT 11
B31136
tissue kallikrein (EC 3.4.21.35) 3 precursor, submandibular - rat
N:Alternate names: glandular prokallikrein 3, submandibular
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #ext_change 22-Jun-1999
C:Accession: B31136
R:Chen, Y. P.; Chao, J.; Chao, L.
Biochemistry 27, 7189-7196, 1988
A:Title: Molecular cloning and characterization of two rat renal kallikrein genes.
A:Reference number: A31136; PMID:89088074; PMID:2849988
A:Accession: B31136
A:Molecule type: DNA
A:Residues: 1-259 <CHE>
A:Cross-references: GB:M19648; GB:J02837; NID:g205002; PIDD:NAA51640.1; PID:g205004
A>Note: the authors translated the codon GTC for residue 230 as Cys
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:1-18/Domain: signal sequence #status predicted <Sig>
F:25-251/Domain: tissue prokallikrein 3, submandibular #status predicted <Mat>
F:63-118,211/Active site: His, Asp, Ser #status predicted

Alignment Scores:
Pred. No.:      1,23e-34      Length:      259
Score:          581.50        Matches:     105
Percent Similarity: 61.02%    Conservative: 39
Best Local Similarity: 44.49%  Mismatches: 83
Query Match:    45.61%      Indels:      9
DB:              2           Gaps:        2

```

OY 1 ATATCATGAGGGGTTCAGTAGTGCAGCCTCACTCCAGCCCTGGCAGGACGCCCTGTTCGAG 60
 ::::: ||::::::::::||::: ::||||| ||||| ||:::
Db 25 ValValGlYcIyTrLysCyScgluLysAsnSerGlnProTrpGlnValAlaValIle--- 43

61 AAGACGGGGCTACTCTGTGGGGGAGCGCTCATGGCCCCAGATGGGCTCTGACAGACGCC 120
 44 ---ASNAKGYRIEYSGGLYGLYVALLEULEULEINSPPROSERTRIPVALIETRIALALA 62
 121 CACTGGCCTCAAGCCCCGCTACATAGTTCACTGGGGGACACACACCTCCGAAGGAGAG 180
 63 HICSYTYSERHISASINTRYHISVALLEULEULEINYRGASNAISNEUPHELYASPSGLN 82
 181 GGCTGTAGAGACGCCGGACACGCATCGTAATCTCTCCCAACCCCGGCTTCAC- 234
 83 PROTHEALAGINTYATATGVALVALASNGILINSETPHEPROHISPROASPYTASNPPO 102
 235 -----AAGACGCTCCCAACAAAGACCCAGCCGACATGACATACATGCTGGT 279
 103 PHEMETLYSASNHISTHRIEUPHEPROGLYASAPRASHISERASNPASPLEUMETLEULE 122
 280 AAGATGGCATGCCAGTCTCCATCATCTGGGGCTGTGGACCCCTCAACCTCTCTCAGCC 339
 123 HISLEUSERGUPTROALASPILETHTHASPGLYVALIETLASPLEUPROTHRGU 142
 340 TGTGTCACTGGTGGCAGCTGGCTCATTTCCGGGCTGGGGAGACAGTCCACGCCCCAG 399
 143 GLUPROLYSVALIYLSERTHRCYSLLEALISERGLYTRPBERSETRHLYSPROLEUGU 162
 400 TTACGCTGCTCACACCTTGGCATGGCCAAATCACCATTCATTTGACACAGAACTGT 459
 163 TRGPLUPHEPROASPSAPLEUGLINCYSVALASNIIEASNIIEUSERASNGLUYSCYS 182
 460 GAGAACCCCTTACCCGGGACATCACAGACACCACTGGTGTGTGCGACCGTCCAGGAAGG 519
 183 ILELYSLAHISTHRIEUGMETVALTHASPSVALMETLEUCYSALAGLYLEUGLINCUGLY 202
 520 GGCAGAGACATCTGTCGACGGGTACTCCGGGGGCGCTGTGCTGTAACACAGTCTTCA 579
 203 GLIYTSAPHRHCYSASNGLYASPSERGLCYLPROLEULEULEYASPSGLYVALLEUGN 222
 580 GGCATYATCTCTGGGGCCACAGATCCGTGTCGATCACCCGAAAGCCTGGTGTCTACAG 639
 223 GLIYLETHERSERTRIPSERVALPROCYGLYGLIUTHRASNPARGPROALAIETRYTHR 242
 640 AAAGCTGCAGAAATATGTGAGCTGGATCCAGGAGACGATGAAGAAACAT 687
 243 LYSLEULEULEYSPHETHTSERTRIPLEUGLIVALEUMETLYSGUASN 258

RESULT 12
KOPG

tissue kallikrein (EC 3.4.21.35), pancreatic - pig (tentative sequence)
N/Alternate names: glandular kallikrein; kininogenin
N/Species: Sus scrofa domestica (domestic pig)
C/Date: 24-Apr-1994 #sequence_revision 31-Dec-1993 #text_change 31-Mar-2000
C/Accession: A00938 A92895
R/Tschesche, H.; Mair, G.; Godec, G.; Fiedler, F.; Ehret, W.; Hirschauer, C.; Lemon, .
Adv. Exp. Med. Biol. 120, 245-260, 1979
A/Title: The primary structure of porcine glandular kallikreins.
A/Reference number: A90015
A/Accession: A00938

A/Molecule type: protein
A/Residues: 1-49, GWM,¹53-134, ¹D,¹136-156, ¹H,¹158, ¹B,¹160-224, ¹B,¹226-232 <RSC>
A/Note: the residue identified as 225-Asx is bound to carbonylurate; therefore, we have
R/Bode, W.; Chen, Z.; Bartels, K.; Kutzbach, C.; Schmidt-Kastner, G.; Bartunk, H.
J. Mol. Biol. 164, 237-282, 1983
A/Title: Refined 2 angstrom X-ray crystal structure of porcine pancreatic kallikrein
L, structure and its comparison with bovine trypsin.
A/Reference number: A92895; MUID:83189107; PMID:6551452
A/Contents: X-ray crystallography, 2 angstroms
A/Accession: A92895

A/Molecule type: protein
A/Residues: 1-224,¹B,¹226-232 <BOD>
A/Comment: The protein consists of two chains, A and B, held together by disulfide bo
C/Comment: Tissue kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to releas
C/Superfamily: trypsin; trypsin homology
C/Keywords: glycoprotein; hydrolase; pancreas; serine proteinase

F:1-224/Domain: trypsin homology <TRY>
F:1-80/Product: tissue kallikrein chain A #status experimental <MPRA>
F:79-82/Region: autoolysis loop
F:81-232/Product: tissue kallikrein chain B #status experimental <MPRB>
F:7-144-26-42,121-190,155-169,180-205/Dissulfide bonds: #status experimental
F:41,89,184/Active site: His, Asp, Ser #status experimental
F:78/Binding site: carbonyl (Asn) (covalent) #status experimental
F:225/Binding site: carbonyl (Asn) (partial) #status experimental

Alignment Scores:

Pred. No.:	2,236-34	Length:	232
Score:	578.00	Matches:	102
Percent Similarity:	61.90%	Conservative:	41
Best Local Similarity:	44.16%	Mismatches:	86
Query Match:	45.33%	Indels:	2
DB:	1	Gaps:	1

US-09-856-320A-1_COPY_272_958 (1-687) x KOPG (1-232)

```
QY 1 ATCATCAAGGGGTTGAGTGCAGACCTCCAGCCCTGGAGGAGCCCTGTTCGAG 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 lletleglglYargGlucslulysasnserHisProtrpGlnValAlarleyrHis 20
QY 61 AAGAGCGGCTACTGTGTGGGCGAGCTCATCGCCCAAGATGGCTCTGCACAGCC 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 21 TyrSerSerPheglncysgllyValleuValasnProlystrpValleuThrAla 40
QY 121 CACTGCTCAAGCCCTCATAGTACCTGGGCGAGCACACCTCCAGAGAGGAG 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 41 HiscysLysAsnAspAsnTyrGlnValTrpLeuGlnArgHisAsnLeuPheglu 60
QY 181 GGCCTGAGCAGACCCGAGCAGCCAGTCTCCCAACCCCGGCTTCAACAACAGC 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 AsnThrAlaGlnPhePhegllyValThrAlaAspPheProHisProGlyPheasnLeu 80
QY 241 CTCGCCAACAAAGACCCGAGATGACATGCTGGGAGAGATGGATGCCAGTCTCC 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 81 AlaAspGlyLysAspTyrSerHisAspLeuLeuArgLeuGlnSerProAlaLys 100
QY 301 ATCACTGGCGTGTGTCGAGCCCTCCAGCTCCGTCGTCGTCGTCGTCGTCGTCG 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 101 llettrAspAlaValleuValleuGlnleuProthrGlnGlnProGlnleuGlyserThr 120
QY 361 TGCTCATTTCCGGCTGGGCGAGC-----ACGTCCAGCCCGCAAGTACGCTGCTCAC 414
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 CysgluAlaSerGlyTrpGlySerTrileuProGlyProAsp**PhegluPheProAsp 140
QY 415 ACCTTGGCATGCAGCAACATCATGATGAGCAGCAGAGTGAAGAGCCAGCC 474
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 141 GluileGlnCysValGlnleuThrleuGlnAsnThrPheCysAla**AlaHisPro 160
QY 475 GGCAACATCAGACAGACCATGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 534
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 161 **LysValThrGlnuserMetleuGlnleuGlyTyrleuProGlyLysAspPheCys 180
QY 535 CAGGTCATCTCCGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 594
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 MetGlyAspSerGlyGlyProleuileCysasnGlyMetTrpGlnGlyleThrSerTrp 200
QY 595 GGCAAGATCGGTGTGGGATCACCCGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 654
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 201 GlyHisThrProCysGlySerAlaAsnLysProSerIleTyrThrLysleuIlePheTyr 220
QY 655 GTGCACTGATCCAGAGAGATGAGAAACAAT 687
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 221 LeuAspTrpIleAsn**ThrIleThrGlnAsn 231
```

RESULT 13

A29586
tissue kallikrein (EC 3.4.21.35) hGK-1 precursor - human
N:Alternate names: glandular kallikrein
C:Species: Homo sapiens (man)
C:Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 22-Jun-1999

C:Accession: A29586
R:Schledlich, L.J.; Bennetts, B.H.; Morris, B.J.
DNA 6, 429-437, 1987
A:Title: Primary structure of a human glandular kallikrein gene.
A:Reference number: A29586; MUID:88054467; PMID:2824146
A:Accession: A29586
A:Molecule type: DNA
A:Residues: 1-261 <SCH>
A:Cross-references: GB:M18157; NID:9186640; PIDN:AAA74454.1; PID:9386842
A>Note: the authors translated the codon TAC for residue 43 as Trp

C:Genetics:
A:Introns: 16/1; 69/2; 165/1; 210/3
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:25-253/Domain: trypsin homology <TRY>
F:65,120,213/Active site: His, Asp, Ser #status predicted

Alignment Scores:

Pred. No.:	2,46-34	Length:	261
Score:	577.50	Matches:	106
Percent Similarity:	62.71%	Conservative:	42
Best Local Similarity:	44.92%	Mismatches:	81
Query Match:	45.29%	Indels:	7
DB:	2	Gaps:	1

US-09-856-320A-1_COPY_272_958 (1-687) x A29586 (1-261)

```
QY 1 ATCATCAAGGGGTTGAGTGCAGACCTCCAGCCCTGGAGGAGCCCTGTTCGAG 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 25 lIeValGlyglYTrpGlucslulysasnserHisProtrpGlnValAlaValTyrSer 44
QY 61 AAGAGCGGCTACTGTGTGGGCGAGCTCATCGCCCAAGATGGCTCTGCACAGCC 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 45 HlsglyTrpAlaHisCysgllyGlyValleuValasnProGlnTrpValleuThrAla 64
QY 121 CACTGCTCAAGCCCTCATAGTACCTGGGCGAGCACACCTCCAGAGAGGAG 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 65 HiscysLeuLysAsnSerGlnValTrpLeuGlnArgHisAsnLeuPhegluPro 84
QY 181 GGCCTGAGCAGACCCGAGCAGCCAGTCTCCCAACCCCGGCTTCAACAACAGC 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 85 AspThrGlyGlnAlaGlyAlaProValSerHisSerPheProHisProLeuTyrAsnSer 104
QY 241 CTC-----CCCAACAAAGACCCGAGATGACATGATGATGATGATGATGATGATG 279
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 105 LeuLeuLysHisGlnSerLeuArgProAspGlnLysSerSerHisAspLeuMetleu 124
QY 280 AAGATGCGATGCCAGTCTCATGACCTGGGCTGGGCGAGCCCTGACCTCTCTCACGC 339
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 125 ArgLeuSerGlnProAlaLysIleThrAspValLysValleuGlyleuProThrGln 144
QY 340 TGTGCACTGTGGGCGAGCAGCTGCTCATTTCCGGCTGGGCGAGCAGCTCCAGCCCCAG 399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 145 GluProAlaLeuGlyThrThrCysTyrAlaSerGlyTrpGlySerTrileuProGln 164
QY 400 TTAGCGCTGCTCACACCTTCGATGCGCAACATCACATCATGATGAGCAGCAAGTGT 459
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 165 PheLeuArgProArgSerLeuGlnCysValSerleuHisLeuLeuSerHisAspPheCys 184
QY 460 GAGAACGCTTACCCCGGAGATCACAGACACATGTCGTCGTCGTCGTCGTCGTCGTCG 519
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 185 AlaArgAlaTyrSerGlnLysValThrGlnPheMetleuGlnAlaGlyleuThrThrGly 204
QY 520 GGCAAGATCGGTGTGGGATCACCCGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 579
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 205 GlyLysAspThrCysGlyLysAspSerGlyLysProleuValCysAsnGlyValleuGln 224
QY 580 GGCATTTATCTCTGGGCGAGATCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 639
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 225 GlyIleThrSerTrpGlyProGlnProCysAlaLeuProGlnLysProAlaValTyrThr 244
QY 640 AAAGTCTCAAAATATGTGACTGGATCCAGAGAGATGAGAAACAAT 687
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```


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GenCore version 5.1.6
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OM nucleic acid - nucleic search, using sw model

Run on: October 15, 2003, 16:00:49 ; Search time 250.886 Seconds
(without alignments)
7105.351 Million cell updates/sec

Title: US-09-856-320a-1_COPY_272_958

Perfect score: 687
Sequence: 1 accatcaagggttcgagtg.....aggagacatgaagaacaat 687

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1731049 seqs, 1297405648 residues

Total number of hits satisfying chosen parameters: 3462098

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	687	100.0	1186 14 US-10-205-823-211	Sequence 211, App
2	687	100.0	1204 11 US-09-946-374-169	Sequence 169, App
3	687	100.0	1204 12 US-10-015-387A-169	Sequence 169, App
4	687	100.0	1204 12 US-10-137-870-505	Sequence 505, App
5	687	100.0	1204 12 US-10-140-018-505	Sequence 505, App
6	687	100.0	1204 12 US-10-140-021-505	Sequence 505, App
7	687	100.0	1204 12 US-10-140-214-505	Sequence 505, App
8	687	100.0	1204 12 US-10-140-471-505	Sequence 505, App
9	687	100.0	1204 12 US-10-140-807-505	Sequence 505, App
10	687	100.0	1204 12 US-10-140-922-505	Sequence 505, App
11	687	100.0	1204 12 US-10-140-924-505	Sequence 505, App
12	687	100.0	1204 12 US-10-140-926-505	Sequence 505, App
13	687	100.0	1204 12 US-10-141-698-505	Sequence 505, App
14	687	100.0	1204 12 US-10-141-702-505	Sequence 505, App
15	687	100.0	1204 12 US-10-141-704-505	Sequence 505, App
16	687	100.0	1204 12 US-10-142-421-505	Sequence 505, App

17	687	100.0	1204 12 US-10-142-432-505	Sequence 505, App
18	687	100.0	1204 12 US-10-142-767-505	Sequence 505, App
19	687	100.0	1204 12 US-10-143-033-505	Sequence 505, App
20	687	100.0	1204 12 US-10-144-994-505	Sequence 505, App
21	687	100.0	1204 12 US-10-145-628-505	Sequence 505, App
22	687	100.0	1204 12 US-10-145-631-505	Sequence 505, App
23	687	100.0	1204 12 US-10-145-633-505	Sequence 505, App
24	687	100.0	1204 12 US-10-145-746-505	Sequence 505, App
25	687	100.0	1204 12 US-10-145-748-505	Sequence 505, App
26	687	100.0	1204 12 US-10-145-823-505	Sequence 505, App
27	687	100.0	1204 12 US-10-145-826-505	Sequence 505, App
28	687	100.0	1204 12 US-10-145-870-505	Sequence 505, App
29	687	100.0	1204 12 US-10-145-876-505	Sequence 505, App
30	687	100.0	1204 12 US-10-145-959-505	Sequence 505, App
31	687	100.0	1204 12 US-10-146-724-505	Sequence 505, App
32	687	100.0	1204 12 US-10-146-725-505	Sequence 505, App
33	687	100.0	1204 12 US-10-146-795-505	Sequence 505, App
34	687	100.0	1204 12 US-10-147-485-505	Sequence 505, App
35	687	100.0	1204 12 US-10-147-501-505	Sequence 505, App
36	687	100.0	1204 12 US-10-147-504-505	Sequence 505, App
37	687	100.0	1204 12 US-10-147-506-505	Sequence 505, App
38	687	100.0	1204 12 US-10-147-509-505	Sequence 505, App
39	687	100.0	1204 12 US-10-147-510-505	Sequence 505, App
40	687	100.0	1204 12 US-10-147-511-505	Sequence 505, App
41	687	100.0	1204 12 US-10-147-529-505	Sequence 505, App
42	687	100.0	1204 12 US-10-152-357-505	Sequence 505, App
43	687	100.0	1204 12 US-10-153-586-505	Sequence 505, App
44	687	100.0	1204 12 US-10-158-783-505	Sequence 505, App
45	687	100.0	1204 12 US-10-158-786-505	Sequence 505, App

ALIGNMENTS

RESULT 1
US-10-205-823-211
Sequence 211, Application US/10205823
GENERAL INFORMATION: US20030108963A1
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbacheva, Bella
APPLICANT: Hoersch, Sebastian
APPLICANT: Kametkar, Shubhangi
APPLICANT: Monney, Angela M.
APPLICANT: Glatz, Karen
APPLICANT: Zhao, Xumei
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-044
CURRENT APPLICATION NUMBER: US/10/205,823
PRIOR FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
SOFTWARE: fastseq for Windows Version 4.0
SEQ ID NO 211
LENGTH: 1186
TYPE: DNA
ORGANISM: Homo sapiens
US-10-205-823-211

Query Match 100.0%; Score 687; DB 14; Length 1186;
Best Local Similarity 100.0%; Pred. No. 1,9e-186;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATCTCAAGGGGTTGAGTGCAGACCTTCCAGCCCTGGGAGGAGCCCTTTGGAG 60
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DB 185 ATCTCAAGGGGTTGAGTGCAGACCTTCCAGCCCTGGGAGGAGCCCTTTGGAG 244
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QY 61 AAGAGGGGCTACTCTGTGGGGGAGCGCTCATCGCCCGAGATGGCTCTGACAGAGCC 120
    |||||||
DB 245 AAGAGGGGCTACTCTGTGGGGGAGCGCTCATCGCCCGAGATGGCTCTGACAGAGCC 304
    |||||||
QY 121 CACTGCTCAAGCCCGCTACATATGTTCACTGGGGGAGCAACAACCTTCAGAGAGAG 180
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DB 305 CACTGCTCAAGCCCGCTACATATGTTCACTGGGGGAGCAACAACCTTCAGAGAGAG 364
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QY 181 GGGGTGAGGAGAGCCCGGAGAGCGCATGAGTCTTCCCGACCCCGGCTTCAACAGAGC 240
    |||||||
DB 365 GGGGTGAGGAGAGCCCGGAGAGCGCATGAGTCTTCCCGACCCCGGCTTCAACAGAGC 424
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QY 241 CTCCCAACAAGAGCAACCGCATGATGCTGTGAAGATGGATGCCAGTCTCC 300
    |||||||
DB 425 CTCCCAACAAGAGCAACCGCATGATGCTGTGAAGATGGATGCCAGTCTCC 484
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QY 301 ATCACTGGGCTGTGCAGCCCTCACCCTCTCTACAGCTGTGTCTGTGCGCAGCAGC 360
    |||||||
DB 485 ATCACTGGGCTGTGCAGCCCTCACCCTCTCTACAGCTGTGTGTGCTGTGCGCAGCAGC 544
    |||||||
QY 361 TGGCTCATTTCCGGCTGGGGGAGAGCAAGTCCAGTACCGCCGCTTCAACAGCTTG 420
    |||||||
DB 545 TGGCTCATTTCCGGCTGGGGGAGAGCAAGTCCAGTACCGCCGCTTCAACAGCTTG 604
    |||||||
QY 421 CGATGCGCAACATCACCATTATGAGCAGCAGAGTGTGAAGACCGCTTACCCGGAGAC 480
    |||||||
DB 605 CGATGCGCAACATCACCATTATGAGCAGCAGAGTGTGAAGACCGCTTACCCGGAGAC 664
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QY 481 ATCAAGACACCATGTGTGTGTGCCAGGTGAGAGAGGGGCAAGACCTCTGCCAGGT 540
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DB 665 ATCAAGACACCATGTGTGTGTGCCAGGTGAGAGAGGGGCAAGACCTCTGCCAGGT 724
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QY 541 GACTCGGGGGGCGCTGTGTGTGTACACAGTCTTTCAGAGCATTTATCTCTGGGGGAG 600
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QY 601 GATCGGTGTGGATCACCCGAAAGCGTGTGTGTACAGAAAGTCTCAATATATGTGAGC 660
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DB 785 GATCGGTGTGGATCACCCGAAAGCGTGTGTGTGTACAGAAAGTCTCAATATATGTGAGC 844
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QY 661 TGGATCCAGAGAGCATGAAGAACAT 687
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DB 845 TGGATCCAGAGAGCATGAAGAACAT 871
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RESULT 2
US-09-946-374-169

; Sequence 169, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Christopher J.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paonl, Nicholas F.

```
APPLICANT: Roy, Margaret Ann  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830PICI  
CURRENT FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098803  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098821  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098843  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/099536  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099596  
PRIOR FILING DATE: 1998-09-09  
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PRIOR FILING DATE: 1998-09-09  
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PRIOR FILING DATE: 1998-09-09  
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PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100684  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100710
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;; PRIOR APPLICATION NUMBER: 60/100711
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;; PRIOR APPLICATION NUMBER: 60/100848
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;; PRIOR APPLICATION NUMBER: 60/103679
;; PRIOR FILING DATE: 1998-10-08
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;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105000
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105002
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105104
;; PRIOR FILING DATE: 1998-10-21
;; PRIOR APPLICATION NUMBER: 60/105169
;; PRIOR FILING DATE: 1998-10-22
;; PRIOR APPLICATION NUMBER: 60/105266
;; PRIOR FILING DATE: 1998-10-22
;; PRIOR APPLICATION NUMBER: 60/105693
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105694
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 687; DB 11; Length 1204;
Best Local Similarity 100.0%; Pred. No. 1.9e-186;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCATCAAGGGGTTGAGTGAAGCCTCACTCCAGCCCTGGCAGGACCCCTGTTGAG 60
DB 169 ATCATCAAGGGGTTGAGTGAAGCCTCACTCCAGCCCTGGCAGGACCCCTGTTGAG 228
QY 61 AAGACCGCGCTACTCTGTGTGGGCGACGCTATCGCCCAATGAGTGGTCTGTGACAGAGCC 120
DB 229 AAGACCGCGCTACTCTGTGTGGGCGACGCTATCGCCCAATGAGTGGTCTGTGACAGAGCC 288
QY 121 CACTGCCTCAAGCCCGCTACATAGTTCACCTGGGCGACACAACTCCAGAGAGAG 180
DB 289 CACTGCCTCAAGCCCGCTACATAGTTCACCTGGGCGACACAACTCCAGAGAGAG 348
QY 181 GCGTGTGAGCAGACCCGCGACAGCCACTGATGCTTCCCGCACCCCGGCTTCAACAACAGC 240
DB 349 GCGTGTGAGCAGACCCGCGACAGCCACTGATGCTTCCCGCACCCCGGCTTCAACAACAGC 408
QY 241 CTCGCCAACAAAGACACCCGCAATGACATCATGCTGTGTAAGATGGATCGGCACTTCC 300
DB 409 CTCGCCAACAAAGACACCCGCAATGACATCATGCTGTGTAAGATGGATCGGCACTTCC 468
QY 301 ATCACTGGGCTGTGCGAGACCCCTCAACCCCTCTCTCAAGCTGTGTACATGCTGGACAGGC 360
DB 469 ATCACTGGGCTGTGCGAGACCCCTCAACCCCTCTCTCAAGCTGTGTACATGCTGGACAGGC 528
QY 361 TGCCTCATTTCCGGCTGGGGGAGCAGCTCAGACCCCAATTAAGCCTGCTGCTCAACCTTG 420
DB 529 TGCCTCATTTCCGGCTGGGGGAGCAGCTCAGACCCCAATTAAGCCTGCTGCTCAACCTTG 588
QY 421 CGATGCGCCAAATATACCATCATTTATAGACACGGAAGTGTGAGAACGCTTACCCGGCAAC 480
DB 589 CGATGCGCCAAATATACCATCATTTATAGACACGGAAGTGTGAGAACGCTTACCCGGCAAC 648

OY		481	ATCAGACGACCATGGTGTGTGCCAGCGCTGCAGGAAGGGGGCAAGACTCCGCGCAAGGT	540
Db		649	ATCAGACGACCATGGTGTGTGCCAGCGCTGCAGGAAGGGGGCAAGACTCCGCGCAAGGT	708
OY		541	GACTCCGGGGGCCCTCTGCTGTGTAAACGATCTCTTCAAGGCATTATCTCTGGGGCCAG	600
Db		709	GACTCCGGGGGCCCTCTGCTGTGTAAACGATCTCTTCAAGGCATTATCTCTGGGGCCAG	768
OY		601	GATCCGTTGGGATATACCAGGAGGCTTGTCACAGAAAAGTGTGCAATAATATGTGCAC	660
Db		769	GATCCGTTGGGATATACCAGGAGGCTTGTCACAGAAAAGTGTGCAATAATATGTGCAC	828
OY		661	TGGATCCAGAGACGATGAGAACAAT	687
Db		829	TGGATCCAGAGACGATGAGAACAAT	855
 RESULT 3 US-10-015-387A-169				
:		:	Sequence 169, Application US/10015387A	
:		:	Publication No. US20030135034v1	
:		:	GENERAL INFORMATION:	
:		:	APPLICANT: Baker, Kevin P.	
:		:	APPLICANT: Botstein, David	
:		:	APPLICANT: Desnoyers, Luc	
:		:	APPLICANT: Eaton, Dan I.	
:		:	APPLICANT: Ferrara, Napoleone	
:		:	APPLICANT: Fong, Sherman	
:		:	APPLICANT: Gao, Wei-Qiang	
:		:	APPLICANT: Goddard, Audrey	
:		:	APPLICANT: Godowski, Paul J.	
:		:	APPLICANT: Gueney, Christopher J.	
:		:	APPLICANT: Hillan, Kenneth J.	
:		:	APPLICANT: Pan, James	
:		:	APPLICANT: Paoni, Nicholas F.	
:		:	TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic	
:		:	TITLE OF INVENTION: Acids Encoding the Same	
:		:	FILE REFERENCE: P2830P1C54	
:		:	CURRENT APPLICATION NUMBER: US/10/015,387A	
:		:	CURRENT FILING DATE: 2001-12-12	
:		:	Prior Application removed - See File Wrapper or Palm	
:		:	NUMBER OF SEQ ID NOS: 477	
:		:	SEQ ID NO 169	
:		:	LENGTH: 1204	
:		:	TYPE: DNA	
:		:	ORGANISM: Homo sapiens	
:		:	US-10-015-387A-169	
 Query Match 100.0%; Score 687; DB 12; Length 1204; Best Local Similarity 100.0%; Pred. No. 1,9e-186;				
Matches	687;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
OY		1	ATCATCAAGGGGTTGAGTGCAGGCTTCACCTGCCAGCCCTGGCAGGACGCCCTGTTGAG	60
Db		169	ATCATCAAGGGGTTGAGTGCAGGCTTCACCTGCCAGCCCTGGCAGGACGCCCTGTTGAG	228
OY		61	AAGAGGGGGCTACTGTGTGGGGGCGAGCGTCANCGCCCCCAATAGGCTCTTACAGCACCC	120
Db		229	AAGAGGGGGCTACTGTGTGGGGGCGAGCGTCANCGCCCCCAATAGGCTCTTACAGCACCC	288
OY		121	CACGTGCTCAAGCCCGCTATATAGTTACCTGGGGGAGCACAACCTTCAGAAAGAGAG	180
Db		289	CACGTGCTCAAGCCCGCTATATAGTTACCTGGGGGAGCACAACCTTCAGAAAGAGAG	348
OY		181	GGCTGTGAGCAGACCCGGAGCAGCACTGATGCTTCCCACACCCCGGCTTCAACAACAGC	240
Db		349	GGCTGTGAGCAGACCCGGAGCAGCACTGATGCTTCCCACACCCCGGCTTCAACAACAGC	408
OY		241	CTCCCAACAAGAACACACCGCAATGACATATGCTGTGTGAAGATGTGCGTAGTCTGCC	300
Db		409	CTCCCAACAAGAACACACCGCAATGACATATGCTGTGTGAAGATGTGCGTAGTCTGCC	468

OY	301	ATPACCGGGGCTGTGGACCCCTCAACCCCTCTCAGCGCTGTGACAGCGTGGGACACAGC	360
Dp	469	ATACCTGGGGCTGTGGACCCCTCAACCCCTCTCAGCGCTGTGACAGCGTGGGACACAGC	528
OY	361	TGCGCTCATTTCCGGCTGGGGGAGCAGCGTCCAGCCCGCAGTTACGCGCTGACACACCTTGG	420
Dp	529	TGCGCTCATTTCCGGGCTGGGGGAGCAGCGTCCAGCCCGCAGTTACGCGCTGCTCACACCTTG	588
OY	421	CGATGGGCCAATCATCACTATTGAGCACCGAAGTGTGAAGAGCGCTACCCGGCAC	480
Dp	589	CGATGGGCCAATCATCACTATTGAGCACCGAAGTGTGAAGAGCGCTACCCGGCAC	648
OY	481	ATPACGAGACACCATGGTGTGTGCCAGCGGCGAGAGGGGGCAAGACTCTGCGAAGGT	540
Dp	649	ATPACGAGACACCATGGTGTGTGCCAGCGGCGAGAGGGGGCAAGACTCTGCGAAGGT	708
OY	541	GACTCCGGGGGCCCTCTGGCTGTGTAAACAGCTCTCTCAAGGCATTATCTCCGTGGGCGAG	600
Dp	709	GACTCCGGGGGCCCTCTGGCTGTGTAAACAGCTCTCTCAAGGCATTATCTCCGTGGGCGAG	768
OY	601	GATCCGTGTGCGATCAACCCGAAAGCCTGGTGTCTACACGAAAGTCTGCAATATATGGAC	660
Dp	769	GATCCGTGTGCGATCAACCCGAAAGCCTGGTGTCTACACGAAAGTCTGCAATATATGGAC	828
OY	661	TGGATCCAGGAGCATGGAAGAACT	687
Dp	829	TGGATCCAGGAGCATGGAAGAACT	855

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RESULT 4
US-10-137-870-505
: Sequence 505: Application US/10137870
: Publication No. US20030138883A1
GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen.
: APPLICANT: DeForge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tunas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zhenlu
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3330R1C155
: CURRENT APPLICATION NUMBER: US/10/137,870
: CURRENT FILING DATE: 2002-05-03
: Prior Application removed - See Palm or File Wrapper
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 505
: LENGTH: 1204
: TYPE: DNA
: ORGANISM: Homo Sapien
US-10-137-870-505

Query Match      100.0%; Score 687; DB 12; Length 1204;
Best Local Similarity 100.0%; Pred. No. 1,9e-186;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 ATCATCAAGGGGTGAGATGCAAGCCTCACTCCAGCCCTGGCAGAGGACGCTGTTCAG 60
DB      169 ATCTATCAAGGGGTGAGATGCAAGCCTCACTCCAGCCCTGGCAGAGGACGCTGTTCAG 228

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QY 61 AAGAGCGGCTACTCTGTGGGGGCGACGCTCATCGCCCCAGATGGCTCTGTGACAGAGCC 120
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 229 AAGAGCGGCTACTCTGTGGGGGCGACGCTCATCGCCCCAGATGGCTCTGTGACAGAGCC 288
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 121 CACTGCTCAAGCCCCGGCTACATAGTACCGTGGGGGAGCAACCTCCAGAAAGAGGAG 180
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 289 CACTGCTCAAGCCCCGGCTACATAGTACCGTGGGGGAGCAACCTCCAGAAAGAGGAG 348
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 181 GGCCTGAGACAGACCCGGGAGACAGCCACTGAGTCTTCCCAACCCCGGCTTCAACAGAC 240
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 349 GGCCTGAGACAGACCCGGGAGACAGCCACTGAGTCTTCCCAACCCCGGCTTCAACAGAC 408
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 241 CTCGCCCAACAAAGACACCCGCAATGACATCATGCTGTGAGATGGCATCGCCAGTCTCC 300
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 409 CTCGCCCAACAAAGACACCCGCAATGACATCATGCTGTGAGATGGCATCGCCAGTCTCC 468
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 301 ATCAGCTGGGCTGTGAGACCCCTCACCCTCTCCAGCTGTGTACATGCTGGGACAGC 360
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 469 ATCAGCTGGGCTGTGAGACCCCTCACCCTCTCCAGCTGTGTACATGCTGGGACAGC 528
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 361 TGCCCTCATTTCCGGCTGGGGGAGACAGCTCAGACCCCAAGTTACGCTGCTCAGACCTTG 420
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 529 TGCCCTCATTTCCGGCTGGGGGAGACAGCTCAGACCCCAAGTTACGCTGCTCAGACCTTG 588
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 421 CGATCGGCCAATATCATCATTTGAGACACAGAAAGTGTGAGACGCTTACCCCGGCAAC 480
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 589 CGATCGGCCAATATCATCATTTGAGACACAGAAAGTGTGAGAAAGCGCTTACCCCGGCAAC 648
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 481 ATCAGACACCATGCTGTGTGCCAGCTGAGAGAAAGGGGCAAGAAATCTCTGCCAGAGT 540
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 649 ATCAGACACCATGCTGTGTGCCAGCTGAGAGAAAGGGGCAAGAAATCTCTGCCAGAGT 708
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 541 GACTCCGGGGGCCCTCTGTGTGTAAACAGTCTCTTCAAGGCAATATCTCTGGGGCCAG 600
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 709 GACTCCGGGGGCCCTCTGTGTGTAAACAGTCTCTTCAAGGCAATATCTCTGGGGCCAG 768
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 601 GATCGGTGTGGATATCACCAGAAAGCTGTGTCTTACAGAAAGTGTGAAATATGTGAC 660
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 769 GATCGGTGTGGATATCACCAGAAAGCTGTGTCTTACAGAAAGTGTGAAATATGTGAC 828
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 661 TGGATCCAGAGACGATGAGAACAT 687
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 829 TGGATCCAGAGACGATGAGAACAT 855
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

RESULT 5
US-10-140-018-505
; Sequence 505, Application US/10140018
; Publication No. US20030138885A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria A.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NOCETIC
; FILE REFERENCE: P3330R1C158
; CURRENT APPLICATION NUMBER: US/10/140,018
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
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QY 61 AAGAGCGGCTACTCTGTGGGGGCGACGCTCATCGCCCCAGATGGCTCTGTGACAGAGCC 60
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 229 AAGAGCGGCTACTCTGTGGGGGCGACGCTCATCGCCCCAGATGGCTCTGTGACAGAGCC 228
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 121 CACTGCTCAAGCCCCGGCTACATAGTACCGTGGGGGAGCAACCTCCAGAAAGAGGAG 180
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 289 CACTGCTCAAGCCCCGGCTACATAGTACCGTGGGGGAGCAACCTCCAGAAAGAGGAG 348
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 181 GGCCTGAGACAGACCCGGGAGACAGCCACTGAGTCTTCCCAACCCCGGCTTCAACAGAC 240
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 349 GGCCTGAGACAGACCCGGGAGACAGCCACTGAGTCTTCCCAACCCCGGCTTCAACAGAC 408
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 241 CTCGCCCAACAAAGACACCCGCAATGACATCATGCTGTGAGATGGCATCGCCAGTCTCC 300
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 409 CTCGCCCAACAAAGACACCCGCAATGACATCATGCTGTGAGATGGCATCGCCAGTCTCC 468
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 301 ATCAGCTGGGCTGTGAGACCCCTCACCCTCTCCAGCTGTGTACATGCTGGGACAGC 360
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 469 ATCAGCTGGGCTGTGAGACCCCTCACCCTCTCCAGCTGTGTACATGCTGGGACAGC 528
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 361 TGCCCTCATTTCCGGCTGGGGGAGACAGCTCAGACCCCAAGTTACGCTGCTCAGACCTTG 420
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 529 TGCCCTCATTTCCGGCTGGGGGAGACAGCTCAGACCCCAAGTTACGCTGCTCAGACCTTG 588
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 421 CGATCGGCCAATATCATCATTTGAGACACAGAAAGTGTGAGAAAGCGCTTACCCCGGCAAC 480
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 589 CGATCGGCCAATATCATCATTTGAGACACAGAAAGTGTGAGAAAGCGCTTACCCCGGCAAC 648
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 481 ATCAGACACCATGCTGTGTGCCAGCTGAGAGAAAGGGGCAAGAAATCTCTGCCAGAGT 540
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 649 ATCAGACACCATGCTGTGTGCCAGCTGAGAGAAAGGGGCAAGAAATCTCTGCCAGAGT 708
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 541 GACTCCGGGGGCCCTCTGTGTGTAAACAGTCTCTTCAAGGCAATATCTCTGGGGCCAG 600
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 709 GACTCCGGGGGCCCTCTGTGTGTAAACAGTCTCTTCAAGGCAATATCTCTGGGGCCAG 768
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 601 GATCGGTGTGGATATCACCAGAAAGCTGTGTCTTACAGAAAGTGTGAAATATGTGAC 660
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 769 GATCGGTGTGGATATCACCAGAAAGCTGTGTCTTACAGAAAGTGTGAAATATGTGAC 828
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 661 TGGATCCAGAGACGATGAGAACAT 687
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

QY 829 TGGATCCAGAGACGATGAGAACAT 855
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

RESULT 6
US-10-140-021-505
; Sequence 505, Application US/10140021
; Publication No. US20030138886A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NOCETIC
; FILE REFERENCE: P3330R1C158
; CURRENT APPLICATION NUMBER: US/10/140,018
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
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; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C167
; CURRENT APPLICATION NUMBER: US/10/140,021
; PRIOR APPLICATION REMOVED - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-021-505

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Query Match 100.0%; Score 687; DB 12; Length 1204;

Best Local Similarity 100.0%; Pred. No. 1,9e-186; Mismatches 0; Indels 0; Gaps 0;

Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATCATCAAGGGGTTGAGTGCAAGCCCTCACTCCAGCCCTGGCAGGAGCCCTGTTGAG 60
DB 169 ATCATCAAGGGGTTGAGTGCAAGCCCTCACTCCAGCCCTGGCAGGAGCCCTGTTGAG 228
QY 61 AAGCGGGGCTACTCTGTGGGGGAGCGCTCATGSCCCCGAGATGGSCCTGACAGCAGCC 120
DB 229 AAGCGGGGCTACTCTGTGGGGGAGCGCTCATGSCCCCGAGATGGSCCTGACAGCAGCC 288
QY 121 CACTGCTCAAGCCCGCTCATAGTTCACTGGGGGAGCACAACCTCCAGAAAGAGAG 180
DB 289 CACTGCTCAAGCCCGCTCATAGTTCACTGGGGGAGCACAACCTCCAGAAAGAGAG 348
QY 181 GCGTGTAGCAGACCCGAGACGCACTGAGTCTCTCCCAACCCCGGCTTCAACAGC 240
DB 349 GCGTGTAGCAGACCCGAGACGCACTGAGTCTCTCCCAACCCCGGCTTCAACAGC 408
QY 241 CTCGCCAACAAGACCGCAATGACATGCTGTGTAAGATGGATGGCCAGTCTCC 300
DB 409 CTCGCCAACAAGACCGCAATGACATGCTGTGTAAGATGGATGGCCAGTCTCC 468
QY 301 ATCACTGGGCTGTGACACCCCTCACTCTCTCACTGTGTCACTGTGACAGCAGC 360
DB 469 ATCACTGGGCTGTGACACCCCTCACTCTCTCTCACTGTGTCACTGTGACAGCAGC 528
QY 361 TGCCTCATTTCCGGCTGTGGGAGCAGCTCCAGCCCAAGTTAGCGCTGCTCACACTTG 420
DB 529 TGCCTCATTTCCGGCTGTGGGAGCAGCTCCAGCCCAAGTTAGCGCTGCTCACACTTG 588
QY 421 CGATGGCCCAACATCATCATATTTAGCAGACAGAGTGAAGGCTACCCCGGCAAC 480
DB 589 CGATGGCCCAACATCATCATATTTAGCAGACAGAGTGAAGGCTACCCCGGCAAC 648
QY 481 ATCAAGACACATGATGTGTGCGAGCGTGCAGAGAGGAGGCAAGGATCTCTGCAAGGT 540
DB 649 ATCAAGACACATGATGTGTGCGAGCGTGCAGAGAGGAGGCAAGGATCTCTGCAAGGT 708
QY 541 GACTCGGGGGCCCTCTGTGTGTGAACAGTCTCTTCAAGGATTTATCTCTGGGGCAG 600
DB 709 GACTCGGGGGCCCTCTGTGTGTGAACAGTCTCTTCAAGGATTTATCTCTGGGGCAG 768
QY 601 GATCCGTTGCGATCACCGGAAAGCGTGTACAGAAAGTCTGCAAAATATGTGAC 660
DB 769 GATCCGTTGCGATCACCGGAAAGCGTGTGTACAGAAAGTCTGCAAAATATGTGAC 828
QY 661 TGGATCCAGGAGAGATGAAGAACAT 687
DB 829 TGGATCCAGGAGAGATGAAGAACAT 855

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RESULT 7

US-10-140-274-505

Sequence 505, Application US/10140274

Publication No. US20030143674A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Maury E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P330R1C161

CURRENT APPLICATION NUMBER: US/10/140,274

CURRENT FILING DATE: 2002-05-06

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 505

LENGTH: 1204

TYPE: DNA

ORGANISM: Homo Sapien

US-10-140-274-505

Query Match 100.0%; Score 687; DB 12; Length 1204;

Best Local Similarity 100.0%; Pred. No. 1,9e-186; Mismatches 0; Indels 0; Gaps 0;

Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATCATCAAGGGGTTGAGTGCAAGCCCTCACTCCAGCCCTGGCAGGAGCCCTGTTGAG 60
DB 169 ATCATCAAGGGGTTGAGTGCAAGCCCTCACTCCAGCCCTGGCAGGAGCCCTGTTGAG 228
QY 61 AAGCGGGGCTACTCTGTGGGGGAGCGCTCATGSCCCCGAGATGGSCCTGACAGCAGCC 120
DB 229 AAGCGGGGCTACTCTGTGGGGGAGCGCTCATGSCCCCGAGATGGSCCTGACAGCAGCC 288
QY 121 CACTGCTCAAGCCCGCTCATAGTTCACTGGGGGAGCACAACCTCCAGAAAGAGAG 180
DB 289 CACTGCTCAAGCCCGCTCATAGTTCACTGGGGGAGCACAACCTCCAGAAAGAGAG 348
QY 289 CACTGCTCAAGCCCGCTCATAGTTCACTGGGGGAGCACAACCTCCAGAAAGAGAG 348
QY 181 GCGTGTAGCAGACCCGAGACGCACTGAGTCTCTCCCAAGATGGATGGCCAGTCTCC 240
DB 349 GCGTGTAGCAGACCCGAGACGCACTGAGTCTCTCCCAAGATGGATGGCCAGTCTCC 408
QY 349 GCGTGTAGCAGACCCGAGACGCACTGAGTCTCTCCCAAGATGGATGGCCAGTCTCC 408
QY 421 CTCGCCAACAAGACCGCAATGACATGCTGTGTAAGATGGATGGCCAGTCTCC 300
DB 409 CTCGCCAACAAGACCGCAATGACATGCTGTGTAAGATGGATGGCCAGTCTCC 468
QY 301 ATCACTGGGCTGTGACACCCCTCACTCTCTCACTGTGTCACTGTGACAGCAGC 360
DB 469 ATCACTGGGCTGTGACACCCCTCACTCTCTCTCACTGTGTCACTGTGACAGCAGC 528
QY 361 TGCCTCATTTCCGGCTGTGGGAGCAGCTCCAGCCCAAGTTAGCGCTGCTCACACTTG 420
DB 529 TGCCTCATTTCCGGCTGTGGGAGCAGCTCCAGCCCAAGTTAGCGCTGCTCACACTTG 588
QY 421 CGATGGCCCAACATCATCATATTTAGCAGACAGAGTGAAGGCTACCCCGGCAAC 480
DB 589 CGATGGCCCAACATCATCATATTTAGCAGACAGAGTGAAGGCTACCCCGGCAAC 648

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Db 169 ATCATCAAGGGGTTGAGTGCAGAGCTCACTCCAGCCCTGGCAGGAGCCCTGTTGAG 228
QY 61 AAGACGGGGTACTCTGTGGGGCGAGCCCTATCGCCCGCAGATGGCTCTGACAGCAGCC 120
Db 229 AAGACGGGGTACTCTGTGGGGCGAGCCCTATCGCCCGCAGATGGCTCTGACAGCAGCC 288
QY 121 CACTGCTCAAGCCCGCTACATATGTTACCTGGGGGACAGCAAACTTCAGAGAGAG 180
Db 289 CACTGCTCAAGCCCGCTACATATGTTACCTGGGGGACAGCAAACTTCAGAGAGAG 348
QY 181 GGCTGTAGAGAGAGCCCGAGAGCCATGAGTCTTCCCGCCCGCCGCTTCAGAGAGAG 240
Db 349 GGCTGTAGAGAGAGCCCGAGAGCCATGAGTCTTCCCGCCCGCCGCTTCAGAGAGAG 408
QY 241 CTCCCAACAAAGACACCGCAATGACATCATGCTGGTGAAGATGGATGCCAGCTGCC 300
Db 409 CTCCCAACAAAGACACCGCAATGACATCATGCTGGTGAAGATGGATGCCAGCTGCC 468
QY 301 ATCACTGGGCTGTGGCAACCCCTACCTCTCTCAAGCTGTGTACTGTGGGACAGC 360
Db 469 ATCACTGGGCTGTGGCAACCCCTACCTCTCTCAAGCTGTGTACTGTGGGACAGC 528
QY 361 TGCTCATATTTCCGGGCTGGGGAGCAGCTCCAGCCCGAGTTACGCTGCTCAGACCTTG 420
Db 529 TGCTCATATTTCCGGGCTGGGGAGCAGCTCCAGCCCGAGTTACGCTGCTCAGACCTTG 588
QY 421 CGATGCCCAACATCACCATCATTTGAGCAGCAGCAAGTGTGAAGAGGCTTACCCCGGAC 480
Db 589 CGATGCCCAACATCACCATCATTTGAGCAGCAGCAAGTGTGAAGAGGCTTACCCCGGAC 648
QY 481 ATCAACACACATGATGTGTGTGGCAGGCTGAGAGAGGGGCAAGGACTCTGCGAAGGT 540
Db 649 ATCAACACACATGATGTGTGTGGCAGGCTGAGAGAGGGGCAAGGACTCTGCGAAGGT 708
QY 541 GACTCCGGGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
Db 709 GACTCCGGGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 768
QY 601 GATCCGTTGTGGATCACCCGAAAGCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
Db 769 GATCCGTTGTGGATCACCCGAAAGCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 828
QY 661 TGGATCCAGGAGAGATGAAGAACAT 687
Db 829 TGGATCCAGGAGAGATGAAGAACAT 855

RESULT 10
US-10-140-922-505
; Sequence 505, Application US/10140922
; Publication No. US2003013889A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C179
; CURRENT APPLICATION NUMBER: US/10/140,922
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; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-922-505

Query Match 100.0%; Score 687; DB 12; Length 1204;
Best Local Similarity 100.0%; Pred. No. 1.9e-186;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCATCAAGGGGTTGAGTGCAGAGCTCACTCCAGCCCTGGCAGGAGCCCTGTTGAG 60
Db 169 ATCATCAAGGGGTTGAGTGCAGAGCTCACTCCAGCCCTGGCAGGAGCCCTGTTGAG 228
QY 61 AAGACGGGGTACTCTGTGGGGCGAGCCCTATCGCCCGCAGATGGCTCTGACAGCAGCC 120
Db 229 AAGACGGGGTACTCTGTGGGGCGAGCCCTATCGCCCGCAGATGGCTCTGACAGCAGCC 288
QY 121 CACTGCTCAAGCCCGCTACATATGTTACCTGGGGGACAGCAAACTTCAGAGAGAG 180
Db 289 CACTGCTCAAGCCCGCTACATATGTTACCTGGGGGACAGCAAACTTCAGAGAGAG 348
QY 181 GGCTGTAGAGAGAGCCCGAGAGCCATGAGTCTTCCCGCCCGCCGCTTCAGAGAGAG 240
Db 289 GGCTGTAGAGAGAGCCCGAGAGCCATGAGTCTTCCCGCCCGCCGCTTCAGAGAGAG 348
QY 241 CTCCCAACAAAGACACCGCAATGACATCATGCTGGTGAAGATGGATGCCAGCTGCC 300
Db 349 CTCCCAACAAAGACACCGCAATGACATCATGCTGGTGAAGATGGATGCCAGCTGCC 408
QY 301 ATCACTGGGCTGTGGCAACCCCTACCTCTCTCAAGCTGTGTACTGTGGGACAGC 360
Db 409 ATCACTGGGCTGTGGCAACCCCTACCTCTCTCAAGCTGTGTACTGTGGGACAGC 528
QY 361 TGCTCATATTTCCGGGCTGGGGAGCAGCTCCAGCCCGAGTTACGCTGCTCAGACCTTG 420
Db 421 TGCTCATATTTCCGGGCTGGGGAGCAGCTCCAGCCCGAGTTACGCTGCTCAGACCTTG 588
QY 421 CGATGCCCAACATCACCATCATTTGAGCAGCAGCAAGTGTGAAGAGGCTTACCCCGGAC 480
Db 481 CGATGCCCAACATCACCATCATTTGAGCAGCAGCAAGTGTGAAGAGGCTTACCCCGGAC 540
QY 481 ATCAACACACATGATGTGTGTGGCAGGCTGAGAGAGGGGCAAGGACTCTGCGAAGGT 540
Db 541 ATCAACACACATGATGTGTGTGGCAGGCTGAGAGAGGGGCAAGGACTCTGCGAAGGT 600
QY 541 GACTCCGGGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
Db 589 GACTCCGGGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 708
QY 601 GATCCGTTGTGGATCACCCGAAAGCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
Db 649 GATCCGTTGTGGATCACCCGAAAGCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 768
QY 649 ATCAACACACATGATGTGTGTGGCAGGCTGAGAGAGGGGCAAGGACTCTGCGAAGGT 708
Db 709 ATCAACACACATGATGTGTGTGGCAGGCTGAGAGAGGGGCAAGGACTCTGCGAAGGT 828
QY 709 GACTCCGGGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 828
QY 769 GATCCGTTGTGGATCACCCGAAAGCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 828
Db 829 GATCCGTTGTGGATCACCCGAAAGCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 855

RESULT 11
US-10-140-924-505
; Sequence 505, Application US/10140924
; Publication No. US2003013435A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
```

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; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C177
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-924-505

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Query Match 100.0%; Score 687; DB 12; Length 1204;

Best Local Similarity 100.0%; Pred. No. 1.9e-186; Mismatches 0; Indels 0; Gaps 0;

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; 1 ATCATCAAGGGGTGAGTGAAGCCTCTCCAGCCCTGGCAGGACCCCTGTTGAG 60
; 169 ATCATCAAGGGGTGAGTGAAGCCTCTCCAGCCCTGGCAGGACCCCTGTTGAG 228
; 61 AAGAGCGGGCTACTCTGTGGGGGAGAGCTATCGCCCGAGATGGCTCTGACAGAGCC 120
; 229 AAGAGCGGGCTACTCTGTGGGGGAGAGCTATCGCCCGAGATGGCTCTGACAGAGCC 288
; 121 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGGACACAACTCCAGAGAGGAG 180
; 289 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGGACACAACTCCAGAGAGGAG 348
; 181 GCGTGTGAGCAGACCCGAGCAGCAGTGAATCTCCCGCCGCGCTTCAACAACAGC 240
; 349 GCGTGTGAGCAGACCCGAGCAGCAGTGAATCTCCCGCCGCGCTTCAACAACAGC 408
; 241 CTCGCCAACAAAGACACCGCAATGACATGCTGTGTGAGATGGCATCGCCAGTCTCC 300
; 409 CTCGCCAACAAAGACACCGCAATGACATGCTGTGTGAGATGGCATCGCCAGTCTCC 468
; 301 ATCACCCTGGGCTGTGCGAGACCCCTCACTCTCTCACTGTGTGAGATGGCATCGCCAGC 360
; 469 ATCACCCTGGGCTGTGCGAGACCCCTCACTCTCTCACTGTGTGAGATGGCATCGCCAGC 528
; 361 TGCCTCATATTCGGGCTGGGGGAGCAGATCCAGCCCTTACGCTGCTCAACCTTG 420
; 529 TGCCTCATATTCGGGCTGGGGGAGCAGATCCAGCCCTTACGCTGCTCAACCTTG 588
; 421 CGATCGGCCAACATCAATCAATGAGCAGCAGAAAGTGTGAGAACGCTTACCCCGCAAC 480
; 589 CGATCGGCCAACATCAATCAATGAGCAGCAGAAAGTGTGAGAACGCTTACCCCGCAAC 648
; 481 ATCAGAGACACCATGTGTGTGCGCAGCGTGCAGGAAAGGGGAGAAAGATCCCTGCCAGGT 540
; 649 ATCAGAGACACCATGTGTGTGCGCAGCGTGCAGGAAAGGGGAGAAAGATCCCTGCCAGGT 708
; 541 GACTCCGGGGGCGCTCTGTGTGTAAACAGTCTTCAAGGATTAATCTGCGGGCCAG 600
; 709 GACTCCGGGGGCGCTCTGTGTGTAAACAGTCTTCAAGGATTAATCTGCGGGCCAG 768
; 601 GATCCGTGTGATACCCCGAAGCCTGTGTGTACAGGAAAGTGTGCAAAATATGTGAC 660
; 769 GATCCGTGTGATACCCCGAAGCCTGTGTGTGTACAGGAAAGTGTGCAAAATATGTGAC 828
; 661 TGGATCCAGGAGACATGAAGAACAAT 687

```

Db 829 TGGATCCAGGAGACATGAAGAACAAT 855

RESULT 12

US-10-140-926-505

; Sequence 505, Application US/10140926

; Publication No. US20030134356A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: Deforge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerltsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Collin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P330R1C187

; CURRENT FILING DATE: 2002-05-07

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 505

; LENGTH: 1204

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-140-926-505

Query Match 100.0%; Score 687; DB 12; Length 1204;

Best Local Similarity 100.0%; Pred. No. 1.9e-186; Mismatches 0; Indels 0; Gaps 0;

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; 1 ATCATCAAGGGGTGAGTGAAGCCTCTCCAGCCCTGGCAGGACCCCTGTTGAG 60
; 169 ATCATCAAGGGGTGAGTGAAGCCTCTCCAGCCCTGGCAGGACCCCTGTTGAG 228
; 61 AAGAGCGGGCTACTCTGTGGGGGAGAGCTATCGCCCGAGATGGCTCTGACAGAGCC 120
; 229 AAGAGCGGGCTACTCTGTGGGGGAGAGCTATCGCCCGAGATGGCTCTGACAGAGCC 288
; 121 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGGACACAACTCCAGAGAGGAG 180
; 289 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGGACACAACTCCAGAGAGGAG 348
; 181 GCGTGTGAGCAGACCCGAGCAGCAGTGAATCTCCCGCCGCGCTTCAACAACAGC 240
; 349 GCGTGTGAGCAGACCCGAGCAGCAGTGAATCTCCCGCCGCGCTTCAACAACAGC 408
; 241 CTCGCCAACAAAGACACCGCAATGACATGCTGTGTGAGATGGCATCGCCAGTCTCC 300
; 409 CTCGCCAACAAAGACACCGCAATGACATGCTGTGTGAGATGGCATCGCCAGTCTCC 468
; 409 ATCAGAGACACCATGTGTGTGCGCAGCGTGCAGGAAAGGGGAGAAAGATCCCTGCCAGGT 540
; 649 ATCAGAGACACCATGTGTGTGCGCAGCGTGCAGGAAAGGGGAGAAAGATCCCTGCCAGGT 708
; 301 ATCACCCTGGGCTGTGCGAGACCCCTCACTCTCTCACTGTGTGAGATGGCATCGCCAGC 360
; 469 ATCACCCTGGGCTGTGCGAGACCCCTCACTCTCTCACTGTGTGAGATGGCATCGCCAGC 528
; 469 GACTCCGGGGGCGCTCTGTGTGTAAACAGTCTTCAAGGATTAATCTGCGGGCCAG 588
; 601 GATCCGTGTGATACCCCGAAGCCTGTGTGTACAGGAAAGTGTGCAAAATATGTGAC 660
; 769 GATCCGTGTGATACCCCGAAGCCTGTGTGTGTACAGGAAAGTGTGCAAAATATGTGAC 828
; 661 TGGATCCAGGAGACATGAAGAACAAT 687

```

Dh 589 CGATGCCCAACATACCATCATTTGAGCACCAGAAAGTGTGAGAAAGCCCTACCCGGGCAAC 648
Qy 481 ATCAGACACACATGATGTGTGTCAGGCGTGCAGAGAGGGGCGAGAGAGATCTCTGCAGAGGT 540
Dh 649 ATCAGACACACATGATGTGTGTCAGGCGTGCAGAGAGGGGCGAGAGAGATCTCTGCAGAGGT 708
Qy 541 GACTCCGGGGGCGCTGTGTGTGTACCAAGTCTCTCAAGGCAATATCTCTGGGGCGAG 600
Dh 709 GACTCCGGGGGCGCTGTGTGTGTACCAAGTCTCTCAAGGCAATATCTCTGGGGCGAG 768
Qy 601 GATCCGTGTGCGATCACCCGAAAGCCTGTGTGTACAGAAAGTCTGCAAAATATGTGGAC 660
Dh 769 GATCCGTGTGCGATCACCCGAAAGCCTGTGTGTGTACAGAAAGTCTGCAAAATATGTGGAC 828
Qy 661 TGGATCCAGAGAGACGATGAAGAACAT 687
Dh 829 TGGATCCAGAGAGACGATGAAGAACAT 855

RESULT 13

US-10-141-698-505
Sequence 505, Application US/10141698
Publication No. US20030134357A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C206
CURRENT APPLICATION NUMBER: US/10/141,698
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 505
LENGTH: 1204
TYPE: DNA
ORGANISM: Homo Sapien
US-10-141-698-505

Query Match 100.0%; Score 687; DB 12; Length 1204;
Best Local Similarity 100.0%; Pred. No. 1,9e-186;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCATCAAGGGGCTGAGTGCAGAGCTACATCCAGCCCTGGGAGGCGAGCCCTGTGAG 60
Dh 169 ATCATCAAGGGGCTGAGTGCAGAGCTACATCCAGCCCTGGGAGGCGAGCCCTGTGAG 228
Qy 61 AAGACGGGCTACTCTGTGGGGGAGCGCTCATCGCCCGAGATGGCTCTGACAGCAGCC 120
Dh 229 AAGACGGGCTACTCTGTGGGGGAGCGCTCATCGCCCGAGATGGCTCTGACAGCAGCC 288
Qy 121 CACTGCTCAAGCCCGCTACATAGTTACCTGGGGGAGACAAACCTTCAGAAAGAGAG 180
Dh 289 CACTGCTCAAGCCCGCTACATAGTTACCTGGGGGAGACAAACCTTCAGAAAGAGAG 348
Qy 181 GGCTGTAG 240
Dh 349 GGCTGTAG 408

Qy 241 CTCCCAACAAAGACACACCCCAATGACATCATGTGTGGAAGATGGCATGCGAGTCTCC 300
Dh 409 CTCCCAACAAAGACACACCCCAATGACATCATGTGTGGAAGATGGCATGCGAGTCTCC 468
Qy 301 ATCAGTGGGCTGTGACACCCCTCACCCTCTCTCTACAGCTGTGTCTACTGTGCGACAGC 360
Dh 469 ATCAGTGGGCTGTGACACCCCTCACCCTCTCTCTACAGCTGTGTCTACTGTGCGACAGC 528
Qy 361 TGCCTCAATTCGCGCTGGGGGAGCAGTCCAGCCCGAGTTCAGGCTGCGCTCACACCTTG 420
Dh 529 TGCCTCAATTCGCGCTGGGGGAGCAGTCCAGCCCGAGTTCAGGCTGCGCTCACACCTTG 588
Qy 421 CGATGCCCAACATACCATCATTTAGACACACAGAGTGTAGAAAGCGCTTACCCGGGCAAC 480
Dh 589 CGATGCCCAACATACCATCATTTAGACACACAGAGTGTAGAAAGCGCTTACCCGGGCAAC 648
Qy 481 ATCAGACACACATGATGTGTGTGCGAGGCTGACAGAAAGGGGCGAAGACATCTCTCGCAGGT 540
Dh 649 ATCAGACACACATGATGTGTGTGCGAGGCTGACAGAAAGGGGCGAAGACATCTCTCGCAGGT 708
Qy 541 GACTCCGGGGGCGCTGTGTGTGTGTACCAAGTCTCTCAAGGCAATATCTCTGCGGGCGAG 600
Dh 709 GACTCCGGGGGCGCTGTGTGTGTGTGTACCAAGTCTCTCAAGGCAATATCTCTGCGGGCGAG 768
Qy 601 GATCCGTGTGCGATCACCCGAAAGCCTGTGTGTGTACAGAAAGTCTGCAAAATATGTGGAC 660
Dh 769 GATCCGTGTGCGATCACCCGAAAGCCTGTGTGTGTGTACAGAAAGTCTGCAAAATATGTGGAC 828
Qy 661 TGGATCCAGAGAGACGATGAAGAACAT 687
Dh 829 TGGATCCAGAGAGACGATGAAGAACAT 855

RESULT 14

US-10-141-702-505
Sequence 505, Application US/10141702
Publication No. US20030134358A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C208
CURRENT APPLICATION NUMBER: US/10/141,702
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 505
LENGTH: 1204
TYPE: DNA
ORGANISM: Homo Sapien
US-10-141-702-505

Query Match 100.0%; Score 687; DB 12; Length 1204;
Best Local Similarity 100.0%; Pred. No. 1,9e-186;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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OY 1 ATCATCAAGGGGTTGAGTGCAGAGCTCTACTCTCCAGCCCTGGCAGAGACCCCTGTTCCAG 60
    |||||||
Db 169 ATCATCAAGGGGTTGAGTGCAGAGCTCTACTCTCCAGCCCTGGCAGAGACCCCTGTTCCAG 228
OY 61 AAGACGGGGCTACTCTGTGGGGGCGAGCGTACGCGCCCAAGTGGCTCTGTGACAGAGC 120
    |||||||
Db 229 AAGACGGGGCTACTCTGTGGGGGCGAGCGTACGCGCCCAAGTGGCTCTGTGACAGAGC 288
OY 121 CACTGCTCAAGCCCGCTACTACTAGTTCACCTGGGGGCGAGCACAACCTCCAGAAAGAGAG 180
    |||||||
Db 289 CACTGCTCAAGCCCGCTACTACTAGTTCACCTGGGGGCGAGCACAACCTCCAGAAAGAGAG 348
OY 181 GCGCTGTAGACAGACCCCGGACAGACCTAGTCTTCCCGCCCGGCTTCAACAACAGC 240
    |||||||
Db 349 GCGCTGTAGACAGACCCCGGACAGACCTAGTCTTCCCGCCCGGCTTCAACAACAGC 408
OY 241 CTCCCAACAAGACCCGCAATGACATGATGCTGGTGAAGATGGATGGCATGGCATGCTCC 300
    |||||||
Db 409 CTCCCAACAAGACCCGCAATGACATGATGCTGGTGAAGATGGATGGCATGGCATGCTCC 468
OY 301 ATCACTGGGCTGTGCGAGACCCCTCACCTCTCTCAGCTGTGTACTGTGCGACAGC 360
    |||||||
Db 469 ATCACTGGGCTGTGCGAGACCCCTCACCTCTCTCAGCTGTGTACTGTGCGACAGC 528
OY 361 TGCCCTCATTTCCGGCTGGGGGCGAGCAGCTTCAGCCCCCGATTACGCTGCTTACACCTTG 420
    |||||||
Db 529 TGCCCTCATTTCCGGCTGGGGGCGAGCAGCTTCAGCCCCCGATTACGCTGCTTACACCTTG 588
OY 421 CGATCGCGCAACATCATCATGATGAGCAGCAGAAAGTGAAGAGCGCTACCCCGGCAAC 480
    |||||||
Db 589 CGATCGCGCAACATCATCATGATGAGCAGCAGAAAGTGAAGAGCGCTACCCCGGCAAC 648
OY 481 ATCAAGACACCATGCTGTGCGAGCGTGCAGGAAGGGGGCGAAGAGCTCTGCCAGGAT 540
    |||||||
Db 649 ATCAAGACACCATGCTGTGCGAGCGTGCAGGAAGGGGGCGAAGAGCTCTGCCAGGAT 708
OY 541 GACTCCGGGGGCGCTCTGTGTCTGTACCAAGTCTCTTCAAGGCAATATCTCTGGGGCCAG 600
    |||||||
Db 709 GACTCCGGGGGCGCTCTGTGTCTGTACCAAGTCTCTTCAAGGCAATATCTCTGGGGCCAG 768
OY 601 GATCCGTGTGATGATCAGCCGAAAGCGTGTGCTCTACAGAAAGTCTGCAAAATATGTGAC 660
    |||||||
Db 769 GATCCGTGTGATGATCAGCCGAAAGCGTGTGCTCTACAGAAAGTCTGCAAAATATGTGAC 828
OY 661 TGGATCCAGAGAGCATGAAGAACAAT 687
    |||||||
Db 829 TGGATCCAGAGAGCATGAAGAACAAT 855

```

RESULT 15

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US-10-141-704-505
; Sequence 505, Application US/10141704
; Publication No. US20030134359A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zhen
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; ACIDS ENCODING THE SAME

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; FILE REFERENCE: P3330R1C209
; CURRENT APPLICATION NUMBER: US/10/141,704
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-141-704-505

Query Match. 100.0%; Score 687; DB 12; Length 1204;
Best Local Similarity 100.0%; Pred. No. 1,9e-186;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATCATCAAGGGGTTGAGTGCAGAGCTCTACTCTCCAGCCCTGGCAGAGACCCCTGTTCCAG 60
    |||||||
Db 169 ATCATCAAGGGGTTGAGTGCAGAGCTCTACTCTCCAGCCCTGGCAGAGACCCCTGTTCCAG 228
OY 61 AAGACGGGGCTACTCTGTGGGGGCGAGCGTACGCGCCCAAGTGGCTCTGTGACAGAGC 120
    |||||||
Db 229 AAGACGGGGCTACTCTGTGGGGGCGAGCGTACGCGCCCAAGTGGCTCTGTGACAGAGC 288
OY 121 CACTGCTCAAGCCCGCTACTACTAGTTCACCTGGGGGCGAGCACAACCTCCAGAAAGAGAG 180
    |||||||
Db 289 CACTGCTCAAGCCCGCTACTACTAGTTCACCTGGGGGCGAGCACAACCTCCAGAAAGAGAG 348
OY 181 GCGCTGTAGACAGACCCCGGACAGACCTAGTCTTCCCGCCCGGCTTCAACAACAGC 240
    |||||||
Db 349 GCGCTGTAGACAGACCCCGGACAGACCTAGTCTTCCCGCCCGGCTTCAACAACAGC 408
OY 241 CTCCCAACAAGACCCGCAATGACATGATGCTGGTGAAGATGGATGGCATGGCATGCTCC 300
    |||||||
Db 409 CTCCCAACAAGACCCGCAATGACATGATGCTGGTGAAGATGGATGGCATGGCATGCTCC 468
OY 301 ATCACTGGGCTGTGCGAGACCCCTCACCTCTCTCAGCTGTGTACTGTGCGACAGC 360
    |||||||
Db 469 ATCACTGGGCTGTGCGAGACCCCTCACCTCTCTCAGCTGTGTACTGTGCGACAGC 528
OY 361 TGCCCTCATTTCCGGCTGGGGGCGAGCAGCTTCAGCCCCCGATTACGCTGCTTACACCTTG 420
    |||||||
Db 529 TGCCCTCATTTCCGGCTGGGGGCGAGCAGCTTCAGCCCCCGATTACGCTGCTTACACCTTG 588
OY 421 CGATCGCGCAACATCATCATGATGAGCAGCAGAAAGTGAAGAGCGCTACCCCGGCAAC 480
    |||||||
Db 589 CGATCGCGCAACATCATCATGATGAGCAGCAGAAAGTGAAGAGCGCTACCCCGGCAAC 648
OY 481 ATCAAGACACCATGCTGTGCGAGCGTGCAGGAAGGGGGCGAAGAGCTCTGCCAGGAT 540
    |||||||
Db 649 ATCAAGACACCATGCTGTGCGAGCGTGCAGGAAGGGGGCGAAGAGCTCTGCCAGGAT 708
OY 541 GACTCCGGGGGCGCTCTGTGTCTGTACCAAGTCTCTTCAAGGCAATATCTCTGGGGCCAG 600
    |||||||
Db 709 GACTCCGGGGGCGCTCTGTGTCTGTACCAAGTCTCTTCAAGGCAATATCTCTGGGGCCAG 768
OY 601 GATCCGTGTGATGATCAGCCGAAAGCGTGTGCTCTACAGAAAGTCTGCAAAATATGTGAC 660
    |||||||
Db 769 GATCCGTGTGATGATCAGCCGAAAGCGTGTGCTCTACAGAAAGTCTGCAAAATATGTGAC 828
OY 661 TGGATCCAGAGAGCATGAAGAACAAT 687
    |||||||
Db 829 TGGATCCAGAGAGCATGAAGAACAAT 855

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 15, 2003, 12:59:38 ; Search time 64.2767 Seconds
(without alignments)
4717.579 Million cell updates/sec

Title: US-09-856-320A-1_COPY_272_958

Perfect score: 687
Sequence: 1 atcacaaggggttcgagtg.....agagacgacgtaagaacaat 687

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: /cgn2_6/ptodata/2/lna/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/lna/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/lna/6B_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	687	100.0	1192	3	US-08-944-483-8
2	687	100.0	1314	3	US-09-025-059-2
3	686.6	99.9	1292	4	US-09-205-258-189
4	685.8	99.8	1146	4	US-09-205-258-247
5	685.2	99.7	1166	3	US-08-944-483-7
6	660	96.1	1052	4	US-09-386-642-10
7	654.2	95.2	833	2	US-08-790-137-2
8	464.6	67.6	618	4	US-09-280-116-3
9	287	41.8	662	4	US-09-702-705-109
10	287	41.8	662	4	US-09-736-457-109
11	262.4	38.2	472	4	US-09-280-116-136
12	250	36.4	250	3	US-08-944-483-4
13	237.4	34.6	239	3	US-08-944-483-3
14	225	32.8	262	3	US-08-944-483-5
15	223.6	32.5	994	3	US-09-008-271A-19
16	220.4	32.1	1049	4	US-09-070-526-1
17	219.2	31.9	1049	4	US-09-386-642-9
18	191.8	27.9	1570	4	US-09-996-243-308
19	187.6	27.3	825	3	US-09-120-582-1
20	187.6	27.3	897	2	US-08-956-267A-1
21	182.4	26.6	1476	2	US-08-824-874-2
22	182.4	26.6	1476	2	US-09-210-084-2
23	182.4	26.6	1476	4	US-09-764-762-2
24	177.8	25.9	1341	4	US-08-983-075D-6
25	177.8	25.9	1358	4	US-08-983-075D-8
26	176.2	25.6	711	3	US-08-622-046B-2
27	176.2	25.6	711	3	US-08-622-046B-13

28	176.2	25.6	711	3	US-09-100-264-2	Sequence 2, Appl1
29	176.2	25.6	711	4	US-08-843-076D-2	Sequence 2, Appl1
30	176.2	25.6	760	3	US-08-768-859A-7	Sequence 7, Appl1
31	176.2	25.6	760	3	US-08-767-820A-7	Sequence 7, Appl1
32	176.2	25.6	766	3	US-08-768-859A-9	Sequence 9, Appl1
33	176.2	25.6	766	3	US-08-767-820A-9	Sequence 9, Appl1
34	176.2	25.6	766	3	US-08-622-046B-6	Sequence 6, Appl1
35	176.2	25.6	766	3	US-08-622-046B-17	Sequence 17, Appl1
36	176.2	25.6	766	4	US-09-100-264-6	Sequence 6, Appl1
37	176.2	25.6	822	3	US-08-843-076D-6	Sequence 6, Appl1
38	176.2	25.6	822	3	US-09-100-264-8	Sequence 8, Appl1
39	176.2	25.6	832	3	US-08-768-859A-5	Sequence 5, Appl1
40	176.2	25.6	832	3	US-08-768-859A-20	Sequence 20, Appl1
41	176.2	25.6	832	3	US-08-767-820A-5	Sequence 5, Appl1
42	176.2	25.6	832	3	US-08-767-820A-20	Sequence 20, Appl1
43	176.2	25.6	832	3	US-08-622-046B-4	Sequence 4, Appl1
44	176.2	25.6	832	3	US-08-622-046B-15	Sequence 15, Appl1
45	176.2	25.6	832	4	US-08-843-076D-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-08-944-483-8
Sequence 8, Application US/08944483
Patent No. 6232456

GENERAL INFORMATION:
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STROPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA: US/08/944,483
APPLICATION NUMBER: US/08/944,483
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1192 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: CDNA
US-08-944-483-8

Query Match 100.0%; Score 687; DB 3; Length 1192;
Best Local Similarity 100.0%; Pred. No. 2.5e-168;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATCATCAAGGGGTTGAGTGCACACCTCCACGCTTCGACGACGACCCCTTTGAG 60
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DB 170 ATCATCAAGGGGTTGAGTGCACACCTCCACGCTTCGACGACGACCCCTTTGAG 229
QY 61 AAGACGGGGCTACTCTGTGGGGGACGCTCATGCGCCCGACAGATGGCTCTGACGACGCC 120
    |||||||
DB 230 AAGACGGGGCTACTCTGTGGGGGACGCTCATGCGCCCGACAGATGGCTCTGACGACGCC 289
QY 121 CACTGCTCAAGCCCGCTACATAGTTCACTGGGGGAGCAACAACCTTCAGAGAGAG 180
    |||||||
DB 290 CACTGCTCAAGCCCGCTACATAGTTCACTGGGGGAGCAACAACCTTCAGAGAGAG 349
QY 181 GGGTGTAGAGACAGCCGGACAGCCACTGAGTCTCTCCCGACCCCGGCTTCACACAGC 240
    |||||||
DB 350 GGGTGTAGAGACAGCCGGACAGCCACTGAGTCTCTCCCGACCCCGGCTTCACACAGC 409
QY 241 CTCCCAACAAGACCAACCGCATGACATCATGCTGGGAGATGGATGCGCCAGTCTCC 300
    |||||||
DB 410 CTCCCAACAAGACCAACCGCATGACATCATGCTGGGAGATGGATGCGCCAGTCTCC 469
QY 301 ATCACTGGGGCTGTGCGACCCCTCACCCTCTCTCAGCTGTCTGACGTGGACAGC 360
    |||||||
DB 470 ATCACTGGGGCTGTGCGACCCCTCACCCTCTCTCAGCTGTCTGACGTGGACAGC 529
QY 361 TGGCTCATTTCCGGCTGGGGGACAGACGTCACAGCCCGCAATTAGCCCTGCTCACACCTTG 420
    |||||||
DB 530 TGGCTCATTTCCGGCTGGGGGACAGACGTCACAGCCCGCAATTAGCCCTGCTCACACCTTG 589
QY 421 CGATCGCCCAACATCACCATCATTTGAGCAGCAGAAAGTGTGAGAACGCCCTACCCGGGAC 480
    |||||||
DB 590 CGATCGCCCAACATCACCATCATTTGAGCAGCAGAAAGTGTGAGAACGCCCTACCCGGGAC 649
QY 481 ATCAAGACACCATGTGTGTGTCAGCGTGCAGGAGAGGGGGCAAGAGCTCTGCCAAGGT 540
    |||||||
DB 650 ATCAAGACACCATGTGTGTGTCAGCGTGCAGGAGAGGGGGCAAGAGCTCTGCCAAGGT 709
QY 541 GACTCGGGGGGCTCTGTGTGTGTGAACAGCTCTTCAAGGCAATTATCTGGGGCCAG 600
    |||||||
DB 710 GACTCGGGGGGCTCTGTGTGTGTGAACAGCTCTTCAAGGCAATTATCTGGGGCCAG 769
QY 601 GATCCGCTGTGATCACCAGCAAGCTGTGTGTACAGAAAGTCTCAAAATATGTGGAC 660
    |||||||
DB 770 GATCCGCTGTGATCACCAGCAAGCTGTGTGTACAGAAAGTCTCAAAATATGTGGAC 829
QY 661 TGGATCCAGAGAGAGATGAAGAACAT 687
    |||||||
DB 830 TGGATCCAGAGAGAGATGAAGAACAT 856
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RESULT 2
US-09-025-059-2
Sequence 2, Application US/09025059
Patent No. 6075136

GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:

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;;
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FASTSEQ for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/025,059
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Billings, Lucy J
;; REGISTRATION NUMBER: 36,749
;; REFERENCE/DOCKET NUMBER: PF-0481 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-855-0555
;; TELEFAX: 650-845-4166
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1314 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: LUNGUTUT10
;; CLONE: 2723646
;; US-09-025-059-2
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Query Match 100.0%; Score 687; DB 3; Length 1314;
Best Local Similarity 100.0%; Pred. No. 2.6e-168;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATCATCAAGGGGTTGAGTGCACACCTCCACGCTTCGACGACGACCCCTTTGAG 60
    |||||||
DB 287 ATCATCAAGGGGTTGAGTGCACACCTCCACGCTTCGACGACGACCCCTTTGAG 346
QY 61 AAGACGGGGCTACTCTGTGGGGGACGCTCATGCGCCCGACAGATGGCTCTGACGACGCC 120
    |||||||
DB 347 AAGACGGGGCTACTCTGTGGGGGACGCTCATGCGCCCGACAGATGGCTCTGACGACGCC 406
QY 121 CACTGCTCAAGCCCGCTACATAGTTCACTGGGGGACAGCAACAACCTTCAGAGAGAG 180
    |||||||
DB 407 CACTGCTCAAGCCCGCTACATAGTTCACTGGGGGACAGCAACAACCTTCAGAGAGAG 466
QY 181 GGGTGTAGAGACAGCCGGAGACCGACGAGTCTTCCCGACCCCGGCTTCACACAGC 240
    |||||||
DB 467 GGGTGTAGAGACAGCCGGAGACCGACGAGTCTTCCCGACCCCGGCTTCACACAGC 526
QY 241 CTCCCAACAAGACACACCGCATGACATCATGCTGTGAGAAAGTGCATGCCAGTCTCC 300
    |||||||
DB 527 CTCCCAACAAGACACACCGCATGACATCATGCTGTGAGAAAGTGCATGCCAGTCTCC 586
QY 587 ATCACTGGGGCTGTGACACCCCTCACCCTCTCTCAGCGTGTGTCATGCTGGACAGC 646
    |||||||
DB 647 TGGCTCATTTCCGGCTGGGGGACAGCACTTCACGCCCCAGTTAGGCTGTCAACACTTG 706
    |||||||
QY 361 TGGCTCATTTCCGGCTGGGGGACAGCACTTCACGCCCCAGTTAGGCTGTCTCACACTTG 420
    |||||||
DB 647 TGGCTCATTTCCGGCTGGGGGACAGCACTTCACGCCCCAGTTAGGCTGTCTCACACTTG 706
    |||||||
QY 421 CGATCGCCCAACATCACCATCATTTGAGCAGCAGAAAGTGTGAGAAAGCTTACCCGGGAC 480
    |||||||
DB 707 CGATCGCCCAACATCACCATCATTTGAGCAGCAGAAAGTGTGAGAAAGCTTACCCGGGAC 766
    |||||||
QY 481 ATCAAGACACCATGTGTGTGTCAGAGGTGCAGAAAGGGGCAAGAGACTCTCCAGAGGT 540
    |||||||
DB 767 ATCAAGACACCATGTGTGTGTCAGAGGTGCAGAAAGGGGCAAGAGACTCTCCAGAGGT 826
    |||||||
QY 541 GACTCGGGGGGCTCTGTGTGTGTGAACAGCTCTTCAAGGCAATTATCTCTGGGGCCAG 600
    |||||||
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Db 827 GACTCCGGGGCCCTTGGTCTGTAAACGACTCTCTTCAAGGCAATTAATCTCGGGCCAG 886
QY 601 GATCCGTGTGCGATCAACCGAAAGCCTGGTGTCTACACGAAAGTCTGCAAAATATGTGAC 660
Db 887 GATCCGTGTGCGATCAACCGAAAGCCTGGTGTCTACACGAAAGTCTGCAAAATATGTGAC 946
QY 661 TGGATCCAGAGACGATGAAGAACAAT 687
Db 947 TGGATCCAGAGACGATGAAGAACAAT 973

RESULT 3
US-09-205-258-189
; Sequence 189, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 189
; LENGTH: 1292
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-205-258-189

Query Match 99.9%; Score 686.6; DB 4; Length 1292;
Best Local Similarity 99.9%; Pred. No. 3.2e-168;
Matches 686; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCATCAAGGGGTTCAGTGCAGAGCCTCACTCCACCCCTGGAGGACGCTGTTGAG 60
Db 270 ATCATCAAGGGGTTCAGTGCAGAGCCTCACTCCACCCCTGGAGGACGCTGTTGAG 329
QY 61 AAGACGGGCTACTCTGTGGGGGAGCGATCGCCAGATGGCTCGACAGAGCC 120
Db 330 AAGACGGGCTACTCTGTGGGGGAGCGATCGCCAGATGGCTCGACAGAGCC 389
QY 121 CACTGCTCAAGCCCGCTACATAGTTCACTGAGGAGCAGCAAACTCCAGAGAGAG 180
Db 390 CACTGCTCAAGCCCGCTACATAGTTCACTGAGGAGCAGCAAACTCCAGAGAGAG 449
QY 181 GGCTGTGACAGACCCGGAGCGCACTGAGTCTTCCACCCCGGCTTCAACACAGC 240
Db 450 GGCTGTGACAGACCCGGAGCGCACTGAGTCTTCCACCCCGGCTTCAACACAGC 509
QY 241 CTCGCCAACAAGACACCGCAATGACATCATCTGTGAAGATGCGATCGCAGTCC 300
Db 510 CTCGCCAACAAGACACCGCAATGACATCATCTGTGAAGATGCGATCGCAGTCC 569
QY 301 ATCACTGGGCTGTGAGACCCCTCACTCTCTCACTGCTGTGACAGTGGACACAG 360
Db 570 ATCACTGGGCTGTGAGACCCCTCACTCTCTCACTGCTGTGACAGTGGACACAG 629
QY 361 TGGCTCATTTCCGGGCGGGGAGCAGCTCAGCCCAAGTACGCTGCTCAACACTTG 420
Db 630 TGGCTCATTTCCGGGCGGGGAGCAGCTCAGCCCAAGTACGCTGCTCAACACTTG 689
QY 421 CGATGGCCCAATCATCACTATTGAGACCAAGATGAGAACGCTAACCCGGGCAAC 480
Db 690 CGATGGCCCAATCATCACTATTGAGACCAAGATGAGAACGCTAACCCGGGCAAC 749
QY 481 ATCAAGACCAATGCTGTGTGACAGCTGTGAGAAAGGGGCAAGACTCTGCGAGGCT 540

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Db 750 ATCAGACACCATGTTGTGCCAGCTGCAAGAAAGGGGCAAGACTCTGCCAGGGT 809
OY 541 GACTCCGGGGCCCTGTGTGTGTACAGTCTCTTCAAGCATTATCTCTGGGGCCAG 600
Db 810 GACTCCGGGGCCCTGTGTGTGTGTACAGTCTCTTCAAGCATTATCTCTGGGGCCAG 869
OY 601 GATCCGTGTGCGATACCCGGAAGCGTGTGTCTACAGAAAGTCTGCAAAATATGTGAC 660
Db 870 GATCCGTGTGCGATACCCGGAAGCGTGTGTCTACAGAAAGTCTGCAAAATATGTGAC 929
OY 661 TGGATCCAGAGAGATGAAGACAT 687
Db 930 TGGATCCAGAGAGATGAAGACAT 956
RESULT 4
US-09-205-258-247
Sequence 247, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
EARLIER FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916

EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
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EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 247
LENGTH: 1146
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (20)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (35)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (36)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (37)
OTHER INFORMATION: n equals a,t,g, or c
US-09-205-258-247
Query Match 99.8%; Score 685.8; DB 4; Length 1146;
Best Local Similarity 99.6%; Pred. No. 5e-168;
Matches 684; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATCATCAAGGGGTTGAGTGCAGGCTTCCAGGCTGGGAGGAGGCGCTTTTCGAG 60
Db 124 ATCATCAAGGGGTTGAGTGCAGGCTTCCAGGCTGGGAGGAGGCGCTTTTCGAG 183
OY 61 AAGAGCGGCTACTCTGTGGGCGAGCCTCATGCGCCCAAGATGCTCTGACAGAGCC 120
Db 184 AAGAGCGGCTACTCTGTGGGCGAGCCTCATGCGCCCAAGATGCTCTGACAGAGCC 243
OY 121 CACTGCTCAAGCCCGCTCATGATGTCACCTGGGGAGAGACAACCTCCAGAGAGAG 180
Db 244 CACTGCTCAAGCCCGCTCATGATGTCACCTGGGGAGAGACAACCTCCAGAGAGAG 303

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QY 181 GGCTGTGACAGACCCGGACAGCCACTGAGTCTTCCCGACCCCGGCTTCAACAACAGC 240
D 304 GGCTGTGACAGACCCGGACAGCCACTGAGTCTTCCCGACCCCGGCTTCAACAACAGC 363
QY 241 CTCGCCAACAAGACACCGCAATGATCATGCTGTGTAAGATGTCATGCGAGCTCC 300
D 364 CTCGCCAACAAGACACCGCAATGATCATGCTGTGTAAGATGTCATGCGAGCTCC 423
QY 301 ATCAGCTGGGCTGTGGGACCCCTCACCCCTCTCAGCTGTGTCACTGCTGGCAGCAGC 360
D 424 ATCAGCTGGGCTGTGGGACCCCTCACCCCTCTCAGCTGTGTCACTGCTGGCAGCAGC 483
QY 361 TGCCTCATTTCCGGGCTGGGGGACAGCAGCTCAGCCCAATTTACGCTGCTCAGACCTTG 420
D 484 TGTCTCATTTCCGGGCTGGGGGACAGCAGCTCAGCCCAATTTACGCTGCTCAGACCTTG 543
QY 421 CGATGGCGCAACATCATCATTTGAGCAGCAGAAAGTGTGAGAAAGCTTACCCCGGCAAC 480
D 544 SGATGGCGCAACATCATCATTTGAGCAGCAGAAAGTGTGAGAAAGCTTACCCCGGCAAC 603
QY 481 ATCAGAGACACCATGCTGTGTGCGACGCTGACAGAAAGGGGCAAGGACTCTGCCAGGCT 540
D 604 ATCAGAGACACCATGCTGTGTGCGACGCTGACAGAAAGGGGCAAGGACTCTGCCAGGCT 663
QY 541 GACTCGGGGGGCTCTGTGTGTATACAGCTCTTTCAAGGCAATTTATCTGTGGGCGCAG 600
D 664 GACTCGGGGGGCTCTGTGTGTATACAGCTCTTTCAAGGCAATTTATCTGTGGGCGCAG 723
QY 601 GATCGGTGTGCGATACCCGGAAGGCTGTGTCTACAGAAAGTGTGCAAAATATGTGGAC 660
D 724 GATCGGTGTGCGATACCCGGAAGGCTGTGTCTACAGAAAGTGTGCAAAATATGTGGAC 783
QY 661 TGGATCCAGAGACGATGAGAACAAT 687
D 784 TGGATCCAGAGACGATGAGAACAAT 810

RESULT 5
US-08-944-483-7
; Sequence 7, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLAS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STEWART, KENT D.
; APPLICANT: STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1166 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-944-483-7

Query Match      99.7%; Score 685.2; DB 3; Length 1166;
Best Local Similarity 99.6%; Pred. No. 7,2e-168;
Matches 684; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATCATCAAGGGGTTCGAGTGCAGAGCTCACTCCAGCCCTGGCAGGACGCTGTTGAG 60
D 166 ATCATCAAGGGGTTCGAGTGCAGAGCTCACTCCAGCCCTGGCAGGACGCTGTTGAG 225
QY 61 AAGACGGGCTACTCTGTGGGGGAGCGCTATCGCCCCAGATGCTCTGACAGAGCC 120
D 226 AAGACGGGCTACTCTGTGGGGGAGCGCTATCGCCCCAGATGCTCTGACAGAGCC 285
QY 121 CACTGCTTAAGCCCGCTACATAGTTCACTTGGGGACACACAACTCCAGAAAGAGAG 180
D 286 CACTGCTTAAGCCCGCTACATAGTTCACTTGGGGGACACACAACTCCAGAAAGAGAG 345
QY 181 GGCTGTGACAGACCCGGACAGCCACTGATGCTTCCCGACCCCGGCTTCAACAACAGC 240
D 346 GGCTGTGACAGACCCGGACAGCCACTGATGCTTCCCGACCCCGGCTTCAACAACAGC 405
QY 241 CTCGCCAACAAGACACCGCAATGATCATGCTGTGTAAGATGTCATGCGAGCTCC 300
D 406 CTCGCCAACAAGACACCGCAATGATCATGCTGTGTAAGATGTCATGCGAGCTCC 465
QY 301 ATCAGCTGGGCTGTGGGACCCCTCACCCCTCTCAGCTGTGTCACTGCTGGCAGCAGC 360
D 466 ATCAGCTGGGCTGTGGGACCCCTCACCCCTCTCAGCTGTGTCACTGCTGGCAGCAGC 525
QY 361 TGCCTCATTTCCGGGCTGGGGGACAGCAGCTCAGCCCAATTTACGCTGCTCAGACCTTG 420
D 526 TGCCTCATTTCCGGGCTGGGGGACAGCAGCTCAGCCCAATTTACGCTGCTCAGACCTTG 585
QY 421 CGATGGCGCAACATCATCATTTGAGCAGCAGAAAGTGTGAGAAAGCTTACCCCGGCAAC 480
D 586 CGATGGCGCAACATCATCATTTGAGCAGCAGAAAGTGTGAGAAAGCTTACCCCGGCAAC 645
QY 481 ATCAGAGACACCATGCTGTGTGCGACGCTGACAGAAAGGGGCAAGGACTCTGCCAGGCT 540
D 646 ATCAGAGACACCATGCTGTGTGCGACGCTGACAGAAAGGGGCAAGGACTCTGCCAGGCT 705
QY 541 GACTCGGGGGGCTCTGTGTGTATACAGCTCTTTCAAGGCAATTTATCTGTGGGCGCAG 600
D 706 GACTCGGGGGGCTCTGTGTGTATACAGCTCTTTCAAGGCAATTTATCTGTGGGCGCAG 765
QY 601 GATCGGTGTGCGATACCCGGAAGGCTGTGTCTACAGAAAGTGTGCAAAATATGTGGAC 660
D 766 GATCGGTGTGCGATACCCGGAAGGCTGTGTCTACAGAAAGTGTGCAAAATATGTGGAC 825
QY 661 TGGATCCAGAGACGATGAGAACAAT 687
D 826 TGGATCCAGAGACGATGAGAACAAT 852

RESULT 6
US-09-386-642-10
; Sequence 10, Application US/09386642
; Patent No. 6420157

```

GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Q1, Jensen
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 1052
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-10

Query Match 96.1%; Score 660; DB 4; Length 1052;

Best Local Similarity 100.0%; Pred. No. 2,2e-161;

Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 28 CACTCCAGCCCTGGCAGGAGCCCTGTGAGAAAGCGGGCTACTCTGTGGGGCAGC 87
DB 196 CACTCCAGCCCTGGCAGGAGCCCTGTGAGAAAGCGGGCTACTCTGTGGGGCAGC 255
QY 88 CTCATCGCCCGCAGATGGCTCTGACAGCAGCCCACTGCTCAAGCCCGCTACATAGTT 147
DB 256 CTCATCGCCCGCAGATGGCTCTGACAGCAGCCCACTGCTCAAGCCCGCTACATAGTT 315
QY 148 CACTGGGGGAGCAGCAACCTTCAGAAAGAGAGAGGGCTGTGAGAGACCCGAGCAGCACT 207
DB 316 CACTGGGGGAGCAGCAACCTTCAGAAAGAGAGAGGGCTGTGAGAGACCCGAGCAGCACT 375
QY 208 GAGTCCTTCCCGCCCGCGGGCTTACAGAACAGCTCCCAAGAAAGACCGAATGAC 267
DB 376 GAGTCCTTCCCGCCCGCGGGCTTACAGAACAGCTCCCAAGAAAGACCGAATGAC 435
QY 268 ATCATGCTGTGAGATGGCATCGCAGTCATCACTGCGCTGTGCGACCCCTGACC 327
DB 436 ATCATGCTGTGAGATGGCATCGCAGTCATCACTGCGCTGTGCGACCCCTGACC 495
QY 328 CTCCTCCAGCGCTGTGACACTGTGGCAGCAACGCTGCTCATTTCCGGTGGGGAGCAGC 387
DB 496 CTCCTCCAGCGCTGTGACACTGTGGCAGCAACGCTGCTCATTTCCGGTGGGGAGCAGC 555
QY 388 TCCAGCCCGCAGTACGCTGCGTCACACCTTGGATGGCGCCACATCACCATTATGAG 447
DB 556 TCCAGCCCGCAGTACGCTGCGTCACACCTTGGATGGCGCCACATCACCATTATGAG 615
QY 448 CACCAGAGTGTGAGAACGCTTACCCCGGCAACATCAGACAGACCATGTTGTGCAGC 507
DB 616 CACCAGAGTGTGAGAACGCTTACCCCGGCAACATCAGACAGCATGTTGTGCAGC 675
QY 508 GTGAGAGAGAGGGGAGAGGACTCTGCCAGGGGTACTCCGGGGCCCTCTGGTGTGTAAC 567
DB 676 GTGAGAGAGAGGGGAGAGGACTCTGCCAGGGGTACTCCGGGGCCCTCTGGTGTGTAAC 735
QY 568 CAGTCTTTCAGAGCATTTATCTCTGTGGGCGAGGATCGTGTGGATCACCCGAAAGCCT 627
DB 736 CAGTCTTTCAGAGCATTTATCTCTGTGGGCGAGGATCGTGTGGATCACCCGAAAGCCT 795
QY 628 GGTGTTCACAGAAAGTCTCCAAATATGTGAGTGCATTCAGAGAGAGATGAAAGCAAT 687
DB 796 GGTGTTCACAGAAAGTCTCCAAATATGTGAGTGCATTCAGAGAGAGATGAAAGCAAT 855
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RESULT 7
US-08-790-137-2

; Sequence 2, Application US/08790137

; Patent No. 5840871

; GENERAL INFORMATION:

```
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Goli, Surya K.  
TITLE OF INVENTION: A NOVEL PROSTATE-ASSOCIATED  
TITLE OF INVENTION: KALIKREIN  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/790,137  
FILING DATE: Filed Herewith  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0195 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 833 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-790-137-2
```

Query Match 95.2%; Score 654.2; DB 2; Length 833;
Best Local Similarity 97.6%; Pred. No. 6.5e-160;
Matches 662; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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QY 10 GGGTGCAGTGCAGCACTCCACTCCAGCCCTGGAGGAGCAGCCCTGTTCAGAGAGCAGCG 69
DB 108 GGGTGCAGTGCAGCACTCCACTCCAGCCCTGGAGGAGCAGCCCTGTTCAGAGAGCAGCG 167
QY 70 CTACTCTGTGGGGGAGAGCTCATGCCCCAGATGCTCTGTGAGAGCAGCCACTGCTC 129
DB 168 CTACTCTGTGGGGGAGAGCTCATGCCCCAGATGCTCTGTGAGAGCAGCCACTGCTC 227
QY 130 AAGCCCGCTACATAGTTCACTGCGGAGAGCAACCTCCAGAAAGAGAGGGCTGTGAG 189
DB 228 AAGCCCGCTACATAGTTCACTGCGGAGAGCAACCTCCAGAAAGAGAGGGCTGTGAG 287
QY 190 CAGACCCGGAGCAGCACTGAGTCTTCCCGCCAGCCCGGGCTTCAACAACAGCCTCCCAAC 249
DB 288 CAGACCCGGAGCAGCACTGAGTCTTCCCGCCAGCCCGGGCTTCAACAACAGCCTCCCAAC 347
QY 250 AAAGACACCGCATAGCATCATGCTGTGAAATGGCATTCGCAAGTCTCATCACTGG 309
DB 348 AAAGACACCGCATAGCATCATGCTGTGAAATGGCATTCGCAAGTCTCATCACTGG 407
QY 310 GCTGTGAGACCCCTACACCTCTCTCAAGCTGTGTCACTGCTGGACACAGCTGCTCATTT 369
DB 408 GCTGTGAGACCCCTACACCTCTCTCTCAAGCTGTGTCACTGCTGGACACAGCTGCTCATTT 467
QY 370 TCGGCTGGGGGAGCAGCAGTCCAGGCCCACTTACGCTGCTCAACACTTTCAGATGGCC 429
DB 468 TCGGCTGGGGGAGCAGCAGTCCAGGCCCACTTACGCTGCTCAACACTTTCAGATGGCC 527
QY 430 AACATCACTCATTTGAGCAGCAGAAATGTGTGAGAACCTTACCCCGGCAACATCAGCAGC 489
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Db 528 AACATCACCATCATTTGAGCACCAGAAAGTGTGAAGAGCCCTACCCCGCAACATCAACAG 587
Qy 490 ACCATGCTGTGTCACAGCGCTGCAGAGAGGGGCAAGAGACTCTGCCAGGGTACTCCGG 549
Db 588 ACCATGCTGTGTCACAGCGCTGCAGAGAGGGGCAAGAGACTCTGCCAGGGTACTCCGG 647
Qy 550 GAGCCCTGTGCTGTGAACAGTCTCTCAAGGCAATTAATCTCTGGGGCCAGATCCGCT 609
Db 648 GAGCCCTGTGCTGTGAACAGTCTCTCAAGGCAATTAATCTCTGGGGCCAGATCCGCT 707
Qy 610 GCGATCACCCGGAAGCCTGTGTCTACAGAAAGTCTGCAAAATATGTGATCGATCAG 669
Db 708 GCGATCACCCGGAAGCCTGTGTCTACAGAAAGTCTGCAAAATATGTGATCGATCAG 767
Qy 670 GAGACGATGAGACAAAT 687
Db 768 GAGACGATGAGACAAAT 785
```

```
RESULT 8
US-09-280-116-3
; Sequence 3, Application US/09280116A
; Patent No. 6311427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: trypsin-like serine proteases
US-09-280-116-3
```

```
Query Match 67.6%; Score 464.6; DB 4; Length 618;
Best Local Similarity 91.8%; Pred. No. 5.4e-111;
Matches 559; Conservative 0; Mismatches 14; Indels 36; Gaps 5;

Qy 66 GCGGCTACTCTGTGGGGGAGCGCTATCGCCCCGAGATGCTCTGACAGACGCCACTG 125
Db 1 GCGGCTACTCTGTGGGGGAGC-CTCATCG-CTCAGATGGCTCTGACAGACGCCACTG 58
Qy 126 CTTCAAGCCCGCTACATAGTTCACTGGGGGAGACAACCTCCAGAGAGAGAGGGCTG 185
Db 59 CTTCAAGCCCGCTACATAGTTCACTGGGGGAGACAACCTCCAGAGAGAGAGGGCTG 118
Qy 186 TGAGCAGACCGGAGACGCACTGAGTCTTCCGCCACCCCGGCTTCAACAACAGGCTCC 245
Db 119 TGAGCAGACCGGAGACGCACTGAGTCTTCCGCCACCCCGGCTTCAACAACAGGCTCC 178
Qy 246 CAACAAGACACCGCAATGACATCATCTGTGTGAAGATGCGATCGCAAT-CTCCATCA 304
Db 179 CAACAAGACACCGCAATGACATCATCTGTGTGAAGATGCGATCGCAATCA 238
Qy 305 CTTGGGCTGTGGAGCCCTCAACCCCTCTCAACGCTGTGATCTGTGACCTGTGGACCACTCC 364
Db 239 CTTGGGCTGTGGAGCCCTCAACCCCTCTCAACGCTGTGATCTGTGACCTGTGGACCACTCC 298
Qy 365 TCATTTCCGGCTGGGGGAGCAGATGCCACCCCAAGTTAGGCTGTGCTCAACCTTGCAT 424
Db 299 TCATTTCCGGCTGGGGGAGCAGATGCCACCCCAAGTTAGGCTGTGCTCAACCTTGCAT 358
Qy 425 GCGCACAATCAATCATTTTGAAGCAGCAGAAAGTGTGAGACGCTTACCCCGGCAACATCA 484
Db 359 GCGCACAATCAATCATTTTGAAGCAGCAGAAAGTGTGAGAAAGGCTTACCCCGGCAACATCA 418
Qy 485 CAGACACCATGTGTGTGCGCAGCGTGCAGAAAGGGGGAAGAGTCCGCGCAGGGTGACT 544
Db 1 CAGACACCATGTGTGTGCGCAGCGTGCAGAAAGGGGGAAGAGTCCGCGCAGGGTGACT 544
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Db 419 CAGACACCATGTGTGTGCGCAGCGTGCAGAAAGGGGGAAGAGTCTCTGCCAAGTCTTT 478
Qy 545 CCGGGGGCCCTGTGTGTGTGTAAACAGTCTCTTCAAGGCAATTAATCTCTGGGG--CCAGGA 602
Db 479 C-----AAAGCAATTAATCTCTGGGGCCAGAGAC 507
Qy 603 TCCGTGTGCGATCACCCGAAAGCCTGTGTGTCTACAGAAAGTGTGCAAAATATGTGACGTG 662
Db 508 TCCGTGTGCGATCACCCGAAAGCCTGTGTGTCTACAGAAAGTGTGCAAAATATGTGACGTG 567
Qy 663 GATCCAGGA 671
Db 568 GATCCAGGA 576
```

```
RESULT 9
US-09-702-705-109
; Sequence 109, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Ranger, Gary
; APPLICANT: Vedvyck, Tom
; APPLICANT: Carter, Darriack
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.47BC14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 662
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-109
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Query Match 41.8%; Score 287; DB 4; Length 662;
Best Local Similarity 100.0%; Pred. No. 4.1e-65;
Matches 287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 401 TACGCTGCTCACACCTTGGGATGGCCCAACATCAATCATTTGAGCACCAGAAAGTGTG 460
Db 14 TACGCTGCTCACACCTTGGGATGGCCCAACATCAATCATTTGAGCACCAGAAAGTGTG 73
Qy 461 AGAAGCCTTACCCCGGCAACATCACAGACACCATGGTGTGTGCGACGTCAGAGAGGG 520
Db 74 AGAAGCCTTACCCCGGCAACATCACAGACACCATGGTGTGTGCGACGTCAGAGAGGG 133
Qy 521 GCAAGACTCTGTCCAGGGGTGACTCCGGGGGCCCTGTGTGTGTGAACAGTCTTTCAAG 580
Db 134 GCAAGACTCTGTCCAGGGGTGACTCCGGGGGCCCTGTGTGTGTGAACAGTCTTTCAAG 193
Qy 581 GCATTAATCTCTGGGGGCAAGATTCGCTGTGATCAACCCGAAAGCCTGTGTCTACAGA 640
Db 194 GCATTAATCTCTGGGGGCAAGATTCGCTGTGATCAACCCGAAAGCCTGTGTCTACAGA 253
Qy 641 AAGTGTCAAAATATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 687
Db 254 AAGTGTCAAAATATGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
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```
RESULT 10
US-09-736-457-109
; Sequence 109, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
```

APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedlick, Tom
APPLICANT: Carter, Darlick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736.457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 109
LENGTH: 662
TYPE: DNA
ORGANISM: Homo sapien
US-09-736-457-109

Query Match 41.8%; Score 287; DB 4; Length 662;
Best Local Similarity 100.0%; Pred. No. 4.1e-65;
Matches 287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 401 TAGCCCTGCTCAACCTGTCGATGCGCAACATCATTGATGAGCACCAGAAAGTGTG 460
DB 14 TAGCCCTGCTCAACCTGTCGATGCGCAACATCATTGATGAGCACCAGAAAGTGTG 73
QY 461 AGAAGCCTTACCCGGCAACATCAGACACACATGCTGTGCCAGGCTGCAGAGAGGG 520
DB 74 AGAAGCCTTACCCGGCAACATCAGACACACATGCTGTGCCAGGCTGCAGAGAGGG 133
QY 521 GCAAGGACTCTGTCGAGAGTACTCCGGGGCCCTGTGCTGTAAACAGTCTTCAAG 580
DB 134 GCAAGGACTCTGTCGAGAGTACTCCGGGGCCCTGTGCTGTAAACAGTCTTCAAG 193
QY 581 GCATTATCTCTGGGGCCAGATCGTGTGCATCACCCGAAAGCCTGTGTTCACGA 640
DB 194 GCATTATCTCTGGGGCCAGATCGTGTGCATCACCCGAAAGCCTGTGTTCACGA 253
QY 641 AAGCTGCAATATATGTGACTGATCCAGAGACGATGAAGAACAAT 687
DB 254 AAGCTGCAATATATGTGACTGATCCAGAGACGATGAAGAACAAT 300

RESULT 11

US-09-280-116-136
Sequence 136, Application US/09280116A
Patent No. 6331427
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
FILE REFERENCE: 5800-24.038800/176965
CURRENT APPLICATION NUMBER: US/09/280.116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 136
LENGTH: 472
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: trypsin-like serine proteases
US-09-280-116-136

Query Match 38.2%; Score 262.4; DB 4; Length 472;
Best Local Similarity 99.6%; Pred. No. 8.2e-59;
Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATCATCAAGGGGTTGAGTGCAGAGCCCTACCTCCAGCCGGGAGAGGCGCCGTTCGAG 60
|||||

DB 209 ATCATCAAGGGGTTGAGTGCAGAGCCCTACCTCCAGCCGTGGCAGAGCCCTGTTCGAG 268
QY 61 AAGAGCGGCTACTCTGTGGGCGACGCTCATCGCCCCAGATGATGCTCTGACAGCAGCC 120
DB 269 AAGAGCGGCTACTCTGTGGGCGACGCTCATCGCCCCAGATGATGCTCTGACAGCAGCC 328
QY 121 CACTGCTCAAGCCCGCTACATATATTTACCTGGGGGAGACACATCTCCAGAAAGAGAG 180
DB 329 CACTGCTCAAGCCCGCTACATATATTTACCTGGGGGAGACACATCTCCAGAAAGAGAG 388
QY 181 GGCTGTAGAGACACCGGAGACGACCATGATGCTCTCCCGACCCCGGCTTCAACACAGC 240
DB 389 GGCTGTAGAGACACCGGAGACGACCATGATGCTCTCCCGACCCCGGCTTCAACACAGC 448
QY 241 CTCCCAACAAGACACCGCAAT 264
DB 449 CTCCCAACAAGACACCGCAAT 472

RESULT 12

US-08-944-483-4
Sequence 4, Application US/08944483
Patent No. 6232456
GENERAL INFORMATION:
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944.483
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183. US. 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-944-483-4

Query Match 36.4%; Score 250; DB 3; Length 250;
Best Local Similarity 100.0%; Pred. No. 1e-55;

Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 GACCACCGAATGACATGCTGTGTAAGATGCGATCCGCTCATCATCCGCGGT 312
|||||
Db 1 GACCACCGAATGACATGCTGTGTAAGATGCGATCCGCTCATCATCCGCGGT 60
QY 313 GGGGACCCCTTACCTCTCTCAGCGCTGTGTACCTGTGGACACAGCTGCTCATTTCC 372
|||||
Db 61 GGGGACCCCTTACCTCTCTCAGCGCTGTGTACCTGTGGACACAGCTGCTCATTTCC 120
QY 373 GGGTGGGGGAGCAGCTGCGAGCCCGGCTTACGCTGCTCAGACCTTGGGATGGCGGAC 432
|||||
Db 121 GGGTGGGGGAGCAGCTGCGAGCCCGGCTTACGCTGCTCAGACCTTGGGATGGCGGAC 180
QY 433 ATCCACCATATTGAGCAGCAGAAAGTGTGAAGCGCTTACCGCGGCAATCAAGACACC 492
|||||
Db 181 ATCCACCATATTGAGCAGCAGAAAGTGTGAAGCGCTTACCGCGGCAATCAAGACACC 240
QY 493 ATGGTGTGTG 502
|||||
Db 241 ATGGTGTGTG 250

RESULT 13

US-08-944-483-3
Sequence 3, Application US/08944483

Patent No. 6232456

GENERAL INFORMATION:

APPLICANT: COHEN, MAURICE

APPLICANT: COLPITTS, TRACEY L.

APPLICANT: FRIEDMAN, PAULA N.

APPLICANT: GRANADOS, EDWARD N.

APPLICANT: KLAAS, MICHAEL R.

APPLICANT: RUSSELL, JOHN C.

APPLICANT: STEWART, KENT D.

APPLICANT: STROPE, STEVEN D.

TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS

TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES

NUMBER OF SEQUENCES: 76

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/944,483

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6183.US.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623

TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 239 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-944-483-3

Query Match

Best Local Similarity 99.6%; Score 237.4; DB 3; Length 239;

Matches 238; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 32 CCCAGCCCTGGGACGAGCCCTGTTGAGAAAGCGGGCTACTCTGTGGGGGAGCGCTCA 91
|||||
Db 1 CCCAGCCCTGGGACGAGCCCTGTTGAGAAAGCGGGCTACTCTGTGGGGGAGCGCTCA 60
QY 92 TCGCCCCCAGATGGCTCTGACGAGCGCCACTGCTCAAGCCCCCTACTATAGTTAC 151
|||||
Db 61 TCGCCCCCAGATGGCTCTGACGAGCGCCACTGCTCAAGCCCCCTACTATAGTTAC 120
QY 152 TGGGGGAGCAGCACTCTCAGAAAGAGAGGGCTGTGAGAGACCCGAGACCGACTGAGT 211
|||||
Db 121 TGGGGGAGCAGCACTCTCAGAAAGAGAGGGCTGTGAGAGACCCGAGACCGACTGAGT 180
QY 212 CCTTCCCCCAGCCCGCTTCAACAGAGCCTCCCAACAAAGACACCGCAATGACATC 270
|||||
Db 181 CCTTCCCCCAGCCCGCTTCAACAGAGCCTCCCAACAAAGACACCGCAATGACATC 239

RESULT 14

US-08-944-483-5
Sequence 5, Application US/08944483

Patent No. 6232456

GENERAL INFORMATION:

APPLICANT: COHEN, MAURICE

APPLICANT: COLPITTS, TRACEY L.

APPLICANT: FRIEDMAN, PAULA N.

APPLICANT: GRANADOS, EDWARD N.

APPLICANT: KLAAS, MICHAEL R.

APPLICANT: RUSSELL, JOHN C.

APPLICANT: STEWART, KENT D.

APPLICANT: STROPE, STEVEN D.

TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS

TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES

NUMBER OF SEQUENCES: 76

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/944,483

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6183.US.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623

TELEX:

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 262 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 15, 2003, 10:56:03 : Search time 241.21 Seconds
(without alignments)
7688.371 Million cell updates/sec

Title: US-09-856-320A-1_COPY_272_958

Perfect score: 687
Sequence: 1 atcatcaaggaggttcgagtg.....agagagacatgaagaacaat 687

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
- 24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*
- 25: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	687	100.0	1106	20	AAZ22638
2	687	100.0	1158	20	AAZ22639
3	687	100.0	1186	24	ABK92131
4	687	100.0	1186	25	ABX76468
5	687	100.0	1192	22	ABX76468
6	687	100.0	1204	21	AAAD14842
7	687	100.0	1204	22	AAAS37072
8	687	100.0	1204	22	AAAS21496
					AAAF54320

9	687	100.0	1204	24	ABL95664
10	687	100.0	1204	24	ABL88175
11	687	100.0	1204	24	ABK33628
12	687	100.0	1204	25	ACA03855
13	687	100.0	1204	25	ACA04276
14	687	100.0	1204	25	ABX89393
15	687	100.0	1301	21	AAA61763
16	687	100.0	1314	21	AAZ30222
17	686.6	99.9	1292	22	ABA83372
18	685.8	99.8	1146	20	AAV84589
19	685.8	99.8	1146	22	ABA83430
20	685.2	99.7	1166	22	AAAD14841
21	684.6	99.7	1191	20	AAK97777
22	673	98.0	1335	21	AAZ45672
23	660	96.1	1052	21	AAZ87798
24	660	96.1	1052	22	AAZ55270
25	654.2	95.2	833	19	AAV4925
26	601.6	87.6	934	21	AAA61765
27	514.2	74.8	1323	21	AAA61764
28	464.6	67.6	618	24	ABK30233
29	464.2	67.6	762	21	AAH31050
30	464.2	67.6	762	21	AAH31061
31	462.2	67.3	1164	24	ABX51683
32	293.2	42.7	1365	22	AAZ41087
33	293.2	42.7	1375	22	AAZ26876
34	292.4	42.6	924	22	AAZ41622
35	292.4	42.6	924	22	AAZ26948
36	292.4	42.6	924	23	ABK41855
37	291.6	42.4	1438	24	ABQ99555
38	287	41.8	662	22	AAZ68191
39	287	41.8	662	24	ABK38102
40	287	41.8	662	25	ACA10431
41	287	41.8	662	25	ABX93382
42	262.4	38.2	472	24	ABK30366
43	250	36.4	250	22	AAAD14838
44	237.4	34.6	239	22	AAAD14837
45	226.2	32.9	942	20	AAZ11030

ALIGNMENTS

RESULT 1	
AAZ22638	AAZ22638 standard; cDNA; 1106 BP.
ID	AAZ22638;
AC	AAZ22638;
AC	08-DEC-1999 (first entry)
DT	CASB12 nucleotide sequence.
DE	
XX	
XX	
KW	neuropilin; cancer; assay; inhibitor; serine protease; immunogenic; ds.
OS	Homo sapiens.
XX	
XX	
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	14.862
FT	/tag= a
FT	/product= CASB12
PN	W09949055-A1.
PD	30-SEP-1999.
XX	
XX	
PF	17-MAR-1999; 99WO-EP01894.
XX	
PR	20-MAR-1998; 98GB-0006095.
XX	
PA	(SMK) SMITHKLINE BEECHAM BIOLOGICALS.
XX	
PI	Bruck CEM, Cassart J, Coche T, Vinals-Bassols C;

XX WPI; 1999-580450/49.
 DR P-PSDB; AAY42439.
 XX New human serine protease CASB12, for treatment, prevention and
 PT diagnosis of cancer and autoimmune diseases -
 PS Claim 10; Page 47; 58bp; English.
 XX This is the nucleotide sequence of the CASB12 gene. The nucleotide
 CC sequence of AA22638 shows homology with neuropilin and the encoded
 CC protein AAY42439 is structurally related to other proteins of the
 CC serine protease family, having homology and/or structural similarity
 CC with neuropilin. It is expected that as well as similar structure, these
 CC proteins will also share similar biological functions and properties.
 CC The CASB12 polypeptides and polynucleotides can be used to develop
 CC methods for identifying agonists and antagonists/inhibitors of these
 CC molecules, and thereby treating conditions associated with CASB12
 CC polypeptide imbalance. The invention also provides for diagnostic assays
 CC for detecting diseases associated with inappropriate CASB12 polypeptide
 CC activity or levels.
 CC Since CASB12 is either specifically expressed or highly over-expressed
 CC in tumors compared to normal cells, the polypeptides and polynucleotides
 CC of the invention are believed to be important immunogens for specific
 CC prophylactic or therapeutic immunization against tumors. The
 CC polypeptides and polynucleotides can therefore be targeted by antigen
 CC specific immune reactions (which result in the destruction of the tumor
 CC cell) or they can be used to diagnose the occurrence of tumor cells.
 SQ Sequence 1106 BP; 247 A; 348 C; 287 G; 224 T; 0 other;
 Query Match 100.0%; Score 687; DB 20; Length 1106;
 Best Local Similarity 100.0%; Pred. No. 7.1e-137;
 Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATCATCAAGGGGCTCGATGCAAGCCCTACCTCCAGCCGCGGAGAGCCCTGTGAG 60
 Db 173 ATCTTCAAGGGGCTTCGATGCAAGCCCTACCTCCAGCCGCGGAGAGCCCTGTGAG 232
 QY 61 AAGACGGGCTACTCTGTGGGGGAGCGCTATGCCCCAGATGGCTCTGACAGCACC 120
 Db 233 AAGACGGGCTACTCTGTGGGGGAGCGCTATGCCCCAGATGGCTCTGACAGCACC 292
 QY 121 CACTGCTCAAGCCCGCTACATAGTTACCTGGGGGAGACAACTCCAGAGAGAG 180
 Db 293 CACTGCTCAAGCCCGCTACATAGTTACCTGGGGGAGACAACTCCAGAGAGAG 352
 QY 181 GGGGTGAGAGACCGGAGAGCCACTGAGTCTCCCGACCCCGGCTTCAACAGAGC 240
 Db 353 GGGGTGAGAGACCGGAGAGCCACTGAGTCTCCCGACCCCGGCTTCAACAGAGC 412
 QY 241 CTCGCCAACAAGACACCGCAATGACATCATGCTGGTGAAGATGGCATGCCAGTCTCC 300
 Db 413 CTCGCCAACAAGACACCGCAATGACATCATGCTGGTGAAGATGGCATGCCAGTCTCC 472
 QY 301 ATACACGGGCTGTGGGACCCCTCACCCTCTCTCAGCGTGTGTCATGCTGGACACG 360
 Db 473 ATACACGGGCTGTGGGACCCCTCACCCTCTCTCAGCGTGTGTCATGCTGGACACG 532
 QY 361 TGCTCATTTCCGGCTGTGGGAGAGCTCCAGCCCGGCTTACAGCCCTGACACCTTG 420
 Db 533 TGCTCATTTCCGGCTGTGGGAGAGCTCCAGCCCGGCTTACAGCCCTGACACCTTG 592
 QY 421 CGATGGCCCAACATCACCATCATTTGAGACACAGAAAGTGTGAGAAAGCGCTACCCGGAC 480
 Db 593 CGATGGCCCAACATCACCATCATTTGAGACACAGAAAGTGTGAGAAAGCGCTACCCGGAC 652
 QY 481 ATACAGAGACACATGCTGTGTGCCAGGCTGACAGAGAGGGGCAAGAGCTCTGCGACGGT 540
 Db 653 ATACAGAGACACATGCTGTGTGCCAGGCTGACAGAGAGGGGCAAGAGCTCTGCGACGGT 712
 QY 541 GACTCCGGGGGCGCTGTGCTGTGAACCAAGTCTTTAAAGCAATATCTCTGGGGCCAG 600
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 713 GACTCCGGGGGCGCTGTGCTGTGAACCAAGTCTTTCAAGGCAATTATCTCTGGGGCCAG 772
 QY 601 GATCCGTGTGGATCACCCGAAAGCCTGTGTCTACAGAAAGTCTCAATATGTGAC 660
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 Db 773 GATCCGTGTGGATCACCCGAAAGCCTGTGTGTCTACAGAAAGTCTCAATATGTGAC 832
 QY 661 TGGATCCAGAGACGATGAAGACAAT 687
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 833 TGGATCCAGAGACGATGAAGACAAT 859
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 RESULT 2
 AA22639
 ID AA22639 standard; cDNA; 1158 BP.
 XX
 AC AA22639;
 XX
 DT 08-DEC-1999 (first entry)
 XX
 DE CASB12 derived from Expressed Sequence Tag sequences.
 XX
 KW neuropilin; cancer; assay; inhibitor; serine protease; immunogenic;
 KW autoimmune disease; ds.
 OS
 OS Homo sapiens.
 FH
 FH Key Location/Qualifiers
 FT CDS 84..932
 FT /*tag= a
 FT /product= CASB12
 XX
 XX W09949055-A1.
 FN
 FN 30-SEP-1999.
 XX
 XX 17-MAR-1999; 99WO-EP01894.
 PR 20-MAR-1998; 98GB-0006095.
 XX
 PA (SWIK) SMITHKLINE BEECHAM BIOLOGICALS.
 PA
 PI Bruck CEM, Cassart J, Coche T, Vinals-Bassols C;
 XX
 DR WPI; 1999-580450/49.
 DR P-PSDB; AAY42440.
 XX
 PT New human serine protease CASB12, for treatment, prevention and
 PT diagnosis of cancer and autoimmune diseases -
 PS Claim 26; Page 49; 58bp; English.
 XX This is the nucleotide sequence of the CASB12 gene derived from
 CC Expressed Sequence Tag (EST) search for tumor-specific and
 CC tumor-associated antigens. The nucleotide sequence of AA22638 shows
 CC homology with neuropilin and the encoded protein AAY42439 is structurally
 CC related to other proteins of the serine protease family, having homology
 CC and/or structural similarity with neuropilin. It is expected that as well
 CC as similar structure, these proteins will also share similar biological
 CC functions and properties.
 CC The CASB12 polypeptides and polynucleotides can be used to develop
 CC methods for identifying agonists and antagonists/inhibitors of these
 CC molecules, and thereby treating conditions associated with CASB12
 CC polypeptide imbalance. The invention also provides for diagnostic assays
 CC for detecting diseases associated with inappropriate CASB12 polypeptide
 CC activity or levels.
 CC Since CASB12 is either specifically expressed or highly over-expressed
 CC in tumors compared to normal cells, the polypeptides and polynucleotides
 CC of the invention are believed to be important immunogens for specific
 CC prophylactic or therapeutic immunization against tumors. The
 CC polypeptides and polynucleotides can therefore be targeted by antigen
 CC specific immune reactions (which result in the destruction of the tumor
 CC cell) or they can be used to diagnose the occurrence of tumor cells

Sequence 1158 BP; 274 A; 359 C; 306 G; 219 T; 0 other;

Query Match 100.0%; Score 687; DB 20; Length 1158;
Best Local Similarity 100.0%; Pred. No. 7.1e-137;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATCATCAAGGGGTTGAGTGCAGAGCTTCACTCCAGACCTGGCAGGACCCCTGTTCCAG 60
DB 243 ATCATCAAGGGGTTGAGTGCAGAGCTTCACTCCAGACCTGGCAGGACCCCTGTTCCAG 302
QY 61 AAGAGCGGGCTACTCTGTGGGGGAGAGCTCATCGCCCCAGATGGCTCTGACAGAGCC 120
DB 303 AAGAGCGGGCTACTCTGTGGGGGAGAGCTCATCGCCCCAGATGGCTCTGACAGAGCC 362
QY 121 CACTGCTTCAGACCCCGCTACATAGTTCACTGAGGAGCAGACACCTCCAGAGAGAGAG 180
DB 363 CACTGCTTCAGACCCCGCTACATAGTTCACTGAGGAGCAGACACCTCCAGAGAGAGAG 422
QY 181 GGCTGTGAGCAGACCCCGAGACAGCTAGTCTCTTCCCGACCCCGGCTTCAACAGAC 240
DB 423 GGCTGTGAGCAGACCCCGAGACAGCTAGTCTCTTCCCGACCCCGGCTTCAACAGAC 482
QY 241 CTCCCAACAAAGACACCCGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 483 CTCCCAACAAAGACACCCGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 542
QY 301 ATCACTGGGCTGTGAGACCCCTCAACCTCTCTCACTGATGATGATGATGATGATGATGAT 360
DB 543 ATCACTGGGCTGTGAGACCCCTCAACCTCTCTCACTGATGATGATGATGATGATGATGAT 602
QY 361 TGGCTCATTTTCCGGGTGGGGGAGACAGTTCAGACCCCGAGTTCAGCTGCTTCAACCTT 420
DB 603 TGGCTCATTTTCCGGGTGGGGGAGACAGTTCAGACCCCGAGTTCAGCTGCTTCAACCTT 662
QY 421 CGATCGCCCAACATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 480
DB 663 CGATCGCCCAACATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 722
QY 481 ATCAAGACACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 723 ATCAAGACACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 782
QY 541 GACATCGGGGGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 783 GACATCGGGGGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 842
QY 601 GATCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
DB 843 GATCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 902
QY 661 TGGATTCAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 687
DB 903 TGGATTCAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 929

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RESULT 3

ABK92131
ID ABK92131 standard; DNA; 1186 BP.

AC ABK92131;

XX 15-AUG-2002 (first entry)

DE Prostate cancer-associated DNA sequence #17.

KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;

XX gene therapy; gene; ds.

OS Mammalia.

XX WO200230268-A2.

PN 18-APR-2002.

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XX 12-OCT-2001; 2001WO-US32045.
PF 13-OCT-2000; 2000US-0687576.
XX 08-DEC-2000; 2000US-0733288.
PR 08-DEC-2000; 2000US-0733742.
PR 24-JAN-2001; 2001US-263957P.
PR 16-MAR-2001; 2001US-276791P.
PR 16-MAR-2001; 2001US-276888P.
PR 06-APR-2001; 2001US-281922P.
PR 24-APR-2001; 2001US-286214P.
PR 30-APR-2001; 2001US-0847046.
PR 04-MAY-2001; 2001US-288589P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX Gish KC, Mack DH, Wilson KE, Afar D, Hvezzi P;
PI WPI; 2002-471335/50.
DR P-PSDB; AB61816.
XX
PT Detecting a prostate cancer-associated transcript in a cell in a
PT patient, useful for diagnosing prostate cancer (PC) or screening
PT modulators of PC, by determining if prostate cancer-associated genes
PT are expressed in a prostate tissue
XX
PS Claim 22; Page 313; 436pp; English.
XX
CC The present invention relates to methods of detecting a prostate
CC cancer-associated transcript in a cell from a patient. The method
CC comprises contacting a biological sample from the patient with
CC prostate cancer-associated polynucleotides (designated PC genes) that
CC selectively hybridize to a sequence that is at least 80% identical
CC to them. The prostate cancer-associated polynucleotide sequences
CC are differentially expressed in prostate tumour tissue or in
CC prostate cancer and are derived from the tissues of various
CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
CC The methods of the invention are useful for diagnosing and treating
CC prostate cancer in mammals. The prostate cancer-associated genes are
CC useful for diagnosing or treating prostate cancer, as well as for
CC identifying modulators of prostate cancer or agents that inhibit
CC prostate cancer. The nucleic acid sequences are particularly useful
CC in gene therapy, as a vaccine or in antisense applications.
CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC sequences.
XX
SQ Sequence 1186 BP; 272 A; 368 C; 302 G; 244 T; 0 other;

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Query Match 100.0%; Score 687; DB 24; Length 1186;
Best Local Similarity 100.0%; Pred. No. 7.1e-137;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATCATCAAGGGGTTGAGTGCAGAGCTTCACTCCAGACCTGGCAGGACCCCTGTTCCAG 60
DB 185 ATCATCAAGGGGTTGAGTGCAGAGCTTCACTCCAGACCTGGCAGGACCCCTGTTCCAG 244
QY 61 AAGAGCGGGCTACTCTGTGGGGGAGAGCTCATCGCCCCAGATGGCTCTGACAGAGCC 120
DB 245 AAGAGCGGGCTACTCTGTGGGGGAGAGCTCATCGCCCCAGATGGCTCTGACAGAGCC 304
QY 121 CACTGCTTCAGACCCCGCTACATAGTTCACTGAGGAGCAGACACCTCCAGAGAGAGAG 180
DB 305 CACTGCTTCAGACCCCGCTACATAGTTCACTGAGGAGCAGACACCTCCAGAGAGAGAG 364
QY 181 GGCTGTGAGCAGACCCCGAGACAGCTAGTCTCTTCCCGACCCCGGCTTCAACAGAC 240
DB 365 GGCTGTGAGCAGACCCCGAGACAGCTAGTCTCTTCCCGACCCCGGCTTCAACAGAC 424
QY 241 CTCCCAACAAAGACACCCGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 425 CTCCCAACAAAGACACCCGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 484
QY 301 ATCACTGGGCTGTGAGACCCCTCAACCTCTCTCACTGATGATGATGATGATGATGATGAT 360

```

|||||
Db 485 ATCACCCTGGGCTGTGCACCCCTCACCCTCTCCACGCTGTGTACTGTGGACAGC 544
361 TGCCTCAATTCGCGGCTGGGAGACGCTCCAGCCCGAGTTACGCTGCTGCACACCTTG 420
545 TGCTCATTTCCGGCTGGGAGACGCTCCAGCCCGAGTTACGCTGCTGCACACCTTG 604
Qy 421 CGATGCGCCAAACATCACCATTGAGACACGAGAGTGTGAGAAAGCCCTACCCGCGAAC 480
605 CGATGCGCCAAACATCACCATTGAGACACGAGAGTGTGAGAAAGCCCTACCCGCGAAC 664
Qy 481 ATCAGACACACATGATGTGTGCGAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 540
665 ATCAGACACACATGATGTGTGCGAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 724
Qy 541 GACTCCGCGGGGCGCCCTGTGTCTGTACACAGTCTCTTCAAGGCAATATCTCCGCGGCGAG 600
725 GACTCCGCGGGGCGCCCTGTGTCTGTACACAGTCTCTTCAAGGCAATATCTCCGCGGCGAG 784
Qy 601 GATCCGCTGTGCGATCACCAGCCGAGGCTGTGTCTACACGAAAGTCTGCAAAATATGTGGAC 660
785 GATCCGCTGTGCGATCACCAGCCGAGGCTGTGTCTACACGAAAGTCTGCAAAATATGTGGAC 844
Db 661 TGGATCCAGGAGACGATGAAGAACAAT 687
845 TGGATCCAGGAGACGATGAAGAACAAT 871

RESULT 4

ID ABX76468 standard; DNM: 1186 BP.
AC ABX76468;

02-APR-2003 (first entry)

Lung cancer-associated polynucleotide #332.

Lung cancer-associated polynucleotide; gene; ds; cytosolic; emphysema;
antitumorigenic; antiproliferative; non-small cell lung cancer; atelectasis;
small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

Unidentified.

WO200286443-A2.

31-OCT-2002.

18-APR-2002; 2002WO-US12476.

18-APR-2001; 2001US-284770P.

10-MAY-2001; 2001US-290492P.

09-NOV-2001; 2001US-339245P.

13-NOV-2001; 2001US-350666P.

29-NOV-2001; 2001US-334370P.

12-APR-2002; 2002US-372246P.

(EOSB-) EOS BIOTECHNOLOGY INC.

Aziz N, Murray R;

WPI; 2003-093161/08.

P-PSDB; ABUS6739.

Claim 22; Page 443; 453pp; English.

The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the invention.

Sequence 1186 BP; 272 A; 368 C; 302 G; 244 T; 0 other;

Query Match 100.0%; Score 687; DB 25; Length 1186;

Best Local Similarity 100.0%; Pred. No. 7.1e-137; Mismatches 0; Gaps 0;

Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCATCAAGGGGTTGAGTCAAGCCCTCACTCCAGCCCTGCGAGCGCCCTGTTTCGAG 60
185 ATCATCAAGGGGTTGAGTCAAGCCCTCACTCCAGCCCTGCGAGCGCCCTGTTTCGAG 244
Qy 61 AAGACGGGCTACTCTGTGGGAGCGCTATGAGCCCGCAGATGCTCTGACAGAGCC 120
245 AAGACGGGCTACTCTGTGGGAGCGCTATGAGCCCGCAGATGCTCTGACAGAGCC 304
Qy 121 CACTGCTCAAGCCCGCTCAATAGTTCACCTGGGAGAGACAACTCCGAAGAGAGAG 180
305 CACTGCTCAAGCCCGCTCAATAGTTCACCTGGGAGAGAGACAACTCCGAAGAGAGAG 364
Qy 181 GCGTGTGAGAGACAGCCGAGACCGCACTGAGTCTTCCCGACCCCGGCTTCAACAGAG 240
365 GCGTGTGAGAGACAGCCGAGACCGCACTGAGTCTTCCCGACCCCGGCTTCAACAGAG 424
Qy 241 CTCCCAACAAAGAACCCGCAATGATATGCTGTGAGATGAGATGAGATGAGATGAG 300
425 CTCCCAACAAAGAACCCGCAATGATATGCTGTGAGATGAGATGAGATGAGATGAG 484
Qy 301 ATCAGCTGGGCTGTGCAGCCCTCAACCTCCCTCAAGCTGTGACCTGTGACAGCAGC 360
485 ATCAGCTGGGCTGTGCAGCCCTCAACCTCCCTCAAGCTGTGACCTGTGACAGCAGC 544
Qy 361 TGCCTCAATTCGCGGCTGGGAGACGCTCCAGCCCGAGTTACGCTGCTGCACACCTTG 420
545 TGCTCATTTCCGGCTGGGAGACGCTCCAGCCCGAGTTACGCTGCTGCACACCTTG 604
Qy 421 CGATGCGCCAAACATCACCATTGAGACACGAGAGTGTGAGAAAGCCCTACCCGCGAAC 480
605 CGATGCGCCAAACATCACCATTGAGACACGAGAGTGTGAGAAAGCCCTACCCGCGAAC 664
Qy 481 ATCAGACACACATGATGTGTGCGAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGT 540
665 ATCAGACACACATGATGTGTGCGAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGT 724
Qy 541 GACTCCGCGGGGCGCCCTGTGTCTGTAAACAGTCTCTTCAAGGCAATATCTCCGCGGCGAG 600
725 GACTCCGCGGGGCGCCCTGTGTCTGTAAACAGTCTCTTCAAGGCAATATCTCCGCGGCGAG 784
Qy 601 GATCCGCTGTGCGATCACCAGCCGAGGCTGTGTCTACACGAAAGTCTGCAAAATATGTGGAC 660
785 GATCCGCTGTGCGATCACCAGCCGAGGCTGTGTCTACACGAAAGTCTGCAAAATATGTGGAC 844
Qy 661 TGGATCCAGGAGACGATGAAGAACAAT 687
845 TGGATCCAGGAGACGATGAAGAACAAT 871

ID	AD14842	standard: DNA; 1192 BP.
XX	AD14842;	
XX	01-NOV-2001	(first entry)
XX	Human PS133 gene contig.	
XX	Human; PS133; prostate disease; cancer; immunogen; gene therapy; EST;	
XX	expressed sequence tag; cytosolic; ds.	
XX	Homo sapiens.	
XX	Key	Location/Qualifiers
XX	CDS	107..859
XX	FT	/tag= a
XX	FT	/product= "Human PS133 protein"
XX	FT	/transl_except= (pos:188..196, aa:Cys-Pro)
XX	FT	/transl_except= (pos:224..232, aa:Phe-Lys)
XX	US6232456-B1.	
XX	15-MAY-2001.	
XX	06-0CT-1997;	97US-0944483.
XX	06-0CT-1997;	97US-0944483.
XX	(ABBO) ABBOTT LAB.	
XX	Cohen M, Colpitts TL, Friedman PN, Granados E, Klass MR;	
XX	Russell JC, Stewart KD, Stroupe SD;	
XX	WPI: 2001-366357/38.	
XX	P-PSDB; AAE08017.	
XX	New PS133 polynucleotides, useful for detecting, diagnosing, staging,	
XX	monitoring, prognosing, preventing, treating or determining the	
XX	predisposition of an individual to a prostate disease, e.g. cancer -	
XX	Claim 1; Column 71-74; 93pp: English.	
XX	The patent discloses PS133 polynucleotides and polypeptides which	
XX	are indicative of prostate disease. The patent also provides a method	
XX	for detecting PS133 protein in a test sample. The polynucleotides of	
XX	the invention are useful for detecting, diagnosing, staging, monitoring,	
XX	prognosing, preventing, treating or determining the predisposition of	
XX	an individual to prostate diseases such as cancer. PS133-derived	
XX	polynucleotides are used for the detection of normal or altered gene	
XX	expression, in assays for detecting, amplifying or quantifying genes	
XX	or nucleic acids relating to prostate tissue diseases and conditions,	
XX	and to produce probes which can be used in the detection of nucleic	
XX	acids in a sample. PS133 proteins are used as immunogens for the	
XX	production of antibodies. PS133 sequences are also used in gene	
XX	therapy. The present sequence is human PS133 gene contig.	
XX	Sequence 1192 BP; 279 A; 385 C; 290 G; 238 T; 0 other;	
XX	Query Match	100.0%; Score 687; DB 22; Length 1192;
XX	Best Local Similarity	100.0%; Pred. No. 7,1e-137;
XX	Matches	687; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX	1 ATCATCAAGGGGTTGCACTGCAAGCCTCACTCCAGCCCTGGCAGCAGCCCTGTTGAG	60
XX		
XX	170 ATCATCAAGGGGTTGCACTGCAAGCCTCACTCCAGCCCTGGCAGCAGCCCTGTTGAG	229
XX	61 AAGACGGCGCTACTCTGTGGGGCGACGCTCAATCGCCCGCAATGGCTCTCTGACAGAGCC	120
XX		
XX	230 AAGACGGCGCTACTCTGTGGGGCGACGCTCAATCGCCCGCAATGGCTCTCTGACAGAGCC	289

OY	121	CAGTCCCTCAAGCCCGGCTACATAGTTCACCTGGGGGACAGACAACCTCCGAAGGGAG	180
Db	230	CAGTCCCTCAAGCCCGGCTACATAGTTCACCTGGGGGACAGACAACCTCCGAAGGGAG	349
OY	181	GCGTGTGAGCAGACCCCGGACGCCACACTGAGTCTTCCCGCACCCCGGCTTCAACACAGC	240
Db	350	GCGTGTGAGCAGACCCCGGACGCCACACTGAGTCTTCCCGCACCCCGGCTTCAACACAGC	409
OY	241	CTCCCAACAAAGACCCCGGACATGATGCTGTGTGAGATGGCATGCGCATGCTCC	300
Db	410	CTCCCAACAAAGACCCCGGACATGATGCTGTGTGAGATGGCATGCGCATGCTCC	469
OY	301	ATCACCTGGGGGTGGGAGACCCCGCACCCCTCTCCACGCTGTCTACTGCTGGCACAGC	360
Db	470	ATCACCTGGGGGTGGGAGACCCCGCACCCCTCTCCACGCTGTCTACTGCTGGCACAGC	529
OY	361	TGCGTCATATTCGGGCTGGGGGACAGCAGTCCAGCCCGCAATAGCGCTGCTCACACCTTG	420
Db	530	TGCGTCATATTCGGGCTGGGGGACAGCAGTCCAGCCCGCAATAGCGCTGCTCACACCTTG	589
OY	421	CGATCGGCCACATATACCATTCATTGAGCACCCAGAGTGTGAGAGAGCTTACCCGGCAC	480
Db	590	CGATCGGCCACATATACCATTCATTGAGCACCCAGAGTGTGAGAGAGCTTACCCGGCAC	649
OY	481	ATCACAGACACCATGATGTGTGTGCCAGCGTCCAGGAGGGGGGCAAGGACATCCCTCCAGGGT	540
Db	650	ATCACAGACACCATGATGTGTGTGCCAGCGTCCAGGAGGGGGGCAAGGACATCCCTCCAGGGT	709
OY	541	GACTCCGGGGGCGCTGTGTGTGTACCAAGTCTTCAAGGCAATATTCCTCTGGGCCAG	600
Db	710	GACTCCGGGGGCGCTGTGTGTGTGTACCAAGTCTTCAAGGCAATATTCCTCTGGGCCAG	769
OY	601	GATCGGTGTGCGATACCCGGAAGGCTGGTGTCTACAGAAAGTCTGCAATATGTGGAC	660
Db	770	GATCGGTGTGCGATACCCGGAAGGCTGGTGTCTACAGAAAGTCTGCAATATGTGGAC	829
OY	661	TGGATCCAGAGACGATGAGAACAAT	687
Db	830	TGGATCCAGAGACGATGAGAACAAT	856
RESULT 6			
AAA37072			
XX	ID	AAA37072 standard; cDNA; 1204 BP.	
XX	AC	AAA37072;	
XX	DT	08-AUG-2000 (first entry)	
DE	XX	Human PRO1279 (UNQ649) cDNA sequence SEQ ID NO:169.	
XX	KW	Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;	
KW	KW	transmembrane; secretion; Immunoadhesion; pharmaceutical; screening;	
XX	OS	ss.	
XX	OS	Homo sapiens.	
XX	PN	WO20012708-A2.	
XX	PD	09-MAR-2000.	
XX	PF	01-SEP-1999; 99WO-US20111.	
XX	PR	01-SEP-1998; 98US-0098716.	
PR	PR	01-SEP-1998; 98US-0098749.	
PR	PR	01-SEP-1998; 98US-0098750.	
PR	PR	02-SEP-1998; 98US-0098803.	
PR	PR	02-SEP-1998; 98US-0098821.	
PR	PR	02-SEP-1998; 98US-0098843.	
PR	PR	09-SEP-1998; 98US-0099536.	
PR	PR	09-SEP-1998; 98US-0099596.	
PR	PR	09-SEP-1998; 98US-0099598.	

PR 09-SEP-1998; 98US-0099602.
PR 09-SEP-1998; 98US-0099642.
PR 10-SEP-1998; 98US-0099741.
PR 10-SEP-1998; 98US-0099754.
PR 10-SEP-1998; 98US-0099763.
PR 10-SEP-1998; 98US-0099792.
PR 10-SEP-1998; 98US-0099808.
PR 10-SEP-1998; 98US-0099812.
PR 10-SEP-1998; 98US-0099815.
PR 15-SEP-1998; 98US-0100385.
PR 15-SEP-1998; 98US-0100388.
PR 15-SEP-1998; 98US-0100390.
PR 16-SEP-1998; 98US-0100564.
PR 16-SEP-1998; 98US-0100627.
PR 16-SEP-1998; 98US-0100661.
PR 16-SEP-1998; 98US-0100662.
PR 16-SEP-1998; 98US-0100664.
PR 17-SEP-1998; 98US-0100683.
PR 17-SEP-1998; 98US-0100710.
PR 17-SEP-1998; 98US-0100711.
PR 17-SEP-1998; 98US-0100930.
PR 18-SEP-1998; 98US-0100848.
PR 18-SEP-1998; 98US-0100849.
PR 18-SEP-1998; 98US-0101014.
PR 18-SEP-1998; 98US-0101068.
PR 22-SEP-1998; 98US-0101071.
PR 23-SEP-1998; 98US-0101279.
PR 23-SEP-1998; 98US-0101471.
PR 23-SEP-1998; 98US-0101472.
PR 23-SEP-1998; 98US-0101474.
PR 23-SEP-1998; 98US-0101475.
PR 23-SEP-1998; 98US-0101476.
PR 23-SEP-1998; 98US-0101477.
PR 24-SEP-1998; 98US-0101738.
PR 24-SEP-1998; 98US-0101741.
PR 24-SEP-1998; 98US-0101743.
PR 24-SEP-1998; 98US-0101915.
PR 24-SEP-1998; 98US-0101916.
PR 29-SEP-1998; 98US-0102207.
PR 29-SEP-1998; 98US-0102240.
PR 29-SEP-1998; 98US-0102307.
PR 29-SEP-1998; 98US-0102330.
PR 29-SEP-1998; 98US-0102331.
PR 30-SEP-1998; 98US-0102484.
PR 30-SEP-1998; 98US-0102487.
PR 30-SEP-1998; 98US-0102570.
PR 30-SEP-1998; 98US-0102571.
PR 01-OCT-1998; 98US-0102684.
PR 01-OCT-1998; 98US-0102687.
PR 02-OCT-1998; 98US-0102965.
PR 06-OCT-1998; 98US-0103258.
PR 06-OCT-1998; 98US-0103449.
PR 07-OCT-1998; 98US-0103314.
PR 07-OCT-1998; 98US-0103315.
PR 07-OCT-1998; 98US-0103328.
PR 07-OCT-1998; 98US-0103395.
PR 07-OCT-1998; 98US-0103396.
PR 07-OCT-1998; 98US-0103401.
PR 08-OCT-1998; 98US-0103633.
PR 08-OCT-1998; 98US-0103679.
PR 08-OCT-1998; 98US-0103679.
PR 08-OCT-1998; 98US-0103711.
PR 14-OCT-1998; 98US-0104257.
PR 20-OCT-1998; 98US-0104967.
PR 20-OCT-1998; 98US-0105000.
PR 20-OCT-1998; 98US-0105002.
PR 21-OCT-1998; 98US-0105104.
PR 22-OCT-1998; 98US-0105169.
PR 22-OCT-1998; 98US-0105266.

PR 26-OCT-1998; 98US-0105693.
PR 26-OCT-1998; 98US-0105694.
PR 27-OCT-1998; 98US-0105807.
PR 27-OCT-1998; 98US-0105881.
PR 27-OCT-1998; 98US-0105882.
PR 27-OCT-1998; 98US-0106052.
PR 28-OCT-1998; 98US-0106023.
PR 28-OCT-1998; 98US-0106029.
PR 28-OCT-1998; 98US-0106030.
PR 28-OCT-1998; 98US-0106032.
PR 28-OCT-1998; 98US-0106033.
PR 28-OCT-1998; 98US-0106178.
PR 29-OCT-1998; 98US-0106248.
PR 29-OCT-1998; 98US-0106384.
PR 29-OCT-1998; 98US-0106500.
PR 30-OCT-1998; 98US-0106464.
PR 03-NOV-1998; 98US-0106856.
PR 03-NOV-1998; 98US-0106902.
PR 03-NOV-1998; 98US-0106905.
PR 03-NOV-1998; 98US-0106919.
PR 03-NOV-1998; 98US-0106932.
PR 10-NOV-1998; 98US-0106934.
PR 17-NOV-1998; 98US-0107783.
PR 17-NOV-1998; 98US-0108775.
PR 17-NOV-1998; 98US-0108779.
PR 17-NOV-1998; 98US-0108787.
PR 17-NOV-1998; 98US-0108788.
PR 17-NOV-1998; 98US-0108801.
PR 17-NOV-1998; 98US-0108802.
PR 17-NOV-1998; 98US-0108806.
PR 17-NOV-1998; 98US-0108807.
PR 17-NOV-1998; 98US-0108867.
PR 18-NOV-1998; 98US-0108925.
PR 18-NOV-1998; 98US-0108848.
PR 18-NOV-1998; 98US-0108849.
PR 18-NOV-1998; 98US-0108850.
PR 18-NOV-1998; 98US-0108851.
PR 18-NOV-1998; 98US-0108852.
PR 18-NOV-1998; 98US-0108858.
PR 18-NOV-1998; 98US-0108904.

(GETH) GENENTECH INC.

Baker K, Goddard A, Gurney AL, Smith V, Watanabe CR, Wood WI;

WPI: 2000-237871/20.
P-PSDB; AAY9390.

PT New mammalian DNA sequences encoding transmembrane, receptor or
PT secreted PRO polypeptides; useful for screening of potential peptide or
PT small molecule inhibitors of the relevant receptor/ligand interactions
XX
XX Claim 2; Fig 101; 773pp; English.

CC AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC receptor or secreted PRO polypeptides given in AAY9340 to AAY9462. The
CC transmembrane and receptor PRO proteins can be used for screening of
CC potential peptide or small molecule inhibitors of the relevant
CC receptor/ligand interactions. The polypeptides and nucleotide sequences
CC encoding them have various industrial applications, including uses as
CC pharmaceutical and diagnostic agents. AAA37145 to AAA3730 represent
CC PCR primers and hybridisation probes used in the isolation of the PRO
CC polypeptides from the present invention.
XX

SO Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Query Match 100.0%; Score 687; DB 21; Length 1204;
Best Local Similarity 100.0%; Pred. No. 7, 2e-137;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATCATCAAGGGGTTCCAGTGCAGCAAGCTTCACTCCACGCTGCAGGACGACCTGTTCGAG 60
DB 169 ATCATCAAGGGGTTCCAGTGCAGCAAGCTTCACTCCACGCTGCAGGACGACCTGTTCGAG 228

Db 229 AAGAGCGGGCTACTCTGTGGGGGAGACGCTCATGCCCCAGATGGCTCTGACAGCAGCC 288
QY 121 CACTGCTTCAAGCCCGCTACATAGTTACCTGGGGGAGCACAACCTTCAGAAAGAGAG 180
Db 289 CACTGCTTCAAGCCCGCTACATAGTTACCTGGGGGAGCACAACCTTCAGAAAGAGAG 348
QY 181 GCGTGTAGCAGACCCGGAGCAGCAGTGTCTTCCCCCAACCCGGCTTCAACAGC 240
Db 349 GCGTGTAGCAGACCCGGAGCAGCAGTGTCTTCCCCCAACCCGGCTTCAACAGC 408
QY 241 CTCCCAACAAGACCAACCGCATGATCATGTGTGGGAAGATGGATGCCAGTCTCC 300
Db 409 CTCCCAACAAGACCAACCGCATGATCATGTGTGGGAAGATGGATGCCAGTCTCC 468
QY 301 ATCACTGGGGCTGTGCAACCCCTCCTCTCAGCGTGTGTCACTGTGAGCAGC 360
Db 469 ATCACTGGGGCTGTGCAACCCCTCCTCAGCGTGTGTCACTGTGAGCAGC 528
QY 361 TGCTCTATTTCGGGCTGGGGGAGCAGTCCAGCCCAAGTTACGCTTCTCAGACCTTG 420
Db 529 TGCTCTATTTCGGGCTGGGGGAGCAGTCCAGCCCAAGTTACGCTTCTCAGACCTTG 588
QY 421 CGATGCGCAACATCACCATTGATGAGCAGCAGAAAGTGTGAGAACGCTTACCCGGCAAC 480
Db 589 CGATGCGCAACATCACCATTGATGAGCAGCAGAAAGTGTGAGAACGCTTACCCGGCAAC 648
QY 481 ATCAAGACACCATGTGTGTGTGCGAGCGTGCAGAGAGGGGGCAAGAGCTCTGCCAGGGT 540
Db 649 ATCAAGACACCATGTGTGTGTGCGAGCGTGCAGAGAGGGGGCAAGAGCTCTGCCAGGGT 708
QY 541 GATCCCGGGGGCCCTGGTGTGTGTGAACCACTCTTCAAGGCAATATCTCTGGGGCCAG 600
Db 709 GATCCCGGGGGCCCTGGTGTGTGTGAACCACTCTTCAAGGCAATATCTCTGGGGCCAG 768
QY 601 GATCCGTTGGGATCACCCGAAAGCTGTGTCTACAGAAAGTCTGCAATATGTGGAG 660
Db 769 GATCCGTTGGGATCACCCGAAAGCTGTGTCTACAGAAAGTCTGCAATATGTGGAG 828
QY 661 TGGATCCAGAGACGATGAGAACAT 687
Db 829 TGGATCCAGAGACGATGAGAACAT 855

RESULT 8
AAFS4320
ID AAF54320 standard; DNA; 1204 BP.
XX
AC AAF54320;
XX
DT 02-APR-2001 (first entry)
XX
DE DNA encoding protein of the invention #51.
XX
KW Secreted; transmembrane; gene therapy; ss.
XX
OS Unidentified.
XX
PN WO200078961-A1.
XX
PD 28-DEC-2000.
XX
PF 18-FEB-2000; 2000WO-US04342.
XX
PR 23-JUN-1999; 99US-0141037.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 01-SEP-1999; 99WO-US20111.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28551.
PR 16-DEC-1999; 99WO-US01095.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.

XX (GENTH) GENTTECH INC.
PA Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Rong S;
XX Gao W, Goddard A, Goddard PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D;
PI Watanabe CK, Williams PM, Wood WI;
XX WPI: 2001-071395/08.
DR
PT Secreted and transmembrane proteins and nucleic acids designated PRO,
PT useful as hybridization probes, in chromosome and gene mapping and gene
PT therapy -
PS
PS Claim 2: Fig 101; 787bp; English.
XX
CC The present invention relates to secreted and transmembrane proteins.
CC These proteins and the DNA encoding them may be used as hybridization
CC probes, in chromosome and gene mapping and in the generation of
CC anti-sense RNA and DNA. They may also be used to generate either
CC transgenic animals or knockout animals which are in turn useful for
CC development and screening of therapeutically useful reagents.
CC The nucleic acids may also be used in gene therapy.
XX
SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other:
Query Match 100.0%; Score 687; DB 22; Length 1204;
Best Local Similarity 100.0%; Pred. No. 7.2e-137;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATCTCAAGGGGCTTCAAGTGTGCAAGCTTCTCCAGCCCTGGAGGAGCCCTTTGGAG 60
Db 169 ATCTCAAGGGGCTTCAAGTGTGCAAGCTTCTCCAGCCCTGGAGGAGCCCTTTGGAG 228
QY 61 AAGAGCGGGCTACTCTGTGGGGGAGCAGCTCATGCGCCCAAGATGGCTCTGACAGCAGC 120
Db 229 AAGAGCGGGCTACTCTGTGGGGGAGCAGCTCATGCGCCCAAGATGGCTCTGACAGCAGC 288
QY 121 CACTGCTCAAGCCCGCTACATAGTTACCTGGGGGAGCACAACCTTCAGAAAGAGAG 180
Db 289 CACTGCTCAAGCCCGCTACATAGTTACCTGGGGGAGCACAACCTTCAGAAAGAGAG 348
QY 181 GCGTGTAGCAGACCCGGAGCAGCAGTGTCTTCCCCCAAGTTACGCTTCTCAGACCTTG 240
Db 349 GCGTGTAGCAGACCCGGAGCAGCAGTGTCTTCCCCCAAGTTACGCTTCTCAGACCTTG 408
QY 241 CTCCCAACAAGACCAACCGCATGATCATGTGTGGGAAGATGGATGCCAGTCTCC 300
Db 409 CTCCCAACAAGACCAACCGCATGATCATGTGTGGGAAGATGGATGCCAGTCTCC 468
QY 301 ATCACTGGGGCTGTGCAACCCCTCCTCTCAGCGTGTGTCACTGTGAGCAGC 360
Db 469 ATCACTGGGGCTGTGCAACCCCTCCTCTCAGCGTGTGTCACTGTGAGCAGC 528
QY 361 TGCTCTATTTCGGGCTGGGGGAGCAGTCCAGCCCAAGTTACGCTTCTCAGACCTTG 420
Db 529 TGCTCTATTTCGGGCTGGGGGAGCAGTCCAGCCCAAGTTACGCTTCTCAGACCTTG 588
QY 421 CGATGCGCAACATCACCATTGATGAGCAGCAGAAAGTGTGAGAACGCTTACCCGGCAAC 480
Db 589 CGATGCGCAACATCACCATTGATGAGCAGCAGAAAGTGTGAGAACGCTTACCCGGCAAC 648
QY 481 ATCAAGACACCATGTGTGTGTGCGAGCGTGCAGAGAGGGGGCAAGAGCTCTGCCAGGGT 540
Db 649 ATCAAGACACCATGTGTGTGTGCGAGCGTGCAGAGAGGGGGCAAGAGCTCTGCCAGGGT 708
QY 541 GATCCCGGGGGCCCTGGTGTGTGTGAACCACTCTTCAAGGCAATATCTCTGGGGCCAG 600
Db 709 GATCCCGGGGGCCCTGGTGTGTGTGAACCACTCTTCAAGGCAATATCTCTGGGGCCAG 768
QY 601 GATCCGTTGGGATCACCCGAAAGCTGTGTCTACAGAAAGTCTGCAATATGTGGAG 660
Db 769 GATCCGTTGGGATCACCCGAAAGCTGTGTCTACAGAAAGTCTGCAATATGTGGAG 828

OY		661	TGCATCCAGGACGATGTAAACAATT	687
Dn		829	TGGATCCAGGACGATGAAGAACAATT	855
	RESULT 9			
ID	ABLJ5664			
XX	ABLJ5664 standard; cDNA; 1204 BP.			
AC	ABLJ5664;			
XN				
Df	19-JUL-2002 (first entry)			
DE	Human angiogenesis related CDNA PRO1279 SEQ ID NO: 207.			
KW	Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;			
KM	atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;			
KW	cardiac; cytosolic; antiangiogenic; hypotensive; vulnarary;			
XX	antiarteriosclerotic; gene; ss.			
OS	Homo sapiens.			
PX	WO200208284-A2.			
PV				
PD	31-JAN-2002.			
PE	09-JUL-2001; 2001MO-US21735.			
PR	20-JUL-2000; 2000US-219556P.			
PR	25-JUL-2000; 2000US-220624P.			
PR	25-JUL-2000; 2000US-220664P.			
PR	28-JUL-2000; 2000MO-US20710.			
PR	02-AUG-2000; 2000US-222695P.			
PR	17-AUG-2000; 2000US-0643657.			
PR	23-AUG-2000; 2000MO-US2352Z.			
PR	24-AUG-2000; 2000MO-US23328.			
PR	07-SEP-2000; 2000US-230978P.			
PR	15-SEP-2000; 2000US-000000P.			
PR	18-SEP-2000; 2000US-0664610.			
PR	18-SEP-2000; 2000US-0665350.			
PR	24-OCT-2000; 2000US-242922P.			
PR	08-NOV-2000; 2000US-070932B.			
PR	08-NOV-2000; 2000MO-US30952.			
PR	10-NOV-2000; 2000MO-US30873.			
PR	01-DEC-2000; 2000MO-US32678.			
PR	20-DEC-2000; 2000US-0747259.			
PR	20-DEC-2000; 2000MO-US34956.			
PR	22-JAN-2001; 2001US-0767609.			
PR	28-FEB-2001; 2001US-0796498.			
PR	28-FEB-2001; 2001MO-US06620.			
PR	09-MAR-2001; 2001MO-US06666.			
PR	09-MAR-2001; 2001US-0802706.			
PR	14-MAR-2001; 2001US-0808689.			
PR	22-MAR-2001; 2001US-0816744.			
PR	05-APR-2001; 2001US-0828366.			
PR	10-MAY-2001; 2001US-0854208.			
PR	10-MAY-2001; 2001US-0854280.			
PR	25-MAY-2001; 2001US-0866028.			
PR	25-MAY-2001; 2001US-0866034.			
PR	25-MAY-2001; 2001MO-US17092.			
PR	30-MAY-2001; 2001US-0870574.			
PR	30-MAY-2001; 2001MO-US17443.			
PR	01-JUN-2001; 2001MO-US17800.			
PR	20-JUN-2001; 2001MO-US19692.			
PR	28-JUN-2001; 2001MO-US00000.			
PA	(GETH) GENENTECH INC.			
PA	(BAKE/) BAKER K P.			
PA	(FERR/) FERRARA N.			
PA	(GERB/) GERBER H.			
PA	(GERR/) GERRITSEN M E.			
PA	(GODD) GODDARD A.			

	Query Match	100.0%	Score 687	DB 24	Length 1204	
	Best Local Similarity	100.0%	Pred. No. 7.2e-137			
	Matches 687	Conservative	0	Mismatches	0	Indels
XX	(GODO//)	GODOWSKI P J.				
PA	(GURN//)	GURNEI A L.				
PA	(HILL//)	HILLIAN K J.				
PA	(MARS//)	MARSTERS S A.				
PA	(PANU//)	PAN J.				
PA	(PAON//)	PAONI N F.				
PA	(STEP//)	STEPHAN J F.				
PA	(WATA//)	WATANABE C K.				
PA	(WILL//)	WILLIAMS P M.				
PA	(WOOD//)	WOOD W I.				
XX						
PI	Baker KP, Ferrara N, Gerber H, Gertlisen ME, Goddard A;					
PI	Godowski PJ, Guney AU, Hillan KJ, Marsters SA, Pan J, Paoni NF;					
PI	Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;					
XX						
XX	WPI: 2002-171999/22.					
DR	P-PSDB; ABB95526.					
XX						
PT	One hundred and eighty seven nucleic acids encoding PRO polypeptides,					
PT	useful in diagnosis and treatment of cardiovascular (e.g. myocardial					
PT	infarction), endothelial or angiogenic disorders in a mammal -					
XX						
PS	Claim 1; Fig 207; 567pp; English.					
XX						
CC	The present invention provides the protein and coding sequences of human					
CC	PRO proteins. These are useful for treating or diagnosing a					
CC	cardiovascular, endothelial or angiogenic disorder. Including cardiac					
CC	hypertrophy, trauma, cancer, age-related macular degeneration,					
CC	atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,					
CC	angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour					
CC	angiogenesis (such as breast carcinoma and liver carcinoma) and wound					
CC	healing. The present sequence is a coding sequence of the invention.					
XX						
SQ	Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;					
Query Match	100.0%	Score 687	DB 24	Length 1204		
Match	Local Similarity	100.0%	Pred. No. 7.2e-137			
	Matches 687	Conservative	0	Mismatches	0	Indels
QY	1 ATCATCAAGGGGTTGAGTGCAGGCTCATACACCTGAGCCCTGGACAGGACCCCTGTTTCGAG					60
Db	169 ATCATCAAGGGGTTGAGTGCAGGCTCATACACCTGAGCCCTGGACAGGACCCCTGTTTCGAG					228
QY	61 AAGACGGGCTACTCTGTGGGCGACGCTCATGCCGCCAGATGGCTCCTGCACAGCAGCC					120
Db	229 AAGACGGGCTACTCTGTGGGCGACGCTCATGCCGCCAGATGGCTCCTGCACAGCAGCC					288
QY	121 CACGAGCTCAAGCCCGCTTACATATGTTACCTGAGGGGCGACAACTCCAGAAAGAGAG					180
Db	289 CACGAGCTCAAGCCCGCTTACATATGTTACCTGAGGGGCGACAACTCCAGAAAGAGAG					348
QY	181 GCGTGTGAGCAGACCCGGACAGCCACTGAGTCCCTCCCAACCCCGGCTTCAACAAAGC					240
Db	349 GCGTGTGAGCAGACCCGGACAGCCACTGAGTCCCTCCCAACCCCGGCTTCAACAAAGC					408
QY	241 CTCCCAACAAAGACCCGGAATGACATATGCTGTGGTGAAGATGGCATGGCATGCTCC					300
Db	409 CTCCCAACAAAGACCCGGAATGACATATGCTGTGGTGAAGATGGCATGGCATGCTCC					468
QY	301 ATCACTGTGGGCTGTGCGACCCCTCAACCTTCCTCAACCTGTGTACAGCTGGACAGC					360
Db	469 ATCACTGTGGGCTGTGCGACCCCTCAACCTTCCTCAACCTGTGTACAGCTGGACAGC					528
QY	361 TGCTCATTTTCGGGCTGGGCGACAGCTCCAGCCCAAGTACGCTGCTTCACACCTTG					420
Db	529 TGCTCATTTTCGGGCTGGGCGACAGCTCCAGCCCAAGTACGCTGCTTCACACCTTG					588
QY	421 CGATGGCGCAACATCAACCATCATTTGAGACCAAGATGTGAGAAAGCGCTACCCGGGCAAC					480
Db	589 CGATGGCGCAACATCAACCATCATTTGAGACCAAGATGTGAGAAAGCGCTACCCGGGCAAC					648
QY	481 ATCAACAGACCAATGCTGTGTGCGACAGCTGACGAAGAGGGGCAAGGATCTCTGCGAGGCT					540

DB 829 TGGATCCAGACGATGACACAAAT 855

RESULT 12

ACA03855

ID ACA03855 standard; cDNA; 1204 BP.

XX

AC ACA03855;

XX

DT 23-MAY-2003 (first entry)

XX

DE cDNA encoding human PRO polypeptide #253.

XX

KW Human; PRO polypeptide; secreted and transmembrane protein;

KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;

KW differentiation; chondrocyte; tumour; genetic disorder;

KW cytosolic; gene; ss.

XX

OS Homo sapiens.

XX

FN US2003036180-A1.

XX

PD 20-FEB-2003.

XX

PE 09-MAY-2002; 2002US-0143114.

XX

PR 31-MAR-1997; 97WO-US05230.

PR 12-JUN-1998; 98WO-US12456.

PR 14-JUL-1998; 98WO-US14552.

PR 28-AUG-1998; 98WO-US17888.

PR 10-SEP-1998; 98WO-US18824.

PR 14-SEP-1998; 98WO-US19053.

PR 14-SEP-1998; 98WO-US19094.

PR 14-SEP-1998; 98WO-US19177.

PR 16-SEP-1998; 98WO-US19330.

PR 17-SEP-1998; 98WO-US19437.

PR 07-OCT-1998; 98WO-US21141.

PR 29-OCT-1998; 98WO-US22992.

PR 29-OCT-1998; 98WO-US22992.

PR 20-NOV-1998; 98WO-US24855.

PR 01-DEC-1998; 98WO-US25108.

PR 05-JAN-1999; 99WO-US00106.

PR 08-MAR-1999; 99WO-US05028.

PR 10-MAR-1999; 99WO-US05190.

PR 20-APR-1999; 99WO-US08615.

PR 14-MAY-1999; 99WO-US10733.

PR 02-JUN-1999; 99WO-US12252.

PR 01-SEP-1999; 99WO-US20111.

PR 08-SEP-1999; 99WO-US20594.

PR 13-SEP-1999; 99WO-US20944.

PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.

PR 05-OCT-1999; 99WO-US23089.

PR 29-NOV-1999; 99WO-US28214.

PR 30-NOV-1999; 99WO-US28313.

PR 30-NOV-1999; 99WO-US28409.

PR 01-DEC-1999; 99WO-US28301.

PR 01-DEC-1999; 99WO-US28634.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.

PR 02-DEC-1999; 99WO-US28565.

PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.

PR 20-DEC-1999; 99WO-US30999.

PR 22-DEC-1999; 99WO-US30720.

PR 30-DEC-1999; 99WO-US31243.

PR 30-DEC-1999; 99WO-US31274.

PR 05-JAN-2000; 2000WO-US00219.

PR 06-JAN-2000; 2000WO-US00277.

PR 06-JAN-2000; 2000WO-US00376.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.

PR 18-FEB-2000; 2000WO-US04342.

PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.

PR 24-FEB-2000; 2000WO-US05004.

PR 01-MAR-2000; 2000WO-US05601.

PR 02-MAR-2000; 2000WO-US05746.

PR 02-MAR-2000; 2000WO-US05841.

PR 10-MAR-2000; 2000WO-US06319.

PR 15-MAR-2000; 2000WO-US06884.

PR 20-MAR-2000; 2000WO-US07377.

PR 21-MAR-2000; 2000WO-US07532.

PR 30-MAR-2000; 2000WO-US08439.

PR 17-MAY-2000; 2000WO-US13705.

PR 22-MAY-2000; 2000WO-US14042.

PR 30-MAY-2000; 2000WO-US14941.

PR 02-JUN-2000; 2000WO-US15264.

PR 28-JUL-2000; 2000WO-US20710.

PR 11-AUG-2000; 2000WO-US22031.

PR 23-AUG-2000; 2000WO-US23522.

PR 24-AUG-2000; 2000WO-US23528.

PR 08-NOV-2000; 2000WO-US30952.

PR 10-NOV-2000; 2000WO-US30873.

PR 01-DEC-2000; 2000WO-US32678.

PR 20-DEC-2000; 2000WO-US34956.

PR 28-FEB-2001; 2001WO-US06520.

PR 01-MAR-2001; 2001WO-US06666.

PR 25-MAY-2001; 2001WO-US17092.

PR 01-JUN-2001; 2001WO-US17800.

PR 20-JUN-2001; 2001WO-US19692.

PR 22-JUN-2001; 2001WO-US20116.

PR 29-JUN-2001; 2001WO-US21066.

PR 09-JUL-2001; 2001WO-US21735.

PR 20-DEC-2000; 2000WO-US47259.

PR 28-FEB-2001; 2001US-076498.

PR 09-MAR-2001; 2001US-0802706.

PR 14-MAR-2001; 2001US-0808689.

PR 22-MAR-2001; 2001US-0816744.

PR 05-APR-2001; 2001US-0828366.

PR 10-MAY-2001; 2001US-0854208.

PR 10-MAY-2001; 2001US-0854280.

PR 18-MAY-2001; 2001US-0860216.

PR 25-MAY-2001; 2001US-086028.

PR 25-MAY-2001; 2001US-0866034.

PR 01-JUN-2001; 2001US-0872035.

PR 05-JUN-2001; 2001US-0874503.

PR 14-JUN-2001; 2001US-0882636.

PR 19-JUN-2001; 2001US-0886342.

PR 21-JUN-2001; 2001US-0887879.

PR 18-JUL-2001; 2001US-0908827.

PR 06-AUG-2001; 2001US-0924419.

PR 09-AUG-2001; 2001US-0927796.

PR 16-AUG-2001; 2001US-0931836.

PR 19-DEC-2001; 2001US-0028072.

XX

PA (GETH) GENENTECH INC.

XX

PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;

PI Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;

PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX

DR WPI; 2003-332040/31.

DR P-PDSB; AB068822.

XX

PT New secreted and transmembrane PRO nucleic acids, useful for gene

PT therapy, in chromosome and gene mapping, as chromosome markers, in

PT tissue typing, and in chromosome identification

XX

PS Claim 2; Fig 505; 660pp; English.

XX

CC The present invention relates to the isolation of novel human PRO

CC polypeptides, and the polynucleotide sequences encoding them. The

CC PRO polypeptides are secreted and transmembrane proteins. The PRO

CC polypeptides are useful for detecting other PRO polypeptides, for

CC linking bioactive molecules to cells expressing PRO polypeptides,

CC for modulating biological activities of cells expressing PRO
CC polypeptides, and for identifying agonists or antagonists.
CC The PRO polypeptides are useful for stimulating the release of
CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating
CC the proliferation or differentiation of chondrocytes, and detecting the
CC presence of tumours. The polynucleotide sequences encoding PRO
CC polypeptides are useful as hybridisation probes, in chromosome and
CC gene mapping, in the generation of antisense RNA and DNA, in the
CC preparation of PRO polypeptides, for generating transgenic animals or
CC knockout animals, for the genetic analysis of individuals with genetic
CC disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs
CC encoding the human PRO polypeptides of the invention.
CC Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at
CC seqdata.uspto.gov/psipspidentry.html.

xx Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Query Match 100.0%; Score 687; DB 25; Length 1204;
Best Local Similarity 100.0%; Pred. No. 7.2e-137;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCATCAAGGGGTTGAGTGCAGCCCTCCAGCCCTGGCAGCAGCCCTGTTGAG 60
DB 169 ATCATCAAGGGGTTGAGTGCAGCCCTCCAGCCCTGGCAGCAGCCCTGTTGAG 228
QY 61 AAGAGCGGGCTACTGTGTGGGCGAGCGTCATCGCCCCAGATGGCTCTGACAGCAGCC 120
DB 229 AAGAGCGGGCTACTGTGTGGGCGAGCGTCATCGCCCCAGATGGCTCTGACAGCAGCC 288
QY 121 CACTGCTTACAGCCCGCTACATAGTTACCTGGGGGACACACCTCCAGAGAGAGAG 180
DB 289 CACTGCTTACAGCCCGCTACATAGTTACCTGGGGGACACACCTCCAGAGAGAGAG 348
QY 181 GGCTGTAGACAGACCCGAGCAGCACTGATGCTTCCCGCCGGCTTCAACAACAGAC 240
DB 349 GGCTGTAGACAGACCCGAGCAGCACTGATGCTTCCCGCCGGCTTCAACAACAGAC 408
QY 241 CTCGCCAACAAGAGACACCGCATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 409 CTCGCCAACAAGAGACACCGCATGATGATGATGATGATGATGATGATGATGATGAT 468
QY 301 ATCACTGGGCTGTGTGGGCGAGCGTCATCGCCCCAGATGGCTCTGACAGCAGCC 360
DB 469 ATCACTGGGCTGTGTGGGCGAGCGTCATCGCCCCAGATGGCTCTGACAGCAGCC 528
QY 361 TGCCTCATTTCCGGGCTGTGTGGGCGAGCGTCATCGCCCCAGATGGCTCTGACAGC 420
DB 529 TGCCTCATTTCCGGGCTGTGTGGGCGAGCGTCATCGCCCCAGATGGCTCTGACAGC 588
QY 421 CGATGCGGCCAATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 480
DB 589 CGATGCGGCCAATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 648
QY 481 ATCAAGACACCATGTTGT 540
DB 649 ATCAAGACACCATGTTGT 708
QY 541 GACTCCGGGGGCTCTGT 600
DB 709 GACTCCGGGGGCTCTGT 768
QY 601 GATCCGTTGTGCATACCCGGAAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
DB 769 GATCCGTTGTGCATACCCGGAAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 828
QY 661 TGGATCCAGAGACCATGAAGAACAAT 687
DB 829 TGGATCCAGAGACCATGAAGAACAAT 855

RESULT 13
ACA04276

ID	ACA04276 standard; cDNA; 1204 BP.
XX	
AC	ACA04276;
XX	
DT	27-MAY-2003 (first entry)
XX	
DE	Human cDNA encoding a secreted/transmembrane protein, SEQ ID 505.
XX	
KW	Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW	Inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW	infertility; birth defects; premature aging; AIDS; biosensor;
KW	acquired immunodeficiency syndrome; cancer; diabetic complication;
KW	bioreactor; tumour.
XX	
OS	Homo sapiens.
XX	
PN	US2003032155-A1.
XX	
PD	13-FEB-2003.
XX	
PF	03-MAY-2002; 2002US-0137865.
XX	
PR	31-MAR-1997; 97WO-US05230.
PR	12-JUN-1998; 98WO-US12456.
PR	14-JUL-1998; 98WO-US14552.
PR	28-AUG-1998; 98WO-US17888.
PR	10-SEP-1998; 98WO-US18824.
PR	14-SEP-1998; 98WO-US19093.
PR	14-SEP-1998; 98WO-US19094.
PR	14-SEP-1998; 98WO-US19177.
PR	16-SEP-1998; 98WO-US19330.
PR	17-SEP-1998; 98WO-US19437.
PR	07-OCT-1998; 98WO-US21141.
PR	29-OCT-1998; 98WO-US22992.
PR	20-NOV-1998; 98WO-US24855.
PR	01-DEC-1998; 98WO-US25108.
PR	05-JAN-1999; 99WO-US00106.
PR	08-MAR-1999; 99WO-US05028.
PR	10-MAR-1999; 99WO-US05190.
PR	20-APR-1999; 99WO-US08615.
PR	14-MAY-1999; 99WO-US10733.
PR	02-JUN-1999; 99WO-US12252.
PR	01-SEP-1999; 99WO-US20111.
PR	08-SEP-1999; 99WO-US20594.
PR	13-SEP-1999; 99WO-US20944.
PR	15-SEP-1999; 99WO-US21090.
PR	05-OCT-1999; 99WO-US23089.
PR	29-NOV-1999; 99WO-US28214.
PR	30-NOV-1999; 99WO-US28313.
PR	30-NOV-1999; 99WO-US28409.
PR	01-DEC-1999; 99WO-US28301.
PR	01-DEC-1999; 99WO-US28634.
PR	02-DEC-1999; 99WO-US28551.
PR	02-DEC-1999; 99WO-US28564.
PR	16-DEC-1999; 99WO-US30095.
PR	20-DEC-1999; 99WO-US30911.
PR	20-DEC-1999; 99WO-US30999.
PR	22-DEC-1999; 99WO-US30720.
PR	30-DEC-1999; 99WO-US31274.
PR	30-DEC-1999; 99WO-US31243.
PR	05-JAN-2000; 2000WO-US00219.
PR	06-JAN-2000; 2000WO-US00277.
PR	06-JAN-2000; 2000WO-US00376.
PR	11-FEB-2000; 2000WO-US03565.
PR	18-FEB-2000; 2000WO-US04341.
PR	22-FEB-2000; 2000WO-US04342.
PR	24-FEB-2000; 2000WO-US04914.
PR	24-FEB-2000; 2000WO-US05004.
PR	01-MAR-2000; 2000WO-US05601.

02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 18-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX
PA (GENE) GENENTECH INC.
XX
PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,
PI Geritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI: 2003-331925/31.
DR P-PSDB; AB067096.
DR
XX
XX New secreted and transmembrane nucleic acids and polypeptides,
PT designated as PRO, useful for treating inflammation, organ failure,
PT atherosclerosis, cardiac injury, infertility, birth defects, premature
PT aging, AIDS, or cancer -
XX
XX
PS Claim 2; Fig 505; 659pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising, or which is
CC at least 80% identical to, or the full-length coding sequence of, any of
CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
CC (one of 275 secreted or transmembrane proteins). The nucleic acid
CC further comprises the full-length coding sequence of the DNA deposited
CC under American Type Culture Collection (ATCC) accession number in a list
CC given in the specification. Also included are vectors and host
CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO

CC antibodies, PRO extracellular domains and mature sequences, methods
CC of detecting PRO proteins, methods for stimulating the release of
CC TNF-alpha (tumour necrosis factor alpha) from human blood,
CC (and the proliferation of differentiation of chondrocyte cells, the
CC proliferation of, or gene expression in pericyte cells, the release or
CC proteoglycans from cartilage, proliferation of inner ear utricular
CC supporting cells, the proliferation of T-lymphocyte cells, the release
CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the
CC proliferation of endothelial cells), a method for modulating the uptake
CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
CC a method for inhibiting the binding of A-peptide to factor VIIa,
CC or the differentiation of adipocyte cells, a method for detecting the
CC presence of a tumour in a mammal and an oligonucleotide probe derived
CC from any of the nucleotide sequences cited above. The nucleic acids and
CC polypeptides are useful for treating inflammatory diseases, organ
CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
CC diabetic complications. The nucleic acids are useful as hybridisation
CC probes, in chromosome and gene mapping, and in generating antisense RNA
CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
CC biosensors or bioreactors. Both are useful in tissue typing.
CC The present sequence encodes a PRO protein of the invention.
XX

SO Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Query Match 100.0%; Score 687; DB 25; Length 1204;
Best Local Similarity 100.0%; Pred. No. 7.2e-137;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCATCAAGGGGTTGAGTGCAGACCTCATCCAGCCCTGGAGAGAGAGCCCTGTTCAG 60
DB 169 ATCATCAAGGGGTTGAGTGCAGACCTCATCCAGCCCTGGAGAGAGAGCCCTGTTCAG 228
QY 61 AAGAGCGGGCTACTCTGTGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 229 AAGAGCGGGCTACTCTGTGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 288
QY 121 CACTGCTCAAGCCCGGCTACATAGTTCACCTGGGGGAGAGAGAGAGAGAGAGAGAG 180
DB 289 CACTGCTCAAGCCCGGCTACATAGTTCACCTGGGGGAGAGAGAGAGAGAGAGAGAG 348
QY 181 GCGTGTAG 240
DB 349 GCGTGTAG 408
QY 241 CTCGCCAACAAG 300
DB 409 CTCGCCAACAAG 468
QY 301 ATCACTGGGCTGTGGAG 360
DB 469 ATCACTGGGCTGTGGAG 528
QY 361 TGGCTCATTTTCGGGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 529 TGGCTCATTTTCGGGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 588
QY 421 CGATGGCCCAATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 480
DB 589 CGATGGCCCAATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 648
QY 481 ATCAAGAGACACATGT 540
DB 649 ATCAAGAGACACATGT 708
QY 541 GACTCGGGGGGCGGCTGT 600
DB 709 GACTCGGGGGGCGGCTGT 768
QY 601 GATCCGGT 660
DB 769 GATCCGGT 828

QY 661 TGGATCCAGAGACGATGAGACAAAT 687
 DB 829 TGGATCCAGAGACGATGAGACAAAT 855
 RESULT 14
 ABX89393 standard; cDNA, 1204 BP.
 AC ABX89393;
 XX 13-MAY-2003 (first entry)
 DE DNA encoding novel secreted and transmembrane protein PRO1279.
 XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
 KM cardiac insufficiency disorder; cancer; tumour; immune response;
 KM adrenal cortical capillary endothelial growth; c-fos induction;
 KM vascular endothelial growth factor inhibition; VEGF inhibition;
 KM endothelial cell growth inhibitor; T-lymphocytes stimulation;
 KM retinal neurons cell survival; rod photoreceptor cell survival;
 KM retinal disorder; retinitis pigmentosa; kidney disorder;
 KM mammalian kidney mesangial cell proliferation; Berger disease;
 KM dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
 KM chondrocyte redifferentiation; sports injury; arthritis; gene; ss.
 XX Homo sapiens.
 OS US2003017563-A1.
 PN 23-JAN-2003.
 XX 07-MAY-2002; 2002US-0140808.
 PF 31-MAR-1997; 97WO-US05230.
 PR 12-JUN-1998; 98WO-US12456.
 PR 14-JUL-1998; 98WO-US14532.
 PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.
 PR 14-SEP-1998; 98WO-US19177.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 07-OCT-1998; 98WO-US21141.
 PR 29-OCT-1998; 98WO-US22991.
 PR 29-OCT-1998; 98WO-US22992.
 PR 20-NOV-1998; 98WO-US24855.
 PR 01-DEC-1998; 98WO-US25108.
 PR 05-JAN-1999; 99WO-US00106.
 PR 08-MAR-1999; 99WO-US05028.
 PR 10-MAR-1999; 99WO-US05190.
 PR 20-APR-1999; 99WO-US08615.
 PR 14-MAY-1999; 99WO-US10733.
 PR 02-JUN-1999; 99WO-US12252.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 22-DEC-1999; 99WO-US30999.
 PR 22-DEC-1999; 99WO-US30720.

PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 15-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 01-JUN-2001; 2001US-0866034.
 PR 05-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0924796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Beresini M, DeForge L, Desnoyers L, Flyvareff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PU, Guirney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WT, Zhang Z;
 XX WPI; 2003-148238/14.
 DR P-PSDB; AB059903.
 PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
 are therapeutically useful for enhancing immune response and in cancer

PT treatments -

XX Claim 2, Fig 505; 659pp; English.

PS The invention describes an isolated human PRO polypeptide. The PRO

CC polypeptides are useful in detecting PRO polypeptides in a sample, in

CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and

CC in modulating at least one biological activity of a cell expressing a PRO

CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus

CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186

CC stimulate adrenal cortical capillary endothelial growth, and PRO536,

CC PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1256,

CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus

CC useful for treating conditions or disorders where angiogenesis would be

CC beneficial, e.g. wound healing and antagonist of this polypeptide are

CC endothelial growth factor (VEGF) stimulated proliferation of endothelial

CC cells and is thus useful for inhibiting endothelial cell growth in

CC mammals which would be beneficial in inhibiting tumour growth. PRO826,

CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of

CC stimulated T-lymphocytes and are therapeutically useful for enhancing

CC immune response. PRO826, PRO1068 or PRO1312 enhance survival of

CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of

CC rod photoreceptor cells) and therefore are useful for treating retinal

CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813

CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,

CC and therefore are useful for treating kidney disorders associated with

CC decreased mesangial cell function such as Berger disease or other

CC nephropathies associated with dermatitis, herpeticiformis or Crohn's

CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the

CC proliferation and/or redifferentiation of chondrocytes in culture and

CC are thus useful for treating sports injuries, and arthritis. This

CC sequence encodes a novel human PRO protein.

XX

SQ Sequence 1204 BP; 364 A; 364 C; 294 G; 240 T; 0 other:

Query Match 100.0%; Score 687; DB 25; Length 1204;

Best Local Similarity 100.0%; Pred. No. 7.2e-137;

Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 169 ATCATCAAGGGGTTGAGTGCAMGCTTCCAGCCCTGCGAGCGCCCTGTTGAG 228

QY 61 AAGACGGGCTACTCTTGGGGCGAGCTATGCCCCAGANGGCTCTGACAGACC 120

DB 229 AAGACGGGCTACTCTTGGGGCGAGCTATGCCCCAGANGGCTCTGACAGACC 288

QY 121 CACGCGCTCAAGCCCGCTACATAGTTCACCTGGGGGAGACAAACCCGAGAGAGAG 180

DB 289 CACGCGCTCAAGCCCGCTACATAGTTCACCTGGGGGAGACAAACCCGAGAGAGAG 348

QY 181 GGCTGTAGAGAGAGCCCGAGAGCCACTAGTCTCTCCCGACCCCGGCTTCAACAGAG 240

DB 349 GGCTGTAGAGAGAGCCCGAGAGCCACTAGTCTCTCCCGACCCCGGCTTCAACAGAG 408

QY 241 CTGCCCCAAGAAAGCCCGCATGACATATGCTGTGAAGATGGCATGCCAGTCTCC 300

DB 409 CTGCCCCAAGAAAGCCCGCATGACATATGCTGTGAAGATGGCATGCCAGTCTCC 468

QY 301 ATACACGTGGGCTGTGACACCCCTACCCCTCTCCCTACAGCTGTGTGACACAGC 360

DB 469 ATACACGTGGGCTGTGACACCCCTACCCCTCTCCCTACAGCTGTGTGACACAGC 528

QY 361 TGCCCTATTTCGCGTGGGGGAGACAGTCCAGCCCGAGTTAGAGCTGCTCAACCTTG 420

DB 529 TGCCCTATTTCGCGTGGGGGAGACAGTCCAGCCCGAGTTAGAGCTGCTCAACCTTG 588

QY 421 CGATGGCCCAATTCACATCATATTGAGACACAGAGTGTGAAGAGCCCTACCCGGCAGC 480

DB 589 CGATGGCCCAATTCACATCATATTGAGACACAGAGTGTGAAGAGCCCTACCCGGCAGC 648

QY 481 ATCAAGAGACACATGCTGTGTGCGACAGCTGCGAGAGGGGGCAAGAGACTCTCCAGAGGT 540

DB 649 ATCAAGAGACACATGCTGTGTGCGACAGTCCAGAGAGGGGCAAGGACTCTCCAGAGGT 708

QY 541 GACTCCGGGGAGCCCTGCTGTGTGTAAACAGTCTTCAAGGCAATTATCTCTGGGGCAG 800

DB 709 GACTCCGGGGAGCCCTGCTGTGTGTAAACAGTCTTCAAGGCAATTATCTCTGGGGCAG 768

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DB 769 GATCCGTTGTCGATCACCCGAAAGCCCTGCTGTGTGTACACGAAAGTGTGCAATATGTGAC 828

QY 661 TGGATCCAGAGAGACGATGAAGAACAT 687

DB 829 TGGATCCAGAGAGACGATGAAGAACAT 855

RESULT 15

AAA61763

ID AAA61763 standard; cDNA: 1301 BP.

XX

AC AAA61763;

XX

DT 23-OCT-2000 (first entry)

XX

DE cDNA encoding human serine protease BSSP6 (hbSSP6) SEQ ID NO:1.

XX

KW BSSP6; serine protease; human; hbSSP6; mouse; mbSSP6; brain;

KW diagnostic marker; antibody; transgenic animal; Alzheimer's disease;

KW epilepsy; cancer; inflammation; infertility; pancreatitis;

KW prostatic hypertrophy; ss.

XX

OS Homo sapiens.

XX

PN W0200031257-A1.

XX

PD 02-JUN-2000.

XX

PF 19-NOV-1999; 99WO-JP06476.

XX

PR 20-NOV-1998; 98JP-0347802.

XX

PA (FUSO) FUSO PHARM IND LTD.

XX

PI Uemura H, Okui A, Kominami K, Yamaguchi N, Mitsui S;

XX

DR WPI: 2000-40067/34.

XX

DR P-PSDB; AAB11712.

PT Serine protease BSSP6, useful in detecting homologs, mutants and

PT polymorphic variants as markers for diagnosis of Alzheimer's disease,

PT epilepsy, cancer, inflammation, infertility and prostate hypertrophy,

PT using blood or other tissues -

XX

PS Claim 2; Page 67-69; 94pp; Japanese.

XX

CC The invention relates to novel serine proteases designated BSSP6

CC (AAB11712-B11714), and to nucleic acids encoding them (AAA61763-A61765).

CC CC The invention also relates to vectors and transformants comprising BSSP6

CC nucleic acids; transgenic animals in which the expression level of BSSP6

CC can be varied; and an mbSSP6 knockout mouse. The invention additionally

CC encompasses anti-BSSP6 antibodies and methods of production of such

CC antibodies, methods of BSSP6 detection using the antibodies, and the

CC use of BSSP6 proteins or fragments as diagnostic markers for certain

CC medical conditions. Nucleotides encoding BSSP6 were initially

CC isolated in a human brain cDNA library using degenerate PCR primers

CC (AAA61795-A61796) based on conserved regions of serine proteases. The

CC BSSP6 serine proteases and nucleotides encoding them are useful in

CC detecting homologues, mutants and polymorphic variants in biological

CC samples (e.g., blood, urine, brain, prostate gland, placenta, testis

CC and spleen) as diagnostic markers for conditions such as Alzheimer's

CC disease, epilepsy, cancer, inflammation, infertility and prostatic

CC hypertrophy. Sequences AAA61763 and AAA61765 represent cDNAs encoding

CC human BSSP6 variants (hbSSP6), and sequence AAA61764 represents cDNA

CC encoding murine BSSP6 (mBSP6).

XX Sequence 1301 BP; 332 A; 387 C; 330 G; 252 T; 0 other;

Query Match 100.0%; Score 687; DB 21; Length 1301;

Best Local Similarity 100.0%; Pred. No. 7.2e-137;

Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 481 ATCAGAGACCATGCTGTGTGTCAGCAGCTGTCAGAGAGGGGCAAGGACTCTGCCAGGGT 540
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 15, 2003, 11:00:23 ; Search time 3358.63 Seconds

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Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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and is derived by analysis of the total score distribution.

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21	660	96.1	1052	6	AR219287
22	654.2	95.2	833	6	AR060847
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26	514.2	74.8	1213	10	AB016226
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31	287	41.8	662	6	AR272397
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ALIGNMENTS

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DEFINITION Sequence 1 from Patent WO9949055.
ACCESSION AX016287
VERSION AX016287.1 GI:10041854
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS 1 Bruck C.E., Coche T., Cassart J.P. and Vinals-Bassols C.
TITLE Human casb12 polypeptide, a serine protease
JOURNAL Patent: WO 9949055-A 1 30-SEP-1999;

Pred. No. is the number of results predicted by chance to have a

BRUCK CLAUDINE ELVIRE MARIE (BE); SMITHKLINE BEECHAM BIOLOG (BE);
COCHE THIERRY (BE); CASSART JEAN POL (BE); VINALS BASSOLS CARLOTA
(BE)

FEATURES
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Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AAGACGGGGTACTCTGTGGGGGAGCGCTCATCGCCCCAGATGGCTCTGACAGCACC 120
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LOCUS Human CASB 12 polypeptide, a serine protease.
DEFINITION
ACCESSION BD137019
VERSION BD137019.1 GI:23231964
KEYWORDS JP 2002507425-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1106)

REFERENCE
AUTHORS Bruck,C.E.M., Cassart,J.P., Coche,T. and Bassols,C.V.
TITLE Human CASB 12 polypeptide, a serine protease
JOURNAL Patent: JP 2002507425-A 1 12-MAR-2002;
SMITHKLINE BEECHAM BIOLOGICALS SA
OS Homo sapiens (human)
PN JP 2002507425-A/1
PD 12-MAR-2002
PF 17-MAR-1999 JP 2000538015
PI 20-MAR-1998 GB 9806095.7

COMMENT
CLAUDINE ELVIRE MARIE BRUCK,JEAN POL CASSART,THIERRY COCHE, PI
CARLOTA VINALS BASSOLS
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BASE COUNT 247 a 348 c 287 g 224 t
ORIGIN

Query Match 100.0%; Score 687; DB 6; Length 1106;
Best Local Similarity 100.0%; Pred. No. 2.1e-139; Indels 0; Gaps 0;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCATCAAGGGGTTGAGTGCAGAGCCCTACCTCCAGCCCTGGCAGGAGCCCTGTTGAG 60
DB 173 ATCATCAAGGGGTTGAGTGCAGAGCCCTACCTCCAGCCCTGGCAGGAGCCCTGTTGAG 232
QY 61 AAGACGGGGTACTCTGTGGGGGAGCGCTCATCGCCCCAGATGGCTCTGACAGCAGC 120
DB 233 AAGACGGGGTACTCTGTGGGGGAGCGCTCATCGCCCCAGATGGCTCTGACAGCAGC 292
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RESULT 3
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LOCUS Sequence 3 from Patent WO949055.
ACCESSION AX016289
VERSION AX016289.1 GI:10041855
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Bruck,C.E., Coche,T., Cassart,J.P. and Vinals-Bassols,C.
TITLE Human casb12 polypeptide, a serine protease
JOURNAL Patent: WO 949055-A 3 30-SEP-1999;
BRUCK CLAUDE ELVIRE MARIE (BE); SMITHKLINE BEECHAM BIOLOG (BE);
COCHE THIERRY (BE); CASSART JEAN POL (BE); VINALS BASSOLS CARLOTA
(BE)
FEATURES
source location/Qualifiers
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BASE COUNT 274 a 359 c 306 g 219 t
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Best Local Similarity 100.0%; Pred. No. 2,1e-139;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATCATCAAGGGGTTTGAGTGCAGAGCTCACTCCAGCCCTGGCAGAGCCCTGTTCCAG 60
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Oy 181 GGCTGTGAGCAGACCCGGAAGCCAGCTAGTCTTCCCAACCCCGCTTCAACAACAGC 240
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Oy 241 CTCCCAACAAGAGCACCGCAATGATCATGCTGGTGAAGATGGATGGCAGCTCC 300
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Db 843 GATCCGCTGTGCATACCCGGAAGCCTGGTCTCTACAGCAAGTCTGCAATATGTGAC 902
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Db 903 TGGATCCAGAGACGATGAAGAACAAT 929

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LOCUS Human CASB 12 polypeptide, a serine protease.
DEFINITION BD137020
ACCESSION BD137020.1 GI:23231965
VERSION BD137020.1 GI:23231965
KEYWORDS JP 2002507425-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1158)
AUTHORS Bruck,C.E.M., Cassart,J.P., Coche,T. and Bassols,C.V.
TITLE Human CASB 12 polypeptide, a serine protease
JOURNAL Patent: JP 2002507425-A 2 12-MAR-2002;
SMITHKLINE BEECHAM BIOLOGICALS SA
COMMENT OS Homo sapiens (human)
PN JP 2002507425-A/2
PD 12-MAR-2002
PF 17-MAR-1999 JP 2000538015
PR 20-MAR-1998 GB 9806095.7
PI CLAUDE ELVIRE MARIE BRUCK,JEAN POL CASSART,THIERRY COCHE, PI
CARLOTA VINALS BASSOLS
PC C12N15/09,A61K31/70,A61K38/00,A61P35/00,A61P37/02,C07K16/40,
PC C12N1/15,
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PC 68,G01N33/15,
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PC C12N5/00
CC Human CASB 12 polypeptide, a serine protease. FH key
FT source location/Qualifiers
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BASE COUNT 274 a 359 c 306 g 219 t
ORIGIN
Query Match 100.0%; Score 687; DB 6; Length 1158;
Best Local Similarity 100.0%; Pred. No. 2,1e-139;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATCATCAAGGGGTTTGAGTGCAGAGCTCACTCCAGCCCTGGCAGAGCCCTGTTCCAG 60
Db 243 ATCATCAAGGGGTTTGAGTGCAGAGCTCACTCCAGCCCTGGCAGAGCCCTGTTCCAG 302
Oy 61 AAGAGCGGGCTACTGTGTGGGGCGAGCTCATGCCGCCAGATGGGCTCTGACAGCAGCC 120
Db 303 AAGAGCGGGCTACTGTGTGGGGCGAGCTCATGCCGCCAGATGGGCTCTGACAGCAGCC 362
Oy 121 CACTGCTCAAGCCCGCTAGATAGTTCACTGGGGGAGCAACAACCTTCAGAAAGAGAG 180
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QY 241 CTCCCAACAAAGACCCGAGACGCCAGTGTCTCTCCACCCCGGCTTCAACAGAGC 300

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Db 843 GATCCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 902

QY 661 TGGATCCAGAGAGAGATGAAGAACAT 687

Db 903 TGGATCCAGAGAGAGATGAAGAACAT 929

RESULT 5
AB013730 1181 bp mRNA linear PRI 20-JUN-2000

LOCUS Homo sapiens mRNA for Hippostasin, complete cds.
DEFINITION AB013730
ACCESSION AB013730.1 GI:6681453
VERSION
KEYWORDS Hippostasin.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (sites)
AUTHORS Mitsui,S., Yamada,T., Okui,A., Komihama,K., Nemura,H. and Yamaguchi,N.
TITLE A novel isoform of a kallikrein-like protease, TLSP/Hippostasin, (PRSS20), is expressed in the human brain and prostate
JOURNAL Biochem. Biophys. Res. Commun. 272 (1), 205-211 (2000)
MEDLINE 20329229
PUBMED 10872828
2 (bases 1 to 1181)
Yamaguchi,N. and Mitsui,S.
REFERENCE Direct Submission
JOURNAL Submitted (08-MAY-1998) Nozomi Yamaguchi, Kyoto Prefectural University of Medicine, Res. Ins. Geriatrics, Kawaramachi Hirokoji, Kyoto, Kyoto 602-8566, Japan (E-mail:nozomi@koto.kpu-m.ac.jp, Tel:81-75-251-5848, Fax:81-75-251-5848)
FEATURES
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Db 304 CACTGCTCAAGCCCGCTACATATGTTACCTGGGGGACGACAACTCCAGAAAGAGAG 363

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QY 601 GATCCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660

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QY 661 TGGATCCAGAGAGAGATGAAGAACAT 687

Db 844 TGGATCCAGAGAGAGATGAAGAACAT 870

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LOCUS Homo sapiens mRNA for serine protease (TLSP), complete cds.
DEFINITION AB012917
ACCESSION AB012917.1 GI:3649790
VERSION
KEYWORDS TLSP; serine protease (TLSP).

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
 AUTHORS Yoshida,S., Taniguchi,M., Suemoto,T., Oka,T., He,X. and Shiosaka,S.
 TITLE cDNA cloning and expression of a novel serine protease, TLSP
 JOURNAL Biochim. Biophys. Acta 1399 (2-3), 225-228 (1998)
 MEDLINE 98438738
 PUBMED 9765601

REFERENCE
 AUTHORS Yoshida,S.
 TITLE Direct Submission
 JOURNAL Submitted (10-APR-1998) Shigetaka Yoshida, Department of Anatomy 1,
 Asahikawa Medical College, Midorigaoka Higashi 2-1-1, Asahikawa,
 Hokkaido 078-8510, Japan (E-mail: syoshida@asahikawa-med.ac.jp,
 Tel:81-166-68-2300, Fax:81-166-68-2309)

FEATURES
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Query Match 100.0%; Score 687; DB 9; Length 1186;
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 LOCUS ARI52174
 DEFINITION Sequence 8 from patent US 6232456.
 ACCESSION ARI52174
 VERSION ARI52174.1 GI:15118224
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE
 1 (bases 1 to 1192)
 Cohen,M., Colpitts,T.L., Friedman,P.N., Granados,E., Klass,M.R.,
 Russell,J.C., Stewart,K.D. and Stroupe,S.D.
 TITLE Serine protease reagents and methods useful for detecting and
 treating diseases of the prostate
 JOURNAL Patent: US 6232456-A 8 15-MAY-2001;
 FEATURES
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 /organism="unknown"
 BASE COUNT 279 a 385 c 290 g 238 t
 ORIGIN

Query Match 100.0%; Score 687; DB 6; Length 1192;
 Best Local Similarity 100.0%; Pred. No. 2e-139;
 Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 230 AAGACGGGGCTACTGTGTGGGGGAGCGCTCATGCCCCAGATGGCTCTGACAGAGCC 289
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DEFINITION	Sequence 185 from Patent WO0193983.	Linear	PAT 13-FEB-2002
ACCESSION	AX358932		
VERSION	AX358932.1		
KEYWORDS	GI:18675367		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K., and Wood, W.I.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: WO 0193983-A 185 13-DEC-2001; Genentech Inc. (US)		
FEATURES	location/qualifiers		
SOURCE	1..1204		
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Query Match	100.0%;	Score 687;	DB 6;
Best Local Similarity	100.0%;	Pred. No. 2e-139;	
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QY	601	GATCCGTGTGCGATTCACCCCGAAAGCGCTGGTGTCTACACGAAAGTGTGCAATATGTGGAC	660
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DEFINITION	Sequence 185 from Patent WO0208288.		linear
ACCESSION	AX362425		
VERSION	AX362425.1	GI:18694670	
KEYWORDS			
SOURCE			
ORGANISM			
	Homo sapiens (human)		
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REFERENCE			
AUTHORS	1 Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,		
	Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,Y., Stephan,J.P.,		
	Watanabe,C.K. and Wood,W.I.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding		
	the same		
JOURNAL	Patent: WO 0208288-A 185 31-JAN-2002;		
	Genentech, Inc. (US)		
FEATURES			
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BASE COUNT	306 a 364 c 294 g 240 t		
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	Best Local Similarity 100.0%; Pred. No. 2e-139;		
	Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	ATCATCAAGGGGCTTGAAGTCAGACGCTACATCCAGCCCTGGGCGAGGACGCCCTTTGGAG	60
Db	169	ATCATCAAGGGGCTTGAAGTCAGACGCTACATCCAGCCCTGGGCGAGGACGCCCTTTGGAG	228
QY	61	AAGACGGGGCTACTCTGTGGGGCGACGCGTCATCCGCCCCAGATGGCTCTTACAGCAGCC	120
Db	229	AAGACGGGGCTACTCTGTGGGGCGACGCGTCATCCGCCCCAGATGGCTCTTACAGCAGCC	288
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QY 601 GATCCGTGTGATACCCGGAAGCCTGTGTCTACAGAAAGTGTGCAATATGAG 660
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RESULT 10
AX454622 1204 bp DNA linear PAT 06-JUL-2002
LOCUS Sequence 207 from Patent WO0208284.
ACCESSION AX454622
VERSION AX454622.1 GI:21713935
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE 1 Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
AUTHORS Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.

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TITLE Compositions and methods for the diagnosis and treatment of

JOURNAL disorders involving angiogenesis

Patent: WO 0208284-A 207 31-JAN-2002;
 Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
 (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
 Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
 Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
 ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
 Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
 I. (US)

FEATURES
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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 BASE COUNT 306 a 364 c 294 g 240 t
 ORIGIN

Query Match 100.0%; Score 687; DB 6; Length 1204;
 Best Local Similarity 100.0%; Pred. No. 2e-139;

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Db 169 ATCATCAAGGGGTTGAGTGAAGCTCACTCCACCTTGGCAGGACCCCTGTTCAG 228
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QY 421 CGATGGGCCAATCATCATCATTTGAGACAGCAAGTGTGAGAACGCTTACCCGG 480
Db 589 CGATGGGCCAATCATCATCATTTGAGACAGCAAGTGTGAGAACGCTTACCCGG 648
QY 481 ATCAAGACACCATGCTGTGCTGACAGCGTGAGAGAGGGGCAAGGACTCTGCA 540
Db 649 ATCAAGACACCATGCTGTGCTGACAGCGTGAGAGAGGGGCAAGGACTCTGCA 708
QY 541 GACTCCGGGGGCGCTGCTGTGTAAACAGCTCTTTCAAGGCAATATCTCTGG 600
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QY 601 GATCCGTGTGATACCCGGAAGCCTGTGTCTACAGAAAGTGTGCAATATGAG 660
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QY 661 TGGATCCAGAGACGATGAAGAACAT 687
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RESULT 11
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LOCUS Sequence 505 from Patent WO0140466.
ACCESSION AX464372
VERSION AX464372.1 GI:21899202
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE 1 Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E.,
AUTHORS Gao,W.O., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,
Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Wood,W.L. and Zhang,Z.

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TITLE Secreted and transmembrane polypeptides and nucleic acids encoding

JOURNAL same
 Patent: WO 0140466-A 505 07-JUN-2001;
 Genentech Inc. (US)

FEATURES
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/mol_type="genomic DNA"
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BASE COUNT 306 a 364 c 294 g 240 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2e-139;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCATCAAGGGGTTGAGTGCAGAGCTCAGCTCCAGCCCTGGAGGAGCCCTGTCGAG 60
DB 169 ATCATCAAGGGGTTGAGTGCAGAGCTCAGCTCCAGCCCTGGAGGAGCCCTGTCGAG 228

QY 61 AAGAGGGGGCTACTCTGTGGGGCGAGCTCATATGCGCCCGAGATGGCTCTGACAGAGCC 120
DB 229 AAGAGGGGGCTACTCTGTGGGGCGAGCTCATATGCGCCCGAGATGGCTCTGACAGAGCC 288

QY 121 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGGAGAGCAACCTCCAGAAAGAGAGAG 180
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DB 349 GGGTGTAGAGAGAGCCGGAGAGCCATGAGTCTCTCCCGACCCCGGCTTCACAGAGC 408

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QY 301 ATCACTGGGGCTGTGGAGCCCTCAGCTCTCCAGCTGTGTCAGTGGTGGGAGCAGC 360
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QY 361 TGGCTCATTTCCGGCTGGGGAGAGCAGCTCCAGCCCGATGACCTGCTTCACAGCTTG 420
DB 529 TGGCTCATTTCCGGCTGGGGAGAGCAGCTCCAGCCCGATGACCTGCTTCACAGCTTG 588

QY 421 CGATGGCCCAACATCACCATTGATGAGCAGCAGAAAGTGTGAAGAGCCCTACCCGGCAAC 480
DB 589 CGATGGCCCAACATCACCATTGATGAGCAGCAGAAAGTGTGAAGAGCCCTACCCGGCAAC 648

QY 481 ATCAGACAGACCATGATGTGTGCGAGGTGAGAGAGAGGAGGAGAGAGAGTCTGCAAGGT 540
DB 649 ATCAGACAGACCATGATGTGTGCGAGGTGAGAGAGAGAGGAGAGAGAGAGTCTGCAAGGT 708

QY 541 GACTCCGGGGGCCCTGTGTCTGTACACAGTCTCTCAAGGCATTATCTCTGGGGCAG 600
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QY 601 GATCCGTGTGCGATCAGCCGAAAGCCTGTGTCTACAGAAAGTCTCAAAATATGTGGAC 660
DB 769 GATCCGTGTGCGATCAGCCGAAAGCCTGTGTCTACAGAAAGTCTCAAAATATGTGGAC 828

QY 661 TGGATCCAGAGAGAGATGAAGAACAT 687
DB 829 TGGATCCAGAGAGAGATGAAGAACAT 855

RESULT 12
AX491100 1204 bp DNA linear PAT 16-AUG-2002
LOCUS
DEFINITION Sequence 207 from Patent WO0200690.
ACCESSION AX491100
VERSION AX491100.1 GI:22323887
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerltzen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,

Paoletti, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
Patent: WO 0200690-A 207 03-JAN-2002;
Genentech, Inc. (US)
Location/Qualifiers
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BASE COUNT 306 a 364 c 294 g 240 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2e-139;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCATCAAGGGGTTGAGTGCAGAGCTCAGCTCCAGCCCTGGAGGAGCCCTGTCGAG 60
DB 169 ATCATCAAGGGGTTGAGTGCAGAGCTCAGCTCCAGCCCTGGAGGAGCCCTGTCGAG 228

QY 61 AAGAGGGGGCTACTCTGTGGGGCGAGCTCATATGCGCCCGAGATGGCTCTGACAGAGCC 120
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QY 121 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGGAGAGCAACCTCCAGAAAGAGAGAG 180
DB 289 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGGAGAGCAACCTCCAGAAAGAGAGAG 348

QY 181 GGGTGTAGAGAGAGCCGGAGAGCCATGAGTCTCTCCCGACCCCGGCTTCACAGAGC 240
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QY 241 CTCGCCAACAAGACACCCGATGACATCATGCTGTGAAGATGCGATGCCAGTCTCC 300
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QY 301 ATCACTGGGGCTGTGGAGCCCTCAGCTCTCCAGCTGTGTCAGTGGTGGGAGCAGC 360
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QY 361 TGGCTCATTTCCGGCTGGGGAGAGCAGCTCCAGCCCGATGACCTGCTTCACAGCTTG 420
DB 529 TGGCTCATTTCCGGCTGGGGAGAGCAGCTCCAGCCCGATGACCTGCTTCACAGCTTG 588

QY 421 CGATGGCCCAACATCACCATTGATGAGCAGCAGAAAGTGTGAAGAGCCCTACCCGGCAAC 480
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QY 481 ATCAGACAGACCATGATGTGTGCGAGGTGAGAGAGAGGAGAGAGAGTCTGCAAGGT 540
DB 649 ATCAGACAGACCATGATGTGTGCGAGGTGAGAGAGAGGAGAGAGAGTCTGCAAGGT 708

QY 541 GACTCCGGGGGCCCTGTGTCTGTACACAGTCTCTCAAGGCATTATCTCTGGGGCAG 600
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QY 601 GATCCGTGTGCGATCAGCCGAAAGCCTGTGTCTACAGAAAGTCTCAAAATATGTGGAC 660
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QY 661 TGGATCCAGAGAGAGATGAAGAACAT 687
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RESULT 13
AX697101 1204 bp DNA linear PAT 02-APR-2003
LOCUS
DEFINITION Sequence 169 from Patent WO0078961.
ACCESSION AX697101
VERSION AX697101.1 GI:29498066

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Homiidae; Homo.

AUTHORS Ferrara, N., Stewart, T.A., Williams, P.M., Baker, K.P., Desnoyers, L., Eaton, D.L., Gao, W.Q., Pan, J., Bolstein, D., Fong, S., Goddard, A., Godowski, P.J., Gueney, A.L., Smith, V., Tumas, D., Wood, W.I., Grimaldi, C.J., Hillan, K.J., Paoni, N.F., Roy, M.A. and Watanabe, C.K. Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: WO 0078961-A 169 28-DEC-2000;

FEATURES Location/Qualifiers

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db_xref="taxon:9606"

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Query Match 100.0%; Score 687; DB 6; Length 1204;

Best Local Similarity 100.0%; Pred. No. 2e-139;

Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61 AAGACGGGCTACTCTGTGGGCGACGCTCATGCCCCAGATGGCTCTGACAGACGC 120

229 AAGACGGGCTACTCTGTGGGCGACGCTCATGCCCCAGATGGCTCTGACAGACGC 288

121 CACTGCTCAACGCCCGCTACATAGTTCACCTGGGGGACACACACCTCCAGAGGAGG 180

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181 GCGCTGAGCAGACCCCGACACGACGCTGCTTCCCGACCCCGGCTTCAACAACAGC 240

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361 TGCCTCATTTCCGGCTGGGGGACAGCTCCAGCCGCCCAATTACGCTGCTGCTGCTGCT 420

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649 ATCAAGACACCATGCTGTGCTCCAGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 708

541 GACTCGGGGGGCTCTGCTGTATACAGTCTTTCAGAGGATATATCTCTGGGGCCAG 600

709 GACTCGGGGGGCTCTGCTGTATACAGTCTTTCAGAGGATATATCTCTGGGGCCAG 768

601 GATCGGTGTGATATCAACCCGAAAGCTGTGTATACGAAAGTGTGAAATATGTGAGC 660

769 GATCGGTGTGATATCAACCCGAAAGCTGTGTGTATACGAAAGTGTGAAATATGTGAGC 828

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BC022068

LOCUS BC022068

DEFINITION Homo sapiens, kallikrein 11, clone MGC:33060 IMAGE:4824387, mRNA.

ACCESSION BC022068

VERSION BC022068.1 GI:18314497

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1213)

AUTHORS Strausberg, R.

JOURNAL Direct Submission

Submitted (22-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>

CONTACT: MGC help desk

COMMENT Email: cgabs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>

contact: amadan@systemsbiology.org

Anup Madan, Jessica Fahy, Erin Helton, Mark Keltman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>

Series: IRAP Plate: 46 Row: m Column: 6

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5803198.

FEATURES Location/Qualifiers

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BASE COUNT 290 a 376 c 296 g 251 t

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61 AAGACGGGCTACTCTGTGGGCGACGCTCATGCCCCAGATGGCTCTGACAGACGC 120

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

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(without alignments)
2468.773 Million cells updates/sec

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SUMMARIES

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3	1258	98.7	250	12	US-10-137-870-506	Sequence 506, App
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6	1258	98.7	250	12	US-10-140-274-506	Sequence 506, App
7	1258	98.7	250	12	US-10-140-471-506	Sequence 506, App
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11	1258	98.7	250	12	US-10-141-698-506	Sequence 506, App
12	1258	98.7	250	12	US-10-141-702-506	Sequence 506, App
13	1258	98.7	250	12	US-10-141-702-506	Sequence 506, App
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21	1258	98.7	250	12	US-10-145-631-506	Sequence 506, App
22	1258	98.7	250	12	US-10-145-631-506	Sequence 506, App
23	1258	98.7	250	12	US-10-145-746-506	Sequence 506, App
24	1258	98.7	250	12	US-10-145-748-506	Sequence 506, App
25	1258	98.7	250	12	US-10-145-823-506	Sequence 506, App
26	1258	98.7	250	12	US-10-145-826-506	Sequence 506, App
27	1258	98.7	250	12	US-10-145-870-506	Sequence 506, App
28	1258	98.7	250	12	US-10-145-876-506	Sequence 506, App
29	1258	98.7	250	12	US-10-145-959-506	Sequence 506, App
30	1258	98.7	250	12	US-10-146-724-506	Sequence 506, App
31	1258	98.7	250	12	US-10-146-725-506	Sequence 506, App
32	1258	98.7	250	12	US-10-146-795-506	Sequence 506, App
33	1258	98.7	250	12	US-10-147-495-506	Sequence 506, App
34	1258	98.7	250	12	US-10-147-501-506	Sequence 506, App
35	1258	98.7	250	12	US-10-147-506-506	Sequence 506, App
36	1258	98.7	250	12	US-10-147-509-506	Sequence 506, App
37	1258	98.7	250	12	US-10-147-511-506	Sequence 506, App
38	1258	98.7	250	12	US-10-147-511-506	Sequence 506, App
39	1258	98.7	250	12	US-10-147-519-506	Sequence 506, App
40	1258	98.7	250	12	US-10-153-397-506	Sequence 506, App
41	1258	98.7	250	12	US-10-153-397-506	Sequence 506, App
42	1258	98.7	250	12	US-10-158-783-506	Sequence 506, App
43	1258	98.7	250	12	US-10-158-786-506	Sequence 506, App
44	1258	98.7	250	12	US-10-158-786-506	Sequence 506, App
45	1258	98.7	250	12	US-10-006-130A-170	Sequence 170, App

ALIGNMENTS

RESULT 1
US-09-946-374-170
; Sequence 170, Application US/09946374
; Publication No. US20030073129A1
GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunes, Daniel
; APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830P1C1
CURRENT APPLICATION NUMBER: US/09/946,374
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098803
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098821
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098843
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/099536
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099596
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099602
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099642
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099741
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099754
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099763
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PRIOR APPLICATION NUMBER: 60/099792
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099808
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099815
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099816
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100385
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100388
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100390
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100584
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100661
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100662
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100664
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100683
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100684
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100710
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100711
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100848
PRIOR FILING DATE: 1998-09-18

PRIOR APPLICATION NUMBER: 60/100849
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100919
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100930
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101014
PRIOR FILING DATE: 1998-09-18
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PRIOR FILING DATE: 1998-09-23
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PRIOR APPLICATION NUMBER: 60/101743
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101915
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/102207
PRIOR FILING DATE: 1998-09-29
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PRIOR APPLICATION NUMBER: 60/102307
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PRIOR APPLICATION NUMBER: 60/102330
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102331
PRIOR FILING DATE: 1998-09-29
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PRIOR APPLICATION NUMBER: 60/102487
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102570
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102571
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102684
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/102687
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/102965
PRIOR FILING DATE: 1998-10-02
PRIOR APPLICATION NUMBER: 60/103258
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 60/103314
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103315
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103328
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103395
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103396

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; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
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; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807

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Alignment Scores:

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Pred. No.: 6,09e-87 Length: 250
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.67% Indels: 0
DB: 11 Gaps: 0

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US-09-856-320a-1_copy_272_958 (1-687) x US-09-946-374-170 (1-250)

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QY 1 ATCATCAAGGGGTGAGTGCAGAAAGCTCACTCCAGCCCTGGAGGAGCCCTGTTCAG 60
DB 22 IIEIIEIYSGIYPHEGLUCYSYSPRONISSEGINPROTGRIALALALAEUPHEGLU 41
QY 61 AAGAGCGGGTACTGTGTGGGGGAGCGGTACATCGCCCGAGATGGCTCTGTACAGAGCC 120
DB 42 LYSTHARGLEUCYSGIYALATHRLEUILEALAPROAGTGRLEUETHRALALAA 61
QY 121 CACTGCTCAAGCCCCGTACATAGTCACTGTGGGAGACAAACCTCCAGAGAGAG 180
DB 62 HISCYSLEULYSPROAGTGRITLLEVALHISLEUGLYGINHISASNSLEUGLINSGLUGLU 81
QY 181 GGCTGTGAGCAGACCCGGAGCAGCCACTAGTCTTCCCGACCCCGGGCTTCAACAACAGC 240
DB 82 GLYCYSGLUGLINTHRALATHRGLUSERPHEPRONISPROGLYRHEASNSNSER 101
QY 241 CTCGCCCAACAAAGACCCGCAATGACATCATGCTGGGTAAAGATGGCATGCCAGTCTCC 300
DB 102 LEUPROASNLVSAASHISATRGASNSPRIEMELLEVALLYMETALASERPROVALSER 121
QY 301 ATCACTGGGGGTGGAGACCCCTCAACCTTCCTCAGCGTGTGTCACGTGGCAGCCAGC 360
DB 122 IIEIIEIYSGIYPHEGLUCYSYSPRONISSEGINPROTGRIALALALAEUPHEGLU 141
QY 361 TGCCTCATTTCCGGGTGGGGAGCAGCTCAGCCCGCCAGATTACGGCTGCTCAGACACTTG 420
DB 142 CYSLEULIESERGLYTRPOLYSETHRISERSETPROGLINLEUARGLEUPRONISHTRIEUL 161
QY 421 CGATCGGCCCAACATACCATCTATTGAGACCGAAGGTGTGAGAGCGCTTACCCGGGCAAC 480

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DB 162 ARGYSALASANILETHRIIEGLIHISGLINLYSCYSGILUASNAIATYRPROGLYASN 181
QY 481 ATCAAGACACCATGAGTGTGTCCAGCGTCAGAGAGGGGGCAAGACTCTCCGAGGGT 540
DB 182 IIEIIEIYSGIYPHEGLUCYSYSPRONISSEGINPROTGRIALALALAEUPHEGLU 201
QY 541 GACTCGGGGGCCCTGTGTGTGTAACAGTCTTTCAGAGCATTAATCTCTGGGGCCAG 600
DB 202 ASPSERGLYGLYRPROLEUVALCYSAASNGINSERLEUGLNGLYILEEISERTIPGLYGIN 221
QY 601 GATCCCTGTGCCATCAACCCGGAAGCCCTGGTGTATACAGAAAGTCTGCAATATGTGAC 660
DB 222 ASPROCYSALALETHRARGLYSPROGLYVALTYRTHLYVALCYSLYSTYRVALASP 241
QY 661 TCGATCCAGAGCAGATGAAGAACAAT 687
DB 242 TPIIEIIEGLINGLINTHRMETLYSASNAEN 250

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RESULT 2

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US-10-015-387A-170
; Sequence 170, Application US/10015387A
; Publication No. US20030135034A1
; GENERAL INFORMATION:

```

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; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC54
; CURRENT APPLICATION NUMBER: US/10/015,387A
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 170
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-387A-170

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Alignment Scores:

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Pred. No.: 6,09e-87 Length: 250
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.67% Indels: 0
DB: 12 Gaps: 0

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US-09-856-320a-1_copy_272_958 (1-687) x US-10-015-387A-170 (1-250)

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QY 1 ATCATCAAGGGGTGAGTGCAGAAAGCTCACTCCAGCCCTGGAGGAGCCCTGTTCAG 60
DB 22 IIEIIEIYSGIYPHEGLUCYSYSPRONISSEGINPROTGRIALALALAEUPHEGLU 41
QY 61 AAGAGCGGGTACTGTGTGGGGGAGCGGTACATCGCCCGAGATGGCTCTGTACAGAGCC 120
DB 42 LYSTHARGLEUCYSGIYALATHRLEUILEALAPROAGTGRLEUETHRALALAA 61
QY 121 CACTGCTCAAGCCCCGTACATAGTCACTGTGGGAGACAAACCTCCAGAGAGAGAG 180
DB 62 HISCYSLEULYSPROAGTGRITLLEVALHISLEUGLYGINHISASNSLEUGLINSGLUGLU 81
QY 181 GGCTGTGAGCAGACCCGGAGCAGCCACTAGTCTTCCCGACCCCGGGCTTCAACAACAGC 240

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Db 82 GlycylglutInThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 101
QY 241 CTCCCAACAAGACACCCGCAATGACATCATGCTGGTGAAGATGGATCGCCAGTCTCC 300
Db 102 LeuProAsnLysAspHisAspArgAsnAspIleMetLeuValLysMetAlaSerProValSer 121
QY 301 ATCACTGGGCTGTGGCAACCCCTCAACCTCTCTCAACGCTGTGTCACCTGTGGCAACG 360
Db 122 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 141
QY 361 TGCTCATTTCCGGCTGGGGGAGACAGCTCCAGCCCCGATACGCTTCCCTCACACCTTG 420
Db 142 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 161
QY 421 CGATCGCCCAACATCACCATCATGAGACAGACAGAGTGTGAAGAGCTTACCCGCGCAC 480
Db 162 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTrpProGlyAsn 181
QY 481 ATCAACAGACACCATGCTGTGTGCCAGCGTCGACAGAGGGGGCAAGAGACTCTGCCAGG 540
Db 182 IleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly 201
QY 541 GACTCCGGGGGCGCTGT 600
Db 202 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 221
QY 601 GATCCGTTGGGATCACCCGGAAGCCTGGTGTCTACAGAAAGTGTGCAAAATATGTGGAC 660
Db 222 AspProCysAlaIleThrThrArgLysProGlyValIleThrLysValCysLysTyValAsp 241
QY 661 TGGATCCAGAGACGATGAGAACAT 687
Db 242 TrpIleGlnGlnThrMetLysAsnAsn 250

RESULT 3

US-10-137-870-506

; Sequence 506, Application US/10137870

; Publication No. US2003013883A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: Deforge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3330R1C15

; CURRENT APPLICATION NUMBER: US/10/137, 870

; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 506

; LENGTH: 250

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-137-870-506

Alignment Scores:

Pred. No.: 6,09e-87

Length: 1258.00

Matches: 250

Score: 229

Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 98.67%
DB: 12
Gaps: 0

US-09-856-320a-1_copy_272_958 (1-687) x US-10-137-870-506 (1-250)

QY 1 ATCACTCAAGGGGTTGAGTGTGCAACCTTCACTCCAGCCCTGGGAGGCAAGCCCTGTTCAG 60
Db 22 IleIleLysGlyPheGlnCysLysProHisSerIleProTrpGlnAlaIlePheGln 41
QY 61 AAGAGCGGCTACTCTGTGGGGGCAAGCTCATGCCCCAGATGCTCTGACAGCACC 120
Db 42 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThrAlaAla 61
QY 121 CACTGCTCAAGCCCGCTATCATGTTACCTGGGGAGAGCAACATCTCCAGAGAGAG 180
Db 62 HisCysLeuLysProAlaGlyTrpIleValHisLeuIleGlnHisAsnLeuGlnGlyGln 81
QY 181 GCGTGTGAGCAGACCCGAGACAGCCAGTGTCTTCCCAACCCGCGCTTCAACACAGC 240
Db 82 GlycylglutInThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 101
QY 241 CTCCCAACAAGACACCCGCAATGACATCATGCTGGTGAAGATGGATCGCCAGTCTCC 300
Db 102 LeuProAsnLysAspHisAspArgAsnAspIleMetLeuValLysMetAlaSerProValSer 121
QY 301 ATCACTGGGCTGTGGCAACCCCTCAACCTCTCTCAACGCTGTGTCACCTGTGGCAACG 360
Db 122 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 141
QY 361 TGCTCATTTCCGGCTGGGGGAGACAGCTCCAGCCCCGATACGCTTCCCTCACACCTTG 420
Db 142 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 161
QY 421 CGATCGCCCAACATCACCATCATGAGACAGACAGAGTGTGAAGAGCTTACCCGCGCAC 480
Db 162 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTrpProGlyAsn 181
QY 481 ATCAACAGACACCATGCTGTGTGCCAGCGTCGACAGAGGGGGCAAGAGACTCTGCCAGG 540
Db 182 IleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly 201
QY 541 GACTCCGGGGGCGCTGT 600
Db 202 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 221
QY 601 GATCCGTTGGGATCACCCGGAAGCCTGGTGTCTACAGAAAGTGTGCAAAATATGTGGAC 660
Db 222 AspProCysAlaIleThrThrArgLysProGlyValIleThrLysValCysLysTyValAsp 241
QY 661 TGGATCCAGAGACGATGAGAACAT 687
Db 242 TrpIleGlnGlnThrMetLysAsnAsn 250

RESULT 4

US-10-140-018-506

; Sequence 506, Application US/10140018

; Publication No. US2003013885A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: Deforge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3330R1C158
 ; CURRENT APPLICATION NUMBER: US/10/140,018
 ; PRIORITY FILING DATE: 2002-05-06
 ; PRIOR APPLICATION removed - See Palm or File Wrapper
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 506
 ; LENGTH: 250
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-140-018-506

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
6	0.9e-87	1258.00	100.00%	98.67%	250	229	0	0	0	0

US-09-856-320a-1_copy_272_958 (1-687) x US-10-140-018-506 (1-250)

QY 1 ATCATCAAGGGGTTGAGTGCAGAGCCTCCAGCCCTGACAGGAGCCCTGTTGAG 60
 DB 22 ILEILYSGLYPHEGLUCYSLSYSPROHISSEKINPOTRPGILNLALEUPHEGLU 41
 QY 61 AAGAGCGGGCTACTGTGTGGGGGAGCGTCATCGCCCGAGATGGCTCTGCAGAGCC 120
 DB 42 LYSTHARGLEULEUCYSGLYALATHRLEULLEALPROARGTRPLEUETHRALAALA 61
 QY 121 CACTGCTCAAGCCCCCGCTACATAGTACCTGGGGGAGACAACTCCAGAGAGAGAG 180
 DB 62 HISCYSLEULYSPTARGTYRILEVALHISLEUGLYGHNHISASNLEUHLNLSGLUGLU 81
 QY 181 GGCCTGAGCAGACCCGGGAGACCCAGCTGAGTCTCCCGCCAGCCGGCTTCAACAAGAC 240
 DB 82 GLYCSGLUGINTHARGTHRLEUHRGUSERPHEPROHISPROGLYPHEASNNSER 101
 QY 241 CTCGCCAACAAGACCCAGCATGATCATGTGTGTGAGATGGATGGCAGCTTCC 300
 DB 102 LEUPROASNLYSASPHISARGASNAPRIEMELLEVALLYSMETALASERPROVALSER 121
 QY 301 ATCAGCTGGGGTGTGGAGCCCTCAGCTCTCCAGCTGTGTACGTGTGGACAGCAG 360
 DB 122 ILEHTRTPALAVALARPROLEUTHRLEUSERSERARGCYSAITHRALAGLYTHRESER 141
 QY 361 TGCCATATTTCCGGCTGGGGGAGCAGCTGACAGCCCGGATTAGGCTGCTGACAGCTTG 420
 DB 142 CYSLEULIESERGLYTRPGLYSERHRSERPROGLINLEUARGLEUPROHISHREU 161
 QY 421 CGATGCGCAACATCATCATATTGAGCAGCAGAAAGTGTGAGAACGCTTACCCCGGCAAC 480
 DB 162 ARGYSALASNNILEHTRILEGLIHNHISGLNLYSCYSLUASNALATYRPROGLYSYN 181
 QY 481 ATCAAGACACCATGTGTGTGGCAGCTGCGAGGAAAGGGGGAGAGAGATCTCCGCAAGGT 540
 DB 182 ILEHTRAPTRHMEVALCYSALESERVALGNGIUGLYGLYASPSERCTYSGINGLY 201
 QY 541 GACTCGGGGGCCCTGCTGTGTAAACAGTCTTCAAGGATATATCTCCGGGGCCAG 600
 DB 202 ASPSERGLYGLYPROLEUVALCYASNINLSERLEUGINGLYILELIESERTIPGLYN 221
 QY 601 GATCGGTGTGCATCAACCCGAAAGCCTGTGTCTACACGAAAGTGTGCAATATGTGAGC 660
 DB 222 ASPPROCYSALEHTRHARGLYSPROGLYVALTYRTHLYSVALCYLSTYTRVALASP 241
 QY 661 TGGATCCGAGAGAGATGAGAACAT 687
 ||||||||||||||||||||||||||||

DB 242 TRIPLEGLINLUTHRMEILYSASN 250

RESULT 5

US-10-140-021-506
 ; Sequence 506 Application US/10140021
 ; Publication No. US20030138886A1
 ; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerlitsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3330R1C167
 ; CURRENT APPLICATION NUMBER: US/10/140,021
 ; PRIORITY FILING DATE: 2002-05-06
 ; PRIOR APPLICATION removed - See Palm or File Wrapper

; SEQ ID NO 506
 ; LENGTH: 250
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-140-021-506

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
6	0.9e-87	1258.00	100.00%	98.67%	250	229	0	0	0	0

US-09-856-320a-1_copy_272_958 (1-687) x US-10-140-021-506 (1-250)

QY 1 ATCATCAAGGGTGTGAGTGCAGAGCCTCAGCCCTGACAGGAGCCCTGTTGAG 60
 DB 22 ILEILYSGLYPHEGLUCYSLSYSPROHISSEKINPOTRPGILNLALEUPHEGLU 41
 QY 61 AAGAGCGGGCTACTGTGTGGGGGAGCGTCATCGCCCGAGATGGCTCTGCAGAGCC 120
 DB 42 LYSTHARGLEULEUCYSGLYALATHRLEULLEALPROARGTRPLEUETHRALAALA 61
 QY 121 CACTGCTCAAGCCCCCGCTACATAGTACCTGGGGGAGACAACTCCAGAGAGAGAG 180
 DB 62 HISCYSLEULYSPTARGTYRILEVALHISLEUGLYGHNHISASNLEUHLNLSGLUGLU 81
 QY 181 GGCCTGAGCAGACCCGGGAGACCCAGCTGAGTCTCCCGCCAGCCGGCTTCAACAAGAC 240
 DB 82 GLYCSGLUGINTHARGTHRLEUHRGUSERPHEPROHISPROGLYPHEASNNSER 101
 QY 241 CTCGCCAACAAGACCCAGCATGATCATGTGTGTGAGATGGATGGCAGCTTCC 300
 DB 102 LEUPROASNLYSASPHISARGASNAPRIEMELLEVALLYSMETALASERPROVALSER 121
 QY 301 ATCAGCTGGGGTGTGGAGCCCTCAGCTCTCCAGCTGTGTACGTGTGGACAGCAGC 360
 DB 122 ILEHTRTPALAVALARPROLEUTHRLEUSERSERARGCYSAITHRALAGLYTHRESER 141
 QY 361 TGCCATATTTCCGGCTGGGGGAGCAGCTGACAGCCCGGATTAGGCTGCTGACAGCTTG 420
 ||||||||||||||||||||||||||||

TYPE: PRF
ORGANISM: Homo Sapien
US-10-140-471-506

Alignment Scores:

Pred. No.:	6,09e-87	Length:	250
Score:	1258.00	Matches:	229
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	98.67%	Indels:	0
DB:	12	Gaps:	0

US-09-856-320a-1_copy_272_958 (1-687) x US-10-140-471-506 (1-250)

```

QY 1 ATCATCAAGGGGTTCAGTGCAGAGCCCTCACTCCAGCCCTGGACAGACCCCTGTTGAG 60
DB 22 Ilettllysglyrphglicyslysrpionhserrglnprrtgrglmlalaleuphegu 41
QY 61 AAGAGCGGCTACTCTGTGGGGGAGCGCTCATCGGCCCAATGGCTCTGACAGACGCC 120
DB 42 LysThrArgLeuLeuCyseGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAla 61
QY 121 CACTGCTCAAGCCCCGGTACATAGTTCACCTGGGGGACAGACCTCCAGAGAGAG 180
DB 62 HiscysleuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGln 81
QY 181 GCGTGTGAGCAGACCCGGACAGACCCAGTCCCTCCGCCACCCCGGCTTCAACAACAGC 240
DB 82 GlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 101
QY 241 CTCGCCAACAAAGACCCGCAATGACATCATGCTGGTGAAGATGGCATCCGCACTGCC 300
DB 102 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 121
QY 301 ATCAGCTGGGCTGTGCGAGCCCTCACTCCCTCACTGCTGCTGCTGCTGCTGCTGCTG 360
DB 122 IlettlrtrpAlaValArgProleuThrLeuSerSerArgCysValThrAlaGlyThrSer 141
QY 361 TGCTGCATTTCCGGCTGGGGGACAGACGTCACGCCCCCAAGTAAAGCCCTGCACACCTTG 420
DB 142 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 161
QY 421 CGATCGGCCAACATCATCATCTTGAAGACAGAAAGTGTGAAGAGCTTACCCCGGCAAC 480
DB 162 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTrpProGlyAsn 181
QY 481 ATCAGACAGACCATGCTGTGTGCGAGCTGCAGAGGAGGAGGAGGAGGAGGAGGAGT 540
DB 182 IlettlrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGlnGly 201
QY 541 GACTCCGGGGGGCCCTGTGCTGTGAACAGTCTTCAAGGCAATTAATCTCTGGGGCCAG 600
DB 202 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 221
QY 601 GATCGGCTGTGCGATGATACCCGGAAGCCCTGGTGTCAACAGAAAGTGTGCAATATGTGAC 660
DB 222 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTrpValAsp 241
QY 661 TCGATCCAGAGAGCATGAGAAACAAT 687
DB 242 TrpIleGlnGlnThrMetLysAsnAsn 250

```

RESULT 8

US-10-140-807-506
Sequence 506, Application US/10140807
Publication No. US20030134354A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Flivarioff, Ellen
APPLICANT: Gao, Wei-Qiang

```

APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Guiney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330R1C1/74
CURRENT APPLICATION NUMBER: US/10/140,807
CURRENT FILING DATE: 2002-05-07
Prior Application removed - See file wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 506
LENGTH: 250
TYPE: PRF
ORGANISM: Homo Sapien
US-10-140-807-506

Alignment Scores:
Pred. No.: 6,09e-87 Length: 250
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.67% Indels: 0
DB: 12 Gaps: 0

US-09-856-320a-1_copy_272_958 (1-687) x US-10-140-807-506 (1-250)
QY 1 ATCATCAAGGGGTTCAGTGCAGAGCCCTCACTCCAGCCCTGGACAGACCCCTGTTGAG 60
DB 22 Ilettllysglyrphglicyslysrpionhserrglnprrtgrglmlalaleuphegu 41
QY 61 AAGAGCGGCTACTCTGTGGGGGAGCGCTCATCGGCCCAATGGCTCTGACAGACGCC 120
DB 42 LysThrArgLeuLeuCyseGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAla 61
QY 121 CACTGCTCAAGCCCCGGTACATAGTTCACCTGGGGGACAGACCTCCAGAGAGAG 180
DB 62 HiscysleuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGln 81
QY 181 GCGTGTGAGCAGACCCGGACAGACCCAGTCCCTCCGCCACCCCGGCTTCAACAACAGC 240
DB 82 GlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 101
QY 241 CTCGCCAACAAAGACCCGCAATGACATCATGCTGGTGAAGATGGCATCCGCACTGCC 300
DB 102 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 121
QY 301 ATCAGCTGGGCTGTGCGAGCCCTCACTCCCTCACTGCTGCTGCTGCTGCTGCTGCTG 360
DB 122 IlettlrtrpAlaValArgProleuThrLeuSerSerArgCysValThrAlaGlyThrSer 141
QY 361 TGCTGCATTTCCGGCTGGGGGACAGACGTCACGCCCCCAAGTAAAGCCCTGCACACCTTG 420
DB 142 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 161
QY 421 CGATCGGCCAACATCATCATCTTGAAGACAGAAAGTGTGAAGAGCTTACCCCGGCAAC 480
DB 162 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTrpProGlyAsn 181
QY 182 IlettlrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGlnGly 201
QY 541 GACTCCGGGGGGCCCTGTGCTGTGAACAGTCTTCAAGGCAATTAATCTCTGGGGCCAG 600
DB 202 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 221

```

QY 601 GATCCGTGTGGATCACCCGGAAGCCTGTGTCTACACGAAAGTCTGCAAAATATGTGGAC 660
DB 222 AspProCysAlaIleThrAlaGlySerProGlyValIleThrIlySerValCysIlyValAsp 241
QY 661 TGGATCCAGAGACGATGAGAACAAAT 687
DB 242 TriPleGIInIuThrMetIlyAsnAsn 250

RESULT 9

US-10-922-506
Sequence 506, Application US/10140922
Publication No. US20030138889A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Matanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C179
CURRENT APPLICATION NUMBER: US/10/140,922
CURRENT FILING DATE: 2002-05-07
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 506
LENGTH: 250
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-922-506

Alignment Scores:

Pred. No.: 6,09e-87 Length: 250
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.67% Indels: 0
DB: 12 Gaps: 0

US-09-856-320a-1_COPY_272_958 (1-687) x US-10-140-922-506 (1-250)

QY 1 ATATCAAGGGGTTGCGTGCAGAGCCCTACTCCAGCCCGGAGGAGCCCTTTGGAG 60
DB 22 IleIleIlySerIlyPheGlyCysIlySProHISerGlnProIrrglnAlaIlePheGln 41
QY 61 AAGAGCGGCTACTGTGTGGGGGAGCGCTATCGCCCGCCAGATGGCTCTGACAGCAGCC 120
DB 42 IyethrAlrGleuIeuCysglYAlaIthrlleuIleAlaProArgrItrleuIeuThrlAlaIa 61
QY 121 CACTGCCTCAAGCCCGGCTACATAGTTCACTGGGGGAGCACAACCTCGAAGAGAGAG 180
DB 62 HiscysIeuIySProArgrIlyIleValHISleuGlylnHISAsnIeuGlnIySgluGln 81
QY 181 GGGTGTGAGAGACCGGAGCAGCATGATCCCTCCCGCCAGCCCGGCTTCAACAAGAGC 240
DB 82 GlyCysglIeuIlnThrAlrGlnIleAlaIthrlSerPheProHISProGlyPheAsnAsnSer 101
QY 241 CTCGCCAACAAGACGACCGCAATGACATCATGCTGGTGAAGATGGCATGCCAGTCTCC 300
DB 102 IeuProAsnIySPHISArgrAsnAspIleMetIeuValIySmetAlaSerProValSer 121

QY 301 ATCAGTGGGGGTGTGGACCCCTTCAGCCCTGTCTACACGAAAGTCTGCAAAATATGTGGAC 360
DB 122 IleThrItrAlaValArGProIeuThrIeuSerSerArGysValThrAlaGlyThrSer 141
QY 361 TGGCTCATTTCCGGGCTGGGGGAGAGAGCTCCAGCCCGCCAGTTAGCGCTGCTCACACTTG 420
DB 142 CysIeuIleSerGlyIrrPglYSerThrSerSerProGlnIeuArGleuProHISThrIeu 161
QY 421 CGATCGCCCAACATCACCATCATTTAGCACCCAGCAAGTGTGAGAAAGCCCTACCCCGGCAAC 480
DB 162 ArgCysAlaAsnIleThrIleIleGlnHISGlnIySgluSnaIaIyrrProGlyAsn 181
QY 481 ATCAGACAGACCATGTGTGTGGCCAGCGTGCAGAGAGGGGGCAAGAGACTCTTCGACGGT 540
DB 182 IleThrAspThrMetValCysAlaSerValGlnIuGlnIyGlyIySAspSerCysGlnIy 201
QY 541 GACTCGGGGGCCCTGTGTGTGTAACCAAGCTCTTCAAGCATATCTCTGGGGCAG 600
DB 202 AspSerIyGlyProIeuValCysAsnGlnSerIeuIeuIleIleSerIrrPglYGln 221
QY 601 GATCCGTGTGGATCACCCGGAAGCCTGTGTCTACACGAAAGTCTGCAAAATATGTGGAC 660
DB 222 AspProCysAlaIleThrAlaGlySerProGlyValIleThrIlySerValCysIlyValAsp 241
QY 661 TGGATCCAGAGACGATGAGAACAAAT 687
DB 242 TriPleGIInIuThrMetIlyAsnAsn 250

RESULT 10

US-10-924-506
Sequence 506, Application US/10140924
Publication No. US20030134355A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Matanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C177
CURRENT APPLICATION NUMBER: US/10/140,924
CURRENT FILING DATE: 2002-05-07
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 506
LENGTH: 250
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-924-506

Alignment Scores:

Pred. No.: 6,09e-87 Length: 250
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.67% Indels: 0
DB: 12 Gaps: 0

US-09-856-320a-1_COPY_272_958 (1-687) x US-10-140-924-506 (1-250)


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QY 1 ATCATCAAGGGGTTCGAGTGCAGACCTCACTCCCAAGCCCTGGCAGGACCCCTGTTCGAG 60
DB 22 ILEILEYSGLYPHEGLUCYSLYSPRONHISSEKINPROTGRLNALALEUPHEGLU 41
QY 61 AAGACGGGGCTACTGTGTGGGGGAGCGCATCGGCCCCAGATGGCTCTGTGACAGAGCC 120
DB 42 LYSTHARGLEULEUCYSGLYALATHRLEULLALAPROARGTRPREULEUTHRALALE 61
QY 121 CACTGCTTCACGCCCCGCTACATAGTTCACCTGGGGCAGACACCTCCAGAGAGAGAG 180
DB 62 HISCYSLLEULYSPROARGTRYRILEVALHISLEUGLYGINHISASNLEUGLINYSGLUGLU 81
QY 181 GGCCTGTGACAGACCCGGAGACCCACTGATGCTCTCCGCCACCCGGCTTCAACAACAGC 240
DB 82 GLYCYSGIUGLINTHRARGTHRALATHRGUSERPHEPROHISPROGLYPHEASNSNSER 101
QY 241 CTCGCCCAACAAGACCAACCGCAATGACATCATGCTGGTGAATGGCAATGGCAAGCTTCC 300
DB 102 LEUPROASNLYSASPHEISARGASNAPRIEMELLEVALLYSMETALASERPROVALSER 121
QY 301 ATCACTGGGCTGTGTCGACCCCTCACTCTCCACGCTGTGTCACCTGTGACACAGC 360
DB 122 ILETHRTPRALAVAlARGPROLEUTHRIEUSERSERARGCYVALTHRALAGLYHRSER 141
QY 361 TGCCTCATTTCCGGCTGGGGGAGCAGCTCCAGCCCACTTACGCTGCTTACACACTTG 420
DB 142 CYSLLEULISERGLYTRPELYSERTHRSESRPROGLINLEUARGLEUPROHISTHRLEU 161
QY 421 CGATCGGCCAACATCAACATCATTTGAGCAGCAGAAAGTGAGAAAGCCCAACCCGGCAAC 480
DB 162 ARGCYSLALASNNILETHRIELLEGLUNHISGLNLYSCYSGIUNSNALATYRPROGLYASN 181
QY 481 ATCAAGACACCATGATGTGTGCCAGCGTGCAGAGAGGGGGGAGACTCTGTCCAGAGGT 540
DB 182 ILETHRTPRALAVAlARGPROLEUTHRIEUSERSERARGCYVALTHRALAGLYHRSER 201
QY 541 GACTCCGGGGGCGCTCTGTGTCTGTAAACAGTCTTCAAGGCAATATCTCTGGGGCCAG 600
DB 202 ASPSERGLYGLYPROLEUVALCYLSASNGLINSERLEUGLNYLLEISERTTRPGLYGN 221
QY 601 GATCGGTGTGGCATACCCGGAAGCCTGGTCTACAGAAAGTGTGCAAAATATGTGAGC 660
DB 222 ASPPROCYSLALALETHRTARGLYSPROGLYVALTYRTHLYSVALCYLSYSTYRVALASP 241
QY 661 TGGATCCAGAGACGATGAGAACAAT 687
DB 242 TRPLEGLNGLTUHTHMETLYSASN 250
RESULT 11
US-10-140-926-506
; Sequence 506, Application US/10140926
; Publication No. US20030134356A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; ACIDS ENCODING THE SAME
```

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FILE REFERENCE: P3330R1C187
; CURRENT APPLICATION NUMBER: US/10/140,926
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRP
; ORGANISM: Homo Sapien
US-10-140-926-506
Alignment Scores:
Pred. No.: 6,09e-87 Length: 250
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98,67% Indels: 0
DB: 12 Gaps: 0
US-09-856-320a-1_copy_272_958 (1-687) x US-10-140-926-506 (1-250)
QY 1 ATCATCAAGGGGTTCGAGTGCAGACCTCACTCCCAAGCCCTGGCAGGACCCCTGTTCGAG 60
DB 22 ILEILEYSGLYPHEGLUCYSLYSPRONHISSEKINPROTGRLNALALEUPHEGLU 41
QY 61 AAGACGGGGCTACTGTGTGGGGGAGCGCATCGGCCCCAGATGGCTCTGTGACAGAGCC 120
DB 42 LYSTHARGLEULEUCYSGLYALATHRLEULLALAPROARGTRPREULEUTHRALALE 61
QY 121 CACTGCTTCACGCCCCGCTACATAGTTCACCTGGGGCAGACACCTCCAGAGAGAGAG 180
DB 62 HISCYSLLEULYSPROARGTRYRILEVALHISLEUGLYGINHISASNLEUGLINYSGLUGLU 81
QY 181 GGCCTGTGACAGACCCGGAGACCCACTGATGCTCTCCGCCACCCGGCTTCAACAACAGC 240
DB 82 GLYCYSGIUGLINTHRARGTHRALATHRGUSERPHEPROHISPROGLYPHEASNSNSER 101
QY 241 CTCGCCCAACAAGACCAACCGCAATGACATCATGCTGGTGAATGGCAATGGCAAGCTTCC 300
DB 102 LEUPROASNLYSASPHEISARGASNAPRIEMELLEVALLYSMETALASERPROVALSER 121
QY 301 ATCACTGGGCTGTGTCGACCCCTCACTCTCCACGCTGTGTCACCTGTGACACAGC 360
DB 122 ILETHRTPRALAVAlARGPROLEUTHRIEUSERSERARGCYVALTHRALAGLYHRSER 141
QY 361 TGCCTCATTTCCGGCTGGGGGAGCAGCTCCAGCCCACTTACGCTGCTTACACACTTG 420
DB 142 CYSLLEULISERGLYTRPELYSERTHRSESRPROGLINLEUARGLEUPROHISTHRLEU 161
QY 421 CGATCGGCCAACATCAACATCATTTGAGCAGCAGAAAGTGAGAAAGCCCAACCCGGCAAC 480
DB 162 ARGCYSLALASNNILETHRIELLEGLUNHISGLNLYSCYSGIUNSNALATYRPROGLYASN 181
QY 481 ATCAAGACACCATGATGTGTGCCAGCGTGCAGAGAGGGGGGAGACTCTGTCCAGAGGT 540
DB 182 ILETHRTPRALAVAlARGPROLEUTHRIEUSERSERARGCYVALTHRALAGLYHRSER 201
QY 541 GACTCCGGGGGCGCTCTGTGTCTGTAAACAGTCTTCAAGGCAATATCTCTGGGGCCAG 600
DB 202 ASPSERGLYGLYPROLEUVALCYLSASNGLINSERLEUGLNYLLEISERTTRPGLYGN 221
QY 601 GATCGGTGTGGCATACCCGGAAGCCTGGTCTACAGAAAGTGTGCAAAATATGTGAGC 660
DB 222 ASPPROCYSLALALETHRTARGLYSPROGLYVALTYRTHLYSVALCYLSYSTYRVALASP 241
QY 661 TGGATCCAGAGACGATGAGAACAAT 687
DB 242 TRPLEGLNGLTUHTHMETLYSASN 250
RESULT 12
US-10-141-698-506
; Sequence 506, Application US/10141698
; Publication No. US20030134357A1
```

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GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: Deforge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P330R1C206
: CURRENT FILING DATE: 2002-05-08
: Prior Application removed - See Palm or File Wrapper
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 506
: LENGTH: 250
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-141-698-506

Alignment Scores:
Pred. No.: 6,09e-87      Length: 250
Score: 1258.00          Matches: 229
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 98.67%             Indels: 0
DB: 12                     Gaps: 0

US-09-856-320a-1_COPY_272_958 (1-687) x US-10-141-698-506 (1-250)

OY 1 ATCATCAAGGGGCTTCGAGTGCAGCCCTACATCCAGCCGCGAGGAGCCCTGTCGAG 60
Db 22 lIeIleIySglYpHeIglucYsIySPronHISerGIProItrpGlnAlaIaleuPheGlu 41
OY 61 AAGAGCGGCTACTCTGTGGGCGAGCCTCATCGCCCGCCAGATGCTCTGACAGCACC 120
Db 42 lYsthrArgIeuIeuCysGlyAlaIthrLeuIlleAlaProArgTrpLeuIthrAlaIa 61
OY 121 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGGAGACAACTCCAGAAAGAGAGAG 180
Db 62 HiscYsIeuIySProArgTrYrIleValHISleuGIyGlnHISasnIeuGIySglGlu 81
OY 181 GGGGTGAGAGAGAGCCGAGAGCCATGAGTCCTTCCCGCCAGCCCGCTTCAACAGAGC 240
Db 82 GlYcYsIeuIthrAlaIthrAlaIthrIleuSerPheProHISerProGIyPheasnAsnSer 101
OY 241 CTCGCCAACAAGACACACCCCAATGACATCATGCTGTGAAGATGGCATGCCAGTCTCC 300
Db 102 leuProHISnIySPHISarGAsnAspIleMetIeuValIySMeIaIaSerProValSer 121
OY 301 ATGACCTGGGCTGTGACCCCTCACCCCTCTCTACAGCTGTGTCTACCTGTGGCAGCAGC 360
Db 122 lIeIthrAlaIalValArgProIeuIthrLeuSerSerArgCysValIthrAlaGlyThrSer 141
OY 361 TGGCTATTTCCGGCTGGGCGAGAGCTCCAGCCCGCCAGTTAGCCTGGCTCACACCTTG 420
Db 142 CysIeuIleSerGIyTrpGIySerThrSerSerProIleuArgIeuArgProHISthrIeu 161
OY 421 CGATGGCCCAACATCAGCATCATTGTAGCAGACAGAAAGTGTGAAGCGCTACCCCGGAGAC 480
Db 162 ArgCysAlaAsnIleIthrIleIleGIyHISGlnIySglSlnAsnAlaIyTrpGIyAsn 181

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OY 481 ATCAGAGACACCATGTGTGTGCCAGCGGTGCAGAGAGGGGCGAGAGACTCTCCAGAGCT 540
Db 182 lIeIthrAspIhrMetValIcYsAlaSerValGIyGlnIleGIyGlyAspSerCysGlnGly 201
OY 541 GACTCCGGGGGCGCTCTGGTCTGTACCAAGTCTTTCAAGCATATCTCTGGGGCCAG 600
Db 202 AspSerGIyGIyProIeuValIcYsAsnGlnSerIeuIleGIyIleIleSerTrpGIyGln 221
OY 601 GATCCGTTGGCATCACCCGAAAGCTGTGTGTACAGAAAGTCTCAATATGTGGAC 660
Db 222 AspProCysAlaIleIthrAlaIthrArgIySerProGIyValIyTrhrIySValIcYsIyTrValAsp 241
OY 661 TGGATCCAGAGAGACGATGAGAGACAT 687
Db 242 TrpIleGIyGlnIuThrMetIySAsnAsn 250

RESULT 13
US-10-141-702-506
: Sequence 506, Application US/101411702
: Publication No. US20030134358A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: Deforge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P330R1C208
: CURRENT FILING DATE: 2002-05-08
: Prior Application removed - See Palm or File Wrapper
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 506
: LENGTH: 250
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-141-702-506

Alignment Scores:
Pred. No.: 6,09e-87      Length: 250
Score: 1258.00          Matches: 229
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 98.67%             Indels: 0
DB: 12                     Gaps: 0

US-09-856-320a-1_COPY_272_958 (1-687) x US-10-141-702-506 (1-250)

OY 1 ATCATCAAGGGGCTTCGAGTGCAGCCCTACATCCAGCCCTGCGAGGAGCCCTGTCGAG 60
Db 22 lIeIleIySglYpHeIglucYsIySPronHISerGIProItrpGlnAlaIaleuPheGlu 41
OY 61 AAGAGCGGCTACTCTGTGGGCGAGCCTCATCGCCCGCCAGATGCTCTGACAGCACC 120
Db 42 lYsthrArgIeuIeuCysGlyAlaIthrLeuIlleAlaProArgTrpLeuIthrAlaIa 61
OY 121 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGGAGACAACTCCAGAAAGAGAGAG 180
Db 62 HiscYsIeuIySProArgTrYrIleValHISleuGIyGlnHISasnIeuGIySglGlu 81

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QY 181 GGCTGTGACAGACCCGGACAGCCACTGAGTCTTCCCGGCTTCAACAACAC 240
DB 82 GlycylserglnThrArgThrIleThrIleuSerPheProHisProGlyPheAsnAsnSer 101
QY 241 CTCGCCAACAAAGACCCGCAATGACATCATCTGTTGAGATGGCATCGGACGCTCC 300
DB 102 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 121
QY 301 ATCACCCTGGGCTGTGCGAGCCCTCAACCCCTCTCAACGCTGTGCTACTGTGACAC 360
DB 122 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrIleGlyThrSer 141
QY 361 TGCCCATATTTCCGGCTGGGGGACAGACGTCACGCCCCCAATACGCTGCTCAACACTTG 420
DB 142 CysLeuIleSerGlyTyrPheLysSerThrSerProGlnLeuArgLeuProHisThrLeu 161
QY 421 CGATCGGCCAACATCACCATCATTTAGACACAGAAAGTGTGAGAAAGGCTCTGCGACAG 480
DB 162 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaTyrProGlyAsn 181
QY 481 ATCACAAGACCATGCTGTGTGTCAGCGGTGACAGAAAGGGGACGACTCTGCCAGGGT 540
DB 182 IleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly 201
QY 541 GACTCCGGGGGCCCTGTGCTGTAAACCATCTCTTCAAGGCTATATCTCCGCGGCCAG 600
DB 202 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 221
QY 601 GATCCGTGTGCGATCACCCGAAAGCTGGTGTCTACAGCAAGTGTGCAAAATATGTGAC 660
DB 222 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 241
QY 661 TGGATCCAGAGACGATGAAGAACAAT 687
DB 242 TrpIleGlnGlnThrMetLysAsnAsn 250

RESULT 14

US-10-141-704-506
; Sequence 506, Application US/10141704
; Publication No. US20030134359A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Thomas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C209
; CURRENT APPLICATION NUMBER: US/10/141,704
; PRIOR APPLICATION REMOVED - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-141-704-506

Alignment Scores: 6.09e-87 Length: 250
Pred. No.: 6.09e-87

Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.67% Indels: 0
DB: 12 Gaps: 0

US-09-856-320a-1_copy_272_958 (1-687) x US-10-141-704-506 (1-250)

QY 1 ATCATCAAGAGGGTTGAGTGTCAAGGCTTCAACGCTTGGACAGGACGCTGTTCAG 60
DB 22 IleIleLysGlyPheIleLysLysProHisSerGlnProTrpGlnAlaIleLeuPheGlu 41
QY 61 AAGAGCGGCTACTCTGTGTGGGAGACGCTCATCGCCCCCAGATGGCTCTGACAGCAGCC 120
DB 42 LysThrArgLeuIleuLysGlyIleThrIleAlaProArgTrpLeuThrAlaIle 61
QY 121 CACTGCTCAAGCCCGGCTACATGTTACCTCGGGGACACACACCTCCAGAAAGAGAG 180
DB 62 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlu 81
QY 181 GGCTGTGACAGACCCGGACAGCCACTGAGTCTTCCCGGCTTCAACAACAC 240
DB 82 GlycylserglnThrArgThrIleThrIleuSerPheProHisProGlyPheAsnAsnSer 101
QY 241 CTCGCCAACAAAGACCCGCAATGACATCATCTGTTGAGATGGCATCGGACGCTCC 300
DB 102 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 121
QY 301 ATCACCCTGGGCTGTGCGAGCCCTCAACCCCTCTCAACGCTGTGCTACTGTGACAC 360
DB 122 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrIleGlyThrSer 141
QY 361 TGCCCATATTTCCGGCTGGGGGACAGACGTCACGCCCCCAATACGCTGCTCAACACTTG 420
DB 142 CysLeuIleSerGlyTyrPheLysSerThrSerProGlnLeuArgLeuProHisThrLeu 161
QY 421 CGATCGGCCAACATCACCATCATTTAGACACAGAAAGTGTGAGAAAGGCTCTGCGACAG 480
DB 162 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaTyrProGlyAsn 181
QY 481 ATCACAAGACCATGCTGTGTGTCAGCGGTGACAGAAAGGGGACGACTCTGCCAGGGT 540
DB 182 IleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly 201
QY 541 GACTCCGGGGGCCCTGTGCTGTAAACCATCTCTTCAAGGCTATATCTCCGCGGCCAG 600
DB 202 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 221
QY 601 GATCCGTGTGCGATCACCCGAAAGCTGGTGTCTACAGCAAGTGTGCAAAATATGTGAC 660
DB 222 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 241
QY 661 TGGATCCAGAGACGATGAAGAACAAT 687
DB 242 TrpIleGlnGlnThrMetLysAsnAsn 250

RESULT 15
US-10-142-421-506
; Sequence 506, Application US/10142421
; Publication No. US20030134360A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Malanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C218
CURRENT APPLICATION NUMBER: US/10/142,421
CURRENT FILING DATE: 2002-05-09
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 506
LENGTH: 250
TYPE: PRT
ORGANISM: Homo Sapien
US-10-142-421-506

Alignment Scores:

Pred. No.: 6.09e-87 Length: 250
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.67% Indels: 0
DB: 12 Gaps: 0

US-09-856-320a-1_COPY_272_958 (1-687) x US-10-142-421-506 (1-250)

QY 1 ATCATCAAGGGGTTCGAGTCAGAGCTCACTCCAGCCCTGGCAGCAGCCCTGTTCAG 60
DB 22 ILETLEYSGLYRHEGLUCYSLYSPROHISERCLNPROTPRGLNALALALEUPHEGLU 41
QY 61 AAGACGGGCTACTCTGTGGGGCGAGCGCTCATCGCCCCAGATGGCTCTGACAGCAGCC 120
DB 42 LYSRHRGLEUUCYSGLYALATHRLEUILLEALAPROALGTRPLEUATHRALALA 61
QY 121 CACGAGCCTCAAGCCCGCTCATAGTACCTGACCTGGGGAGACACAACTCCAGAAAGAGAG 180
DB 62 HISCYSLYSLYSPROALGTYRILEVALHISLEUGLYINHISASNLEUGLYLSGLUGLU 81
QY 181 GGGTGTGAGCAGACCCGAGAGCCCATGAGTCCCTCCACCCCGGCTTCACACAGC 240
DB 82 GLYCSGLUGLNHRARGYTHRALATHRGLUSERPHEROHNISPROGLYPHEASNASN 101
QY 241 CTCCCAACAAGACACACCCGATGACATCATGCTGTGAAGATGCGATCGCCAGTCTCC 300
DB 102 LEUPROASNLYSPHISARGASNAPRIELETLEUVALIYSMETALASERPROVALSER 121
QY 301 ATCAACCTGGGCTGTGGAGCCCTGACCTCTCCACGCTGTGACATGCTGGGACACAGC 360
DB 122 ILETHTRPALAYALARGPROLEUHRLEUSERSERARGCYVALTHRALAGLYTHR 141
QY 361 TGGCTCATTTCCGGCTGGGCGAGCAGCTCCAGCCCGAGTTACGCTGCTCACACCTTG 420
DB 142 CYSLLEULESERGLYTRPGLYSERTHRSESRPROGLNEUARGLEUPROHNISTH 161
QY 421 CGATGGCCCAACATCACATCATTTGAGCACCAGAAAGTGTGAGAAAGCCCTAACCCGGCAAC 480
DB 162 ARGCYSLALASNLLETHTRIILEGLNHISGLNLYSCYSLUNSNALATYRPROGLYASN 181
QY 481 ATCAGAGACACCATGGTGTGGCAGCGTGCAGGAAGGGGCAAGGACGACTCCTGCCAGGGT 540
DB 182 ILETHTRASPHTMETVALCYSLASERVALGNEUGLYLYLSASPSECYSGINGLY 201
QY 541 GACTCGGGGGCCCTGTGTCTGTAAACAGTCTTTCAGGCAATTATCTCTGGGGCCAG 600
DB 202 ASPSERCLYGLYPROLEUVALCYSLASNLINSERLLEUNGILYILETLESETRPGLYGLN 221
QY 601 GATCGGTGCGCATCACCCGAAAGCTGTGTCTACACGAAAGTGTGCAAAATATGTGAC 660
DB 222 ASPPROCYSLALATLETHTRARGLYSPROGLYVALTYRTHRYSVALCYSLYSTYRVALASP 241
QY 661 TGGATCCAGGAGACGATGAAGAACAAT 687

DB 242 TRIPLEGLINGLUTRIMETLYASNASN 250

Search completed: October 15, 2003, 20:55:06
Job time : 93.6763 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame_plus.n2p model

Run on: October 15, 2003, 17:31:30 ; Search time 32.3111 Seconds

(without alignments)
6749.699 Million cell updates/sec

Title: US-09-856-320A-1_COPY_272_958

Perfect score: 1275

Sequence: 1 atcatcaagggttcgagtg.....aggagacagatgaagaacaat 687

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1107863 segs, 158726573 residues

Total number of hits satisfying chosen parameters: 2215726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-O=/cgn2.1/USPRO_SPOOL/US09856320/runtat.15102003.105638.8500/app_query.fasta_1.2318
-DB=A_Geneseq.19jun03 -OPMT=fastan -SUFFIT=rag -MINMATCH=0.1 -LOOPTC=0
-LOOPTXT=0 -UNITS=bits -STARF=1 -END=1 -MATRIX=blomsm62 -TRANS=human40.cdl
-LIST=45 -DOCLALIGN=200 -THR.SCORE=pcot -THR.MAX=100 -THR.MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pro -NOR=ext -HEAPSIE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09856320.ecgn.1.1-1.40.runtat.15102003.105638.8500 -NCPD=6 -ICPD=3
-NO_MMAP -LARGEREQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq.19jun03.*

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11: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT.*
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22: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1258	98.7	250	21	Human TLSP. Homo
2	1258	98.7	250	21	Human PRO1279 (UNQ)
3	1258	98.7	250	22	Human secreted pro
4	1258	98.7	250	22	Human PRO1279 poly
5	1258	98.7	250	22	Protein of the inv
6	1258	98.7	250	23	Prostate cancer-as
7	1258	98.7	250	23	Human angiogenesis
8	1258	98.7	250	23	Human PRO1279 prot
9	1258	98.7	250	23	Human PRO protein,
10	1258	98.7	250	24	Human PRO polypept
11	1258	98.7	250	24	Human secreted/Cra
12	1258	98.7	250	24	Novel secreted and
13	1258	98.7	250	24	Lung cancer-associ
14	1258	98.7	282	21	CASB12 amino acid
15	1258	98.7	282	21	Human serine prote
16	1258	98.7	282	21	A human prostate-a
17	1252	98.2	281	20	CASB12 polypeptide
18	1235.5	96.9	275	21	Human TLSP. Homo
19	1231	96.5	228	21	Human serine prote
20	1228	96.3	250	20	Human TLSP. Homo
21	1227	96.2	248	22	Extended human sec
22	1219.5	95.6	289	22	Fusion gene with h
23	1219.5	95.6	289	22	Human PS133 consen
24	1182	92.7	228	20	Amino acid sequenc
25	1182	92.7	228	20	Polypeptide fragme
26	1182	92.7	246	20	Human secreted pro
27	1182	92.7	246	21	Polypeptide fragme
28	1062	83.3	276	21	Human secreted pro
29	1014.5	79.6	247	23	Mouse serine prote
30	736	57.7	250	21	Human Serine Prote
31	736	57.7	250	21	Human KLR-L3 prole
32	736	57.7	251	22	Human KLR-L3 prole
33	734	57.6	247	22	Human novel secret
34	733.5	57.4	296	21	Human novel enzyme
35	716	56.2	247	22	Human KLR-L3 prote
36	716	56.2	247	22	Novel human connec
37	716	56.2	247	22	Novel human enzyme
38	688	54.0	275	21	Human neurotrophin
39	684	53.6	260	17	Human recombinant
40	684	53.6	260	18	Human neurotrophin
41	684	53.6	260	18	Mouse neurotrophin
42	682	53.5	256	23	Mouse ischaemic co
43	682	53.5	320	23	Novel human Kallik
44	682	53.5	320	23	Human protease, PR
45	681	53.4	260	20	Amino acid sequenc
					Human PRO322 prote

ALIGNMENTS

RESULT 1

AAAB21325 AAB21325 standard; Protein; 250 AA.

AC AAB21325;

DT 02-FEB-2001 (first entry)

DE Human TLSP.

XX

KW Human; KLR-L1; KLR-L2; KLR-L3; KLR-L4; KLR-L5; KLR-L6; TLSP;

KM trypsin-like serine protease; kallikrein-like protein; serine protease;

OS cytosolic; cancer; prostate cancer.

XX

XX

XX

XX	14-SEP-2000.
PD	
PE	
PF	09-MAR-2000; 2000MO-CA00258.
PG	
PH	11-MAR-1999; 9905-0124260.
PI	01-APR-1999; 9905-0127386.
PJ	21-JUL-1999; 9905-0144919.
PK	
PL	(MOUN) MOUNT SINAI HOSPITAL.
PM	
PN	Yousef GM, Diamandis EP;
PO	
PP	WPI; 2000-587440/55.
PQ	
PR	New kallikrein-like (KLK-L) proteins for diagnosing and treating KLK-L
PS	protein mediated disorders, especially cancer. -
PT	
PV	
PW	
PX	Example 5; Fig 27; 184pp; English.
PY	
PZ	
QA	
QB	
QC	The present sequence is human trypsin-like serine protease (TLSP), a
QD	member of the serine protease family. Kallikreins and
QE	kallikrein-like proteins are a subgroup of the serine protease enzyme
QF	family. They catalyze the selective cleavage of specific polypeptide
QG	precursors to release peptides with potent biological activity. Nucleic
QH	acids encoding kallikrein-like proteins KLK-L1, KLK-L2, KLK-L3, KLK-L4,
QI	KLK-L5 and KLK-L6 have been isolated. The proteins are useful in the
QJ	treatment, monitoring and diagnosis of cancers, especially prostate
QK	cancer. They can also be used to identify a substance that can associate
QL	with or mediate the biological activity of the proteins. Antibodies can
QM	be used to treat conditions mediated by the kallikrein-like proteins.

Alignment Scores:	
Pred. No.:	1,4e-94
Score:	1258.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	98.67%
DB:	21
Length:	250
Matches:	229
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-856-320A-1_COPY_272_958 (1-687) x AAB21325 (1-250)

QY	1	ATGATCAAGGGGEMTTGAGTGCAGCAAGCTCACTCCAGGCTGGAGAGGCAACCTGTTCCAG	60
Db	22	lIeIleIySglYPhgIcUcYlSPProHnISserGIlnPrOtPbIlaIaIaIeupPhgIU	411
QY	61	AAGACGGCGCTACTCTGTGGGGCGAGCGCATCGCCCGCAAGATGGCTCTGACAGCAGCC	12
Db	42	LySthrArgIeuIeucYsgIyAlaIthIleIleIaIaIProArgItrIeuIeuthrIaIaIa	611
QY	121	CACGTGCTCAAGCCCGGCTACATAGTTCACCTGGGGCAGCACAACCTCCAGAAGAGAG	18
Db	62	hIScYsIeuYsProArGTYrIleValhISleUGlYgIhNISmsIeuGIlnYsgIuGI	811
QY	181	GGCTGTGAGAGACGCCGAGAGCCACTGAGTCTTCCCGCCCGCGGCTTCAACAACAC	24
Db	82	GIYcYsGIuIInthrArgIthrAlaItrIGIuSerPherProhISProGIYPhesAnsISser	10
QY	241	CTCCCCCAACAACACACCGGCATGACATCATCTGTGACAGTGGCAATGGCAGCTCC	30
Db	102	LeuPrOhsInYsPhISarISarISAnsPrIleMeIleValYlYSMeIaISerProValSer	12
QY	301	ATCACCTGGGCTGTGGACCCCTCAACCTCTCTCTCAACGGTGTGCTACTCTGGACACAC	36
Db	122	IleIthrTrpAlaIaIaIArgProIeuIthrIeuIserSerArgCYsValIthrIaIaIYhIrrSer	14
QY	361	TGCGCTATTTCGGCGTGGGGGACAGCAGTCCAGGCCCAAGCTTACGCGCTGCACACTTG	42
Db	142	CYSleuIleSerGIYtrpGIYserThrSerSerProGIleuArgIeuProhISthrIleu	16
QY	421	CGATGGGCAACATTCACCATTCATTGAGCACACAGAAATGTGAACAGGCTTACCCGGCAAC	48

Db	162	ArgCysAlaAsnIleIleThrIleIleGluHisGlnIlyCysGluAsnAlaIleTyrProGlyAsn	181
Qy	481	ATCACAGACACCCATGGTGTGTCTGCCAGCGTCGACAGGAAAGGGGCAAGGACTCTGTCCAGGT	540
Db	182	IleIleThrAspIleMetValCysAlaSerValGlnGlnGlyIlyAspSerCysGlnGly	201
Qy	541	GACTCCGGGGCCCTCTGGTCTGTAAACAGTCTTCAAGCAATATTCCTCGGGGCCAG	600
Db	202	AspSerGlyIlyProIleuValCysAsnGlnSerIleuGlnGlyIleIleSerTyrGlyGln	221
Qy	601	GATCCGTGTGCATCACCCGAAAGCCTGTGTCTACACGAAAGTCTGCATATATGAGAC	660
Db	222	AspProCysAlaIleIleThrIleArgIlyProGlyValTyrIleIlyValCysIlyTyrValAsp	241
Qy	661	TGGATCCAGACGACGATGAAGAACAT	687
Db	242	TripIleGlnIleThrMetIlyAsnAsn	250
RESULT 2			
ID	AAy9390	standard; Protein; 250 AA.	
XX	AAy9390;		
AC	AAy9390;		
DT	08-AUG-2000	(first entry)	
DE	Human PRO1279 (UNQ649)	amino acid sequence SEQ ID NO:170.	
XX	XX		
KW	Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;		
XX	transmembrane; secretion; immunoadhesion; pharmaceutical; screening.		
OS	Homo sapiens.		
XX	XX		
PN	WO200012708-A2.		
XX	XX		
PD	09-MAR-2000.		
PE	01-SEP-1999;	99WO-US20111.	
XX	XX		
PR	01-SEP-1998;	98US-0098716.	
PR	01-SEP-1998;	98US-0098749.	
PR	01-SEP-1998;	98US-0098750.	
PR	02-SEP-1998;	98US-0098803.	
PR	02-SEP-1998;	98US-0098821.	
PR	02-SEP-1998;	98US-0098843.	
PR	03-SEP-1998;	98US-0099336.	
PR	03-SEP-1998;	98US-0099396.	
PR	03-SEP-1998;	98US-0099598.	
PR	03-SEP-1998;	98US-0099602.	
PR	03-SEP-1998;	98US-0099642.	
PR	03-SEP-1998;	98US-0099741.	
PR	10-SEP-1998;	98US-0099754.	
PR	10-SEP-1998;	98US-0099763.	
PR	10-SEP-1998;	98US-0099792.	
PR	10-SEP-1998;	98US-0099808.	
PR	10-SEP-1998;	98US-0099812.	
PR	10-SEP-1998;	98US-0099815.	
PR	10-SEP-1998;	98US-0099816.	
PR	15-SEP-1998;	98US-0100385.	
PR	15-SEP-1998;	98US-0100388.	
PR	15-SEP-1998;	98US-0100390.	
PR	16-SEP-1998;	98US-0100584.	
PR	16-SEP-1998;	98US-0100627.	
PR	16-SEP-1998;	98US-0100661.	
PR	16-SEP-1998;	98US-0100662.	
PR	16-SEP-1998;	98US-0100664.	
PR	17-SEP-1998;	98US-0100683.	
PR	17-SEP-1998;	98US-0100684.	
PR	17-SEP-1998;	98US-0100710.	
PR	17-SEP-1998;	98US-0100711.	
PR	17-SEP-1998;	98US-0100919.	
PR	17-SEP-1998;	98US-0100930.	
PR	18-SEP-1998;	98US-0100848.	

Db 122 ILeThrTrpAlaValAlaProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 141
 QY 361 TGCCTCATTTCCGGCTGGGCGACGCTCCAGCCCGATGACGCTGCTGCACACCTTG 420
 Db 142 CysLeuLeuSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 161
 QY 421 CGATGCCCAACATCACCATCATTTGACACACAGAGTGTGAGAACGCCCTACCCGGCAAC 480
 Db 162 ArgCysAlaAsnIleThrIleLeuGlnHisGlnIleCysGlnIleAsnAlaTyrProGlyAsn 181
 QY 481 ATCAGACACACATGATGTGTGCGACGCTGACAGAGGGGAGAGGAGCTCTGCACAGGT 540
 Db 182 ILeThrSprhMetValCysAlaSerValGlnIleGlnIleGlyAspSerCysGlnGly 201
 QY 541 GACTCGGGGGCCCTGTGCTGTGTACCACTCTTCAAGGCATTAATCTCTGGGGCCAG 600
 Db 202 AsperGlyGlyProLeuValCysAsnGlnSerLeuGlnIleIleSerTrpGlyGln 221
 QY 601 GATCCGCTGCGATGACACCCGAAAGCCGTGCTCTACACGAAAGTCTGCAATATGTGAC 660
 Db 222 AsperCysAlaIleThrAlaGlySerProGlyValIleThrIleValCysLysTyrValAsp 241
 QY 661 TGGATCCAGAGACGATGAAGAACAT 687
 Db 242 TrpLeuGlnIleThrMetLysAsnAsn 250

RESULT 3
 ABB50479
 ID ABB50479 standard; Protein: 250 AA.
 AC ABB50479;
 DT 07-FEB-2002 (first entry)
 DE Human secreted protein encoded by gene 179 SEQ ID NO:427.

XX Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;
 KW dermatological; immunosuppressive; anti-inflammatory; immunostimulant;
 KW cytostatic; cardiac; vascular; anti-angiogenic; ophthalmological;
 KW neuroprotective; nootropic; anticonvulsant; antialzheimer's; vulnery;
 KW antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;
 KW multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;
 KW human immunodeficiency virus; hyperproliferative disorder; wound healing;
 KW Gaucher's disease; cardiovascular disease; scleritis syndrome; chemotaxis;
 KW Chaga's cardiomyopathy; coronary arteriosclerosis; angiotensin disorder;
 KW corneal graft neovascularisation; diabetic retinopathy; regeneration;
 KW neurological disorder; Huntington's chorea; Alzheimer's disease;
 KW Parkinson's disease; infectious disease.

XX Homo sapiens.
 OS
 XX
 PN WO200162891-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 21-FEB-2001; 2001WO-US05614.
 XX
 PR 24-FEB-2000; 2000US-184836P.
 PR 29-MAR-2000; 2000US-193170P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI NI J, Ebner R, Lafleur DW, Moore PA, Olsen HS, Rosen CA;
 PI Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;
 PI Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferris AM, Fan P;
 PI Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G;
 PI Zeng Z, Greene JM;
 XX
 DR WPI: 2001-625724/72.
 DR N-PSDB: ABA83372.
 XX
 PT Nucleic acids encoding 207 human secreted polypeptides, useful for preventing, diagnosing and/or treating, e.g. cancers, Parkinson's

PT disease and diabetic retinopathy -
 XX
 PS Claim 11; Page 1181-1182; 1533pp; English.
 XX
 CC ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted
 CC proteins (I) and polynucleotide (II) sequences. (I) and (II) have various
 CC activities based on the tissues and cells the genes are expressed in.
 CC Example of these activities include: immunomodulatory; antisclerotic;
 CC dermatological; immunosuppressive; anti-inflammatory; immunostimulant;
 CC anti-HIV; cytostatic; cardiac; anti-angiogenic; ophthalmological;
 CC neuroprotective; nootropic; anticonvulsant; antialzheimer's; vascular;
 CC antiparkinsonian; antimicrobial; and vulnery. (I) and (II) can be used
 CC in gene therapy and vaccine production. (I) and (II) can be used in the
 CC prevention, diagnosis and treatment of immune disorders (e.g. multiple
 CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus
 CC (HIV) infections), hyperproliferative disorders (e.g. cancers and
 CC Gaucher's disease), cardiovascular diseases (e.g. scleritis syndrome,
 CC Chaga's cardiomyopathy and coronary arteriosclerosis), angiotensin
 CC disorders (e.g. corneal graft neovascularisation and diabetic
 CC retinopathy), neurological disorders (e.g. Huntington's chorea,
 CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or
 CC for promoting wound healing, regeneration and/or chemotaxis. ABA83185 to
 CC ABA83193 and ABB50300 represent sequences used in the exemplification of
 CC the present invention.
 XX
 SQ Sequence 250 AA;
 Alignment Scores:
 Pred. No.: 1,4e-94 Length: 250
 Score: 1258.00 Matches: 229
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 98.67% Indels: 0
 DB: 22 Gaps: 0

US-09-856-320A-1_COPY_272_958 (1-687) x ABB50479 (1-250)

QY 1 ATCATCAAGGGGGTTCAGATGTCAGAGCTCACTCCAGCCCTGGACAGCCCTGTTTCAG 60
 Db 22 ILeThrTrpAlaValAlaProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 141
 QY 61 AAGACGGGCTACTCTGTGGGGGAGCCCTGATGCGCCCGAGAGGCTCTGCACAGCC 120
 Db 42 LysThrArgLeuLeuGlyCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAla 61
 QY 121 CACTGCTCAAGCCCGCTCATATGATGTCACCTGGGAGAGACACCTCGAAGAGAGAG 180
 Db 62 HisCysLeuSerProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnIleGln 81
 QY 181 GCGTGTGAGACAGACCCGAGACCCAGCTGAGTCTTCCCGACCCCGGCTTCAACACAGC 240
 Db 82 GlyCysGlnIleThrArgTrpAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 101
 QY 241 CTCGCCAACAAGACCCGCAATGATGATGCTGTGTAAGATGCGATGCCAGCTCC 300
 Db 102 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 121
 QY 301 ATCAGCTGGGCTGTGACACCCCTACCCCTCTCTCAAGCTGTGTCACTGTGGACACAG 360
 Db 122 ILeThrTrpAlaValAlaProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 141
 QY 361 TGCCTCATTTCCGGCTGGGCGACGCTCCAGCCCGATGACGCTGCTGCACACCTTG 420
 Db 142 CysLeuLeuSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 161
 QY 421 CGATGCCCAACATCACCATCATTTGACACACAGAGTGTGAGAACGCCCTACCCGGCAAC 480
 Db 162 ArgCysAlaAsnIleThrIleLeuGlnHisGlnIleCysGlnIleAsnAlaTyrProGlyAsn 181
 QY 481 ATCAGACACACATGATGTGTGCGACGCTGACAGAGGGGAGAGGCTCTGCACAGGT 540
 Db 182 ILeThrSprhMetValCysAlaSerValGlnIleGlnIleGlyAspSerCysGlnGly 201


```

QY 541 GACTCGGGGGCCCTGTGCTGTACACGACTCTTCAAGCATATATCTGGGGCCAG 600
Db 202 ASPTSGELYLProleuValIcysasnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 221
QY 601 GATCCGTGTGCATCATCCGGAAGCTGTCTACACGAAGTCTGCAATATGTGCAC 660
Db 222 ASPTGCGYAlaIleThrArgLysProGlyValIYrThrLysValIcysLysIYrValAsp 241
QY 661 TGCATCCAGAGACATGAGAACAT 687
Db 242 TPTIleGlnGluThrMetLysAsn 250

RESULT 4
AAU12424
ID AAU12424 standard; Protein; 250 AA.
XX
XX AAU12424;
XX
XX 24-OCT-2001 (first entry)
DE Human PRO1279 polypeptide sequence.
XX
XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;
XX breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
XX cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
XX adipocyte; A-peptide; factor VIIA; gene therapy.
XX
XX Homo sapiens.
XX
XX WO200140466-A2.
XX
XX 07-JUN-2001.
XX
XX 01-DEC-2000; 2000WO-US32678.
XX
XX 01-DEC-1999; 99WO-US28301.
XX 01-DEC-1999; 99WO-US28634.
XX 02-DEC-1999; 99WO-US28551.
XX 02-DEC-1999; 99WO-US28564.
XX 02-DEC-1999; 99WO-US28565.
XX 09-DEC-1999; 99US-0170262.
XX 16-DEC-1999; 99WO-US30095.
XX 20-DEC-1999; 99WO-US30911.
XX 20-DEC-1999; 99WO-US30999.
XX 30-DEC-1999; 99WO-US31243.
XX 06-JAN-2000; 2000WO-US00277.
XX 11-FEB-2000; 2000WO-US00376.
XX 18-FEB-2000; 2000WO-US04341.
XX 18-FEB-2000; 2000WO-US04342.
XX 22-FEB-2000; 2000WO-US04414.
XX 24-FEB-2000; 2000WO-US04914.
XX 24-FEB-2000; 2000WO-US05004.
XX 01-MAR-2000; 2000WO-US05601.
XX 20-MAR-2000; 2000WO-US07377.
XX 21-MAR-2000; 2000WO-US07372.
XX 30-MAR-2000; 2000WO-US08439.
XX 17-MAY-2000; 2000WO-US13705.
XX 22-MAY-2000; 2000WO-US14042.
XX 30-MAY-2000; 2000WO-US14941.
XX 02-JUN-2000; 2000WO-US15264.
XX 10-NOV-2000; 2000WO-US30873.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Flivaroff E, Gao W;
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,
XX Smith V, Stewart RA, Tumas D, Watanabe CK, Wood WL, Zhang Z;
XX WPI; 2001-408281/43.
XX N-PSDB; AAS21496.
XX
XX Isolated, secretory and transmembrane PRO polypeptide used to detect

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PT other PRO polypeptides, link bioactive molecules to cells expressing
PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT lung, breast, prostate, cervical
XX
XX Claim 12; Fig 506; 813bp; English.
XX
CC AAU12172-AAU12446 represent novel human secretory and transmembrane
CC PRO polypeptides. The PRO polypeptides are useful to detect other
CC PRO polypeptides, to link bioactive molecules to cells expressing
CC PRO polypeptides, to modulate biological activities of cells expressing
CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample.
CC Some of the 275 sequences are also useful to stimulate the release of
CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC proliferation or differentiation of chondrocytes, the proliferation or
CC gene expression in pericyte cells, the release of proteoglycans from
CC cartilage, the proliferation of inner ear utricular supporting cells or
CC of T-lymphocytes, the release of a cytokine from peripheral blood
CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC to factor VIIA. The PRO polypeptides can be used in assays to identify
CC molecules involved in binding interactions. The polynucleotides encoding
CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy.
XX
XX
XX Sequence 250 AA:
XX
XX
XX Alignment Scores:
XX Pred. No.: 1.4e-94 Length: 250
XX Score: 1258.00 Matches: 229
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 98.67% Indels: 0
XX DB: 22 Gaps: 0
XX
XX
XX US-09-856-320A-1_COPY_272_958 (1-687) x AAU12424 (1-250)
XX
QY 1 ATCATCAAGGGGGTGTGAGTCAAGGCTTCCTCCAGCCCTGGCAGGACGCTGTTGAG 60
Db 22 ITeIleLysGlyPheGlnCysLysProHisSerGlnProTrpGlnIleAlaLeuPheGln 41
QY 61 AAGACGCGGTACTGTGTGGGGGAGCGCTATCGCCCGCCAGATGGCTCTGACAGAGCC 120
Db 42 LysThrArgLeuLeuLysCysGlyAlaThrIleAlaProArgTrpLeuLeuThrAlaAla 61
QY 121 CACTGCTCAAGCCCCGCTACTAGTCACTGGGGGACACACACCTCCAGAGAGAG 180
Db 62 HisCysLeuLysProArgTrpIleValHisLeuGlnHisAsnIleuGlnLysGln 81
QY 181 GCGTGTGAGCAGACCCGAGCAGCAGCTGAGTCCCTCCCGCCGGGCTTCAACAACAGC 240
Db 82 GlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheHisAsnSer 101
QY 241 CTCCCAACAAAGACACCCGCAATGACATCATGTGTGAGATGGATGGCAGCTTCC 300
Db 102 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 121
QY 301 ATCAGCTGGGCTGTGCGACCCCTCACCTTCTTCAAGCTGTGTACTGTGACACAGC 360
Db 122 ITeHrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 141
QY 361 TGCCCATTTCCGGCTGGGGGAGCAGCTCCACCCCGAGTTGCGCTGCTCCACACCTG 420
Db 142 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 161
QY 421 CGATCGGCCAACATCATCATATTGAGCAGCAGAAGTGTGAGAACGCTTACCCGCGCAAC 480
Db 162 ArgCysAlaAsnIleThrIleGlnHisGlnLysCysGlnAsnAlaIleTrpProLysAsn 181
QY 481 ATCAGACACACCATGTGTGTGCCAGCTGACAGGAAGGGGGGACAGGATCTCTGCCAGGCT 540

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Db 182 ILeThrAspThrMetValCysAlaSerValGlnGlnGlyGlyAspSerCysGlnGly 201
 QY 541 GACTCCGGGGCCCTGTGTCGTGAACAGTCTTCAAGCAATTATCTCTGGGGCCAG 600
 Db 202 AspSerGlyGlyProLeuValCysAsnGlnSerLeuInGlyIleIleSerTrpGlyGln 221
 QY 601 GATCCGCTGTCGATCACCCGAAAGCCTGCTGTCTACACGAAAGTCTCAAAATATGTGAC 660
 Db 222 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTyValAsp 241
 QY 661 TGGATCCAGAGACAGATGAAGAACAAAT 687
 Db 242 TrpIleGlnGlnThrMetLysAsnAsn 250
 RESULT 5
 AAB66139
 ID AAB66139 standard; protein; 250 AA.
 AC AAB66139;
 XX 02-APR-2001 (first entry)
 DT Protein of the invention #51.
 DE Secreted; transmembrane; gene therapy.
 XX
 KM
 XX
 OS Unidentified.
 PN WO200078961-A1.
 PD 28-DEC-2000.
 XX 18-FEB-2000; 2000MO-US04342.
 PE 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 01-SEP-1999; 99MO-US20111.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99MO-US28313.
 PR 02-DEC-1999; 99MO-US28551.
 PR 16-DEC-1999; 99MO-US30095.
 PR 05-JAN-2000; 2000MO-US00219.
 PR 06-JAN-2000; 2000MO-US00376.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D;
 PI Watanabe CK, Williams PM, Wood WI;
 XX WPI; 2001-071395/08.
 DR
 XX
 PT Secreted and transmembrane proteins and nucleic acids designated PRO,
 PT useful as hybridization probes, in chromosome and gene mapping and gene
 PT therapy -
 PT
 PT
 PS Claim 1; Fig 102; 787pp; English.
 XX
 CC The present invention relates to secreted and transmembrane proteins.
 CC These proteins and the DNA encoding them may be used as hybridization
 CC probes, in chromosome and gene mapping and in the generation of
 CC anti-sense RNA and DNA. They may also be used to generate either
 CC transgenic animals or knockout animals which are in turn useful for
 CC development and screening of therapeutically useful reagents.
 CC The nucleic acids may also be used in gene therapy.
 XX
 SO Sequence 250 AA;
 Alignment Scores:
 Pred. No.: 1,4e-94 Length: 250
 Score: 1258.00 Matches: 229

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 98.67% Indels: 0
 DB: 22 Gaps: 0
 US-09-856-320a-1_COPY_272_958 (1-687) x AAB66139 (1-250)
 QY 1 ATCATCAAGGGGTTCGATGTCAMGCTTCACCTCCAGCCCTGGACAGGCCCTGTTCAG 60
 Db 22 IleIleLysGlyPheGlnCysLysProHisSerGlnProIleTrpGlnAlaIlePheGln 41
 QY 61 AAGACGGGCTACTCTGTGGGGAGCCCTATGCCCCAGATGGCTCTGACAGACGCC 120
 Db 42 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThrAlaAla 61
 QY 121 CACTGACCTCAAGCCCGCTCATATGATTCACCTGGGGAGACACAACCTCCAGAGAGAGAG 180
 Db 62 HisCysLeuLysProAlaGlyTrpIleValHisLeuGlyGlnHisAsnLeuGlnGlu 81
 QY 181 GCGTGTGAGCAGACCCCGACAGCCCATGAGTCTTCCCGACCCGCGCTTCAACACAGC 240
 Db 82 GlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 101
 QY 241 CTCCCAACAAGACACCCGCAATGACATCATGCTGTGAAGATGGCATGCCAGTCTCC 300
 Db 102 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 121
 QY 301 ATCACCTGGGCTGTGGACCCCTCACCCCTGCTGACGCTGTGTCATGCTGGACACAGC 360
 Db 122 IleThrTrpAlaValAlaGProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 141
 QY 361 TGCCTCATTTCCGGCTGGGGAGCAGCAGCTCCAGCCCCAGTTAGCCTGCTCACACCTTG 420
 Db 142 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 161
 QY 421 CGATGGCCCAACATCACCATCATGAGCACACAGAGTGAAGACCGCTTCCCCGGCAAC 480
 Db 162 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyProGlyAsn 181
 QY 481 ATCACAGACACCATGCTGTGTGCCAGCGTCAGAGAGGGGAGCAAGACTCTCCAGAGGT 540
 Db 182 IleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyAspSerCysGlnGly 201
 QY 541 GACTCCGGGGCCCTGTGTCGTGAACAGTCTTCAAGCAATTATCTCTGGGGCCAG 600
 Db 202 AspSerGlyGlyProLeuValCysAsnGlnSerLeuInGlyIleIleSerTrpGlyGln 221
 QY 601 GATCCGCTGTCGATCACCCGAAAGCCTGCTGTCTACACGAAAGTCTCAAAATATGTGAC 660
 Db 222 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTyValAsp 241
 QY 661 TGGATCCAGAGACAGATGAAGAACAAAT 687
 Db 242 TrpIleGlnGlnThrMetLysAsnAsn 250
 RESULT 6
 AAB61816
 ID AAB61816 standard; protein; 250 AA.
 AC AAB61816;
 XX 15-AUG-2002 (first entry)
 DT Prostate cancer-associated protein #17.
 DE Prostate cancer-associated protein #17.
 XX
 KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
 XX
 OS Mammalia.
 OS
 XX
 PN WO200230268-A2.
 PD 18-APR-2002.
 XX

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XX PF 12-OCT-2001; 2001WO-US32045.
PR PR 13-OCT-2000; 2000US-0687576.
PR PR 08-DEC-2000; 2000US-0733288.
PR PR 08-DEC-2000; 2000US-0733288.
PR PR 24-JAN-2001; 2001US-263957P.
PR PR 16-MAR-2001; 2001US-276791P.
PR PR 16-MAR-2001; 2001US-276888P.
PR PR 06-APR-2001; 2001US-281922P.
PR PR 24-APR-2001; 2001US-286214P.
PR PR 30-APR-2001; 2001US-0847046.
PR PR 04-MAY-2001; 2001US-288589P.
XX XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX XX
PI Gish KC, Mack DH, Wilson KE, Afari D, Heyezi P;
DR WPI: 2002-471335/50.
XX N-PSDB; ABR92131.
XX XX
PT Detecting a prostate cancer-associated transcript in a cell in a
PT patient, useful for diagnosing prostate cancer (PC) or screening
PT modulators of PC, by determining if prostate cancer-associated genes
PT are expressed in a prostate tissue -
XX XX
PS Claim 27: Page 314; 436pp; English.
XX XX
CC The present invention relates to methods of detecting a prostate
CC cancer-associated transcript in a cell from a patient. The method
CC comprises contacting a biological sample from the patient with
CC prostate cancer-associated polynucleotides (designated PC gene) that
CC selectively hybridise to a sequence that is at least 80% identical
CC to them. The prostate cancer-associated polynucleotide sequences
CC are differentially expressed in prostate tumour tissue or in
CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
CC The methods of the invention are useful for diagnosing and treating
CC prostate cancer in mammals. The prostate cancer-associated genes are
CC useful for diagnosing or treating prostate cancer, as well as for
CC identifying modulators of prostate cancer or agents that inhibit
CC prostate cancer. The nucleic acid sequences are particularly useful
CC in gene therapy, as a vaccine or in antisense applications.
CC ABG61800-ABG61944 represent prostate cancer-associated proteins.
XX XX
SQ Sequence 250 AA;
SQ
Alignment Scores:
Pred. No.: 1,4e-94 Length: 250
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.67% Indels: 0
DB: Gaps: 0
US-09-856-320A-L_COPY_272_958 (1-687) x ABG61816 (1-250)
QY 1 ATCATCAAGGGGTTCGATGTCGAAGCCTTACGCCAGCCCTTGCGAGCCCTGTTGCAG 60
Db |||||||
QY 22 TTTTATTGAGTGGTTCGATGTCGAAGCCTTACGCCAGCCCTTGCGAGCCCTGTTGCAG 60
Db |||||||
QY 61 AAGAGCGGGCTACTCTGTGGGGCGAGCGCTATCGCCCCCAATAGTGGCTTCGACAGCACCC 120
Db |||||||
QY 42 LYTHTATGATGTCGATGTCGAAGCCTTACGCCAGCCCTTGCGAGCCCTGTTGCAG 60
Db |||||||
QY 121 CATCTGCTCAAGCGCCGCTACATGATGTCGAAGCCTTACGCCAGCCCTTGCGAGCCCTGTTGCAG 180
Db |||||||
QY 62 TATCTGCTCAAGCGCCGCTACATGATGTCGAAGCCTTACGCCAGCCCTTGCGAGCCCTGTTGCAG 180
Db |||||||
QY 181 GGCTGTGACAGCACCGCGACAGCCAGTGAAGTCTTCCCGCCAGCCCGGCTTCAACACAGC 240
Db |||||||
QY 82 GTCTGCTCAAGCGCCGCTACATGATGTCGAAGCCTTACGCCAGCCCTTGCGAGCCCTGTTGCAG 240
Db |||||||
QY 241 CTCCTGCTCAAGCGCCGCTACATGATGTCGAAGCCTTACGCCAGCCCTTGCGAGCCCTGTTGCAG 300

```

Db	102	LeuPProAsnLysAspHisArgAsnAspIleMetLeuValLysMetLAsSerProValSer	1211
Qy	301	ATCACCTGGGCTGTGCGAGACCCCTCAACCTCTCTCAGCGTGTGTCACTGCTGGCACACG	360
Db	122	IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer	1411
Qy	361	TGCTCATATTCGGGCTGGGGGCGAGCAGTCCAGCCCCCAGATTACGCTGCTCCACACCTTG	420
Db	142	CysLeuIleSerGlyTrpIleYserThrSerSerProGlnLeuArgLeuProHisThrLeu	161
Qy	421	CGATCGGCCAATATCACTCATTTTAGGACCCAGAAATGTGAGAACCCCTTACCCGGCAAC	480
Db	162	ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTrpProGlyAsn	181
Qy	481	ATCACAGACACCATGATGTTGTGTCCACGCGAGGAAGGGGGCAAGACCTCCAGGGT	540
Db	182	IleThrAspThrMetValCysAlaSerValGlnGlnIleGlyLysAspSerCysGlnGly	201
Qy	541	GACTCCGGGGGCGCTCTGTGTGTGAACAGTCTCTTCAAGGCAATTATCTCGGGGCCAG	600
Db	202	AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln	221
Qy	601	GATCGGTGGCATCAACCCGGAAGCCTGGTGTCTACAGAAAGTGTGCAATATGTGGAC	660
Db	222	AspProCysAlaIleThrArgLysProGlyValTrpThrLysValCysLysIleValAsp	241
Qy	661	TGGATCCAGAGACGATGACAGAACAAT	687
Db	242	TrpIleGlnGluThrMetLysAsnAsn	250
RESULT 7			
AB95526	ID	AB95526 standard; Protein; 250 AA.	
xx	AC	AB95526;	
xx	DT	19-JUL-2002 (first entry)	
xx	DE	Human angiogenesis related protein PRO1279 SEQ ID NO: 208.	
xx	xx	Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer; atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder; antiarteriosclerotic.	
xx	OS	Homo sapiens.	
xx	PN	WO200208284-A2.	
xx	PD	31-JAN-2002.	
xx	PF	09-JUL-2001; 2001WO-US21735.	
xx	PR	20-JUL-2000; 2000US-219556P.	
xx	PR	25-JUL-2000; 2000US-220624P.	
xx	PR	28-JUL-2000; 2000US-220649P.	
xx	PR	02-AUG-2000; 2000US-222695P.	
xx	PR	17-AUG-2000; 2000US-0643657.	
xx	PR	23-AUG-2000; 2000WO-US23522.	
xx	PR	24-AUG-2000; 2000WO-US23328.	
xx	PR	07-SEP-2000; 2000US-230978P.	
xx	PR	15-SEP-2000; 2000US-000000P.	
xx	PR	18-SEP-2000; 2000US-0664610.	
xx	PR	18-SEP-2000; 2000US-0665350.	
xx	PR	24-OCT-2000; 2000US-242922P.	
xx	PR	08-NOV-2000; 2000US-0709238.	
xx	PR	10-NOV-2000; 2000WO-US30952.	
xx	PR	01-DEC-2000; 2000WO-US30873.	
xx	PR	20-DEC-2000; 2000US-0747259.	
xx	PR	20-DEC-2000; 2000WO-US34956.	

PR 22-JAN-2001; 2001US-0767609.
 PR 26-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828368.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 28-JUN-2001; 2001WO-US00000.

XX (GETH) GENENTECH INC.
 PA (BAKE) BAKER K P.
 PA (FERR) FERRARA N.
 PA (GERB) GERBER H.
 PA (GERR) GERRITSEN M E.
 PA (GODD) GODDARD A.
 PA (GODO) GODOWSKI P J.
 PA (GURN) GURNEY A L.
 PA (HILL) HILLMAN K J.
 PA (MARS) MARSTERS S A.
 PA (PANJ) PAN J.
 PA (PAON) PAONI N F.
 PA (STEP) STEPHAN J F.
 PA (WATA) WATANABE C K.
 PA (WILL) WILLIAMS P M.
 PA (WOOD) WOOD W I.

PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillman KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 DR N-PSDB; ABL95664.

WPI: 2002-171999/22.

PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -

PS Claim 11; Fig 208; 567pp; English.

XX The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hyper trophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a PRO protein of the invention.

XX Sequence 250 AA;

Alignment Scores:
 Pred. No.: 1.4e-94 Length: 250
 Score: 1258.00 Matches: 229
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 98.67% Indels: 0
 DB: 23 Gaps: 0

US-09-856-320a-1_copy_272_958 (1-687) x ABB95526 (1-250)

OY 1 ATGATCAAGGGGTTGCGATGCAAGCCTCACTCCAGCGCCGAGGAGCCGTTGAG 60
 DB 22 ITTETLSTLYPNEGILUCYSYSPROHISSETGIPROTPGINDAIAALEUPNEGILU 41

OY 61 AAGACGGGCTACTCTGTGGGGCGAGCCTCATCGCCCGCCAGATGGCTCTGACAGCAGCC 120
 DB 42 LYSTHRTPLAVALARGPROLEUTHRLEUSERTSERARGCYVALTHRALAGLYTHRSER 61
 OY 121 CACTGCTCAAGCCCGCTACATGTTCCACTGGGGCGAGCAGCAACCTCCAGAGGAGCAG 180
 DB 62 HISCYSLEUYSPROAATGYTRILEVALHISLEUPLYGHNHSAENLEUGLNYSGULGN 81
 OY 181 GGCTGTAGCAGACCCGAGCAGCAGCAGTGAAGCTCTCCCGCCGCTTCAACAGCAGC 240
 DB 82 GLYSYSGULGNHTRALAGTHRALAGTHGLUSERTHERPROHISPROGLYPHESANASER 101
 OY 241 CTCCCAACAAGACACACCGCATGACATGATGCTGTGTAAGATGAGCAGCAGCTCC 300
 DB 102 LEUPROANLYSASPHISARGASNPISPLEWETLEUVALYSMETALASERPROVALSER 121
 OY 301 ATCACTGGGCTGTGGCAGCCCTTACCCCTCTCCACAGCTGTGTACCTGCTGGCAGCAGC 360
 DB 122 ILEHTRTPALAVALARPROLEUTHRLEUSERTSERARGCYVALTHRALAGLYTHRSER 141
 OY 361 TGCCATATTCGGGCTGGGCGAGCAGCTCCAGCCCGCATGAGCCTGCTGACAGCTTG 420
 DB 142 CYSLEULESERTGLYTRIPGLYSERTHRSERTPROGLINEUATGLYEUATGLYTHRSER 161
 OY 421 CGATGCGCAACATCACCATCATTTAGACACACAGAGTGTGAGAACGGCTTACCCCGCAAC 480
 DB 162 ARGCYSLAENILHTRILEGILNHISGLINLYSCYSGULNANALATYRPROGLYASN 181
 OY 481 ATCAACACACACATGCTGTGTGGCAGCTGTGACAGAGGCGGAGCAGCTCTGACAGGT 540
 DB 182 ILEHTRAPTHMETVALCYSLASERVALGLINLNYGLYLSASPSERCYSGINGLY 201
 OY 541 GACTCGGGGGCCCTGTGCTGTATACCAAGCTCTTCAAGCATATCTCTGGGGCGAG 600
 DB 202 ASPSERGLYGLYPROLEUVALCYSANGLINSERLEUINGLYILESETRTIPGLYGLN 221
 OY 601 GATCCGTGTGGATCACCCGAAAGCCTGTGTATACAGAAAGTCTCAATATGTGTGAC 660
 DB 222 ASPROCYSLAILETHRTARGLYSPROGLYVALTYRTHRLYSVALCYLSYSTYRVALASP 241
 OY 661 TGGATCCAGAGAGCAGTGAAGCAAT 687
 DB 242 TPTILEGLINGLUTRIMETLYSASNASH 250

RESULT 8
 ABB84920
 ID ABB84920 standard; Protein: 250 AA.

XX ABB84920;

DT 16-MAY-2002 (first entry)

DE Human PRO1279 protein sequence SMO ID NO:208.

XX Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
 KW gene therapy; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 Wound healing; chromosome mapping; gene mapping.

XX Homo sapiens.

PN WO200200690-A2.

PD 03-JAN-2002.

PF 20-JUN-2001; 2001WO-US19692.

PR 23-JUN-2000; 2000US-213637P.

20-JUL-2000: 2000US-219556P.
 PR 25-JUL-2000: 2000US-220624P.
 PR 25-JUL-2000: 2000US-220644P.
 PR 28-JUL-2000: 2000OWO-US20710.
 PR 02-AUG-2000: 2000OWO-222695P.
 PR 17-AUG-2000: 2000OWO-0643657.
 PR 23-AUG-2000: 2000OWO-US23522.
 PR 24-AUG-2000: 2000OWO-US23328.
 PR 07-SEP-2000: 2000US-230978P.
 PR 18-SEP-2000: 2000US-0664610.
 PR 18-SEP-2000: 2000US-0665350.
 PR 24-OCT-2000: 2000US-242922P.
 PR 08-NOV-2000: 2000OWO-0709238.
 PR 08-NOV-2000: 2000OWO-US30952.
 PR 10-NOV-2000: 2000OWO-US30873.
 PR 01-DEC-2000: 2000OWO-US32678.
 PR 20-DEC-2000: 2000US-0747259.
 PR 20-DEC-2000: 2000OWO-US34956.
 PR 22-JAN-2001: 2001US-0767609.
 PR 28-FEB-2001: 2001US-0796498.
 PR 28-FEB-2001: 2001WO-US06520.
 PR 01-MAR-2001: 2001WO-US06666.
 PR 09-MAR-2001: 2001US-0802706.
 PR 14-MAR-2001: 2001US-0808689.
 PR 22-MAR-2001: 2001US-0816744.
 PR 05-APR-2001: 2001US-0828366.
 PR 10-MAY-2001: 2001US-0854208.
 PR 10-MAY-2001: 2001US-0854280.
 PR 25-MAY-2001: 2001US-0866028.
 PR 25-MAY-2001: 2001US-0866034.
 PR 30-MAY-2001: 2001WO-US17092.
 PR 30-MAY-2001: 2001US-0870574.
 PR 01-JUN-2001: 2001WO-US17443.
 PR 01-JUN-2001: 2001WO-US17800.
 (GENE) GENEINTECH INC.
 PA Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WT, Ye W;
 DR N-PSDB: ABL88175.
 XX WPI: 2002-090516/12.
 DR One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -
 XX
 PS Claim 11; Fig 208; 565pp; English.
 XX
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytosstatic,
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
 CC carcinoma) and wound healing. The PRO polynucleotides have applications
 CC in molecular biology, including use as hybridisation probes, and in
 CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
 CC probes used in the exemplification of the present invention.
 XX
 SO Sequence 250 AA:

DB: 23 Gaps: 0
 US-09-856-320a-1_COPY_272_958 (1-687) x ABB84920 (1-250)
 QY 1 ATCATCAAGGGGTGAGTGCAGAGCCTCACTCCAGCCCTGGCAGGACGCTGTCGAG 60
 DB 22 ILEILEYSGLYPHEIDUCYSYSPROHISSESGINPROTGELINLALEUPNEGIL 41
 QY 61 AAGACGCGCTACTGTGTGGGCGAGCGTCAATCGCCCGAGATGAGCTCTGCAGAGCC 120
 DB 42 LYSTHARGLEULEUCYSGLYALATHLEULEIALEIARGLTREPHEUTHRIALALE 61
 QY 121 CACTGCTCAAGCCCGCTACATGATGTCACCTGGGCGACACACCTCCAGAGAGGAG 180
 DB 62 HISCYSEULYSPROARGTYRILEVALHISLEUGLGINHISASNENGLINSGILGIN 81
 QY 181 GGCTGTGAGCAGACCCGAGCAGCAGCTGAGTCCCTCCCGCCGCGCTCAACAGACAG 240
 DB 82 GLYCYSGLVGLNTHARGTHRALATHRGISERPHROHISPROGLYPHEASNSHSE 101
 QY 241 CTCGCCAACAAAGACCCGCAATGACATCATGCTGTGAGATGGCATCGCCAGTCTCC 300
 DB 102 LEUPROASNLYASPHISARGSHNSPILMETLEUVALYMETALASERPROVALSER 121
 QY 301 ATCACCTGGGCTGTGCGAGCCCTCACCTCTCTCACGCTGTGTCACCTGGCAGCAGC 360
 DB 122 ILETHTRPALAVALARGPROLEUTHLEUSERSERARGCYVALTHRALGLYTHSER 141
 QY 361 TGGCTCATTTCCGGCTGGGCGAGCAGCTCCACCCCAATTCGCTGCTCACACTTG 420
 DB 142 CYSLLEULEISERGILYTRPGLYSERTHRSERPROGLINLEARGLEUTHROHIS 161
 QY 421 CGATGCGCCACATCATCATCATGAGCAGCAGAGTGGAGAGAGCCCTACCCCGGACAC 480
 DB 162 ARGCYSAIASNIIETHRIELEIUEHISGLINLSCYSGILNASHIALATYRPROGLYSHN 181
 QY 481 ATCACAGACACCATGCTGTGCGAGCGTGCAGAGAGGGGCGAGACTCTGCCAGGCT 540
 DB 182 ILETHASPTHEVALCYSAISERVALGINGILGLYLYASPERCYSGILNGL 201
 QY 541 GACTCCGGGGGCGCTGTGCTGTAAACGCTCTTCAAGGATATCTCCCTGGGCGAG 600
 DB 202 ASPSERGLYGLYPROLEUVALCYSSANGINSELEUGLNEYILELESERTPELYGIN 221
 QY 601 GATCCGTGTGCATCACCCGAGAGCCTGTGCTACACAGAAAGTCTGCANAATATGTGAC 660
 DB 222 ASPROCYSALALEIETHARGYSPROGLYVALTYRTHLYVALCYSLYSTYRVALASP 241
 QY 661 TGGATCCAGGAGACGATGAGAACAAT 687
 DB 242 TRPILGLINGLUTHRMETLYSASNAN 250
 RESULT 9
 ID AAB83684
 ID AAB83684 standard; Protein; 250 AA.
 XX
 AC AAB83684;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Human PRO protein. Seq ID No 186.
 XX
 KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;
 KW pericyte cell proliferation; chondrocyte cell proliferation;
 KW tumour necrosis factor alpha.
 XX
 OS Homo sapiens.
 XX
 PN WO200208288-A2.
 XX
 PD 31-JAN-2002.
 XX

Alignment Scores:
 Pred. No.: 1.4e-94
 Score: 1258.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 98.67%
 Length: 250
 Matches: 229
 Conservative: 0
 Mismatches: 0
 Indels: 0

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PF 29-JUN-2001; 2001WO-US21066.
XX 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220585P.
PR 25-JUL-2000; 2000US-220605P.
PR 25-JUL-2000; 2000US-220607P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220638P.
PR 25-JUL-2000; 2000US-220664P.
PR 25-JUL-2000; 2000US-220666P.
PR 26-JUL-2000; 2000US-220893P.
PR 28-JUL-2000; 2000WO-US207110.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 15-SEP-2000; 2000US-000000P.
PR 10-NOV-2000; 2000WO-US30873.
PR 28-NOV-2000; 2000US-253646P.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-074725P.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001WO-US17092.
XX (GENE) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2002-172001/22.
DR N-PSDB; ABK33628.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumours
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
PT tumour or liver tumour -
XX
XX Claim 11; Figure 186; 359pp; English.
XX
XX The invention relates to one hundred and twenty two nucleic acids
XX encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
XX encode human secreted proteins. The PRO nucleic acids, polypeptides,
XX agonists and antagonists are useful for treating a PRO related disorder.
XX The PRO polypeptides are useful for diagnosing tumours, especially lung
XX cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
XX liver tumour. The PRO polypeptides are useful for stimulating the
XX proliferation of, or gene expression, in pericyte cells, for stimulating
XX the proliferation or differentiation of chondrocyte cells, for stimulating
XX stimulating the release of tumour necrosis factor-alpha from human blood,
XX for stimulating or inhibiting the proliferation of normal human dermal
XX fibroblast cells. The PRO polypeptide may also be used as molecular
XX weight markers and for tissue typing. The PRO nucleic acids have
XX applications in molecular biology, including use as hybridisation probes,
XX and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
XX protein sequences of the invention.
XX
XX Sequence 250 AA:
XX
XX Alignment Scores:
XX Pred. No.: 1,4e-94 Length: 250
XX Score: 1258.00 Matches: 229
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 98.67% Indels: 0
XX DB: 23 Gaps: 0
XX
XX US-09-856-320a-1_COPY_272_958 (1-687) x AAU83684 (1-250)
XX
XX 1 ATATCAAGGGGTTGAGTCAAGCTCACTCCAGCGCTGGCAGGAGCGCTGTGTTGAG 60
XX |||||||
XX 22 IletlelsgslpnehlsgslslyspnrlserslgnprtrpnlalalaleuPhgln 41
XX |||||||
XX 61 AAGAGCGGCTACTCTGTGGGCGAGCGCTATCGCGCCCAAGATGGCTCTGACAGCACC 120
XX |||||||

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DB 42 LysThrArgLeuLeuCysGlyAlaThrLeuLeuLeuAlaProArgTrpLeuLeuThraAla 61
|||
QY CACTGCGCTCAAGCGCGCTATCATGTTCACTGGGGAGAGACAACTCCGAAGAGAGAG 180
|||
DB HisCysLeuLysProArgTrpIleValHisLeuLysGlnHisAsnLeuGlnLysGln 81
|||
QY 181 GCGTGTAGAGCAGACCGGAGCAGCCATGAGTCTCTCCACCGCGCTTCAACACAGC 240
|||
DB 82 GlyCysGlnGlnThrArgTrpAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 101
|||
QY 241 CTCCCAACAAAGACCAACCGCAATGACATCATGCTGTGAAGATGGATGCCAGTCTCC 300
|||
DB 102 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 121
|||
QY 301 ATCACCGGGGCTGGGAGCGCGCTACCGCTCCGCTCCAGCTGTGCATGCTGTGCACAC 360
|||
DB 122 IletThrPalaValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 141
|||
QY 361 TGCCCTCATTTCCGGCTGGGAGCAGCAGCTCCAGCGCGCTGATGAGTGTAGAAAGCCCTAC 420
|||
DB 142 CysLeuLeuSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 161
|||
QY 421 CGATGCGCGCAATCATCATCATTTGAGCAGCAGCAAGTGTAGAAAGCCCTACCGCGCAC 480
|||
DB 162 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyProGlyAsn 181
|||
QY 481 ATCACAGACACCATGATGTGTGTCAGCGCTCAGAGAGAGGAGGAGCAAGCTCCGAGGGT 540
|||
DB 182 IletThrAspThrMetValCysAlaSerValGlnGlnLysGlnLysAspSerCysGlnGly 201
|||
QY 541 GACTCGCGGGGCGCTGTGTGTGTACCACTCTCTTCAAGGATATCTCTGCGGCGCAG 600
|||
DB 202 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 221
|||
QY 601 GATCGGTGTGGATCCAGCGCAAGCGCTGTGTGTACCGAAAGTCTTCAATATGTGAGAC 660
|||
DB 222 AspProCysAlaIleThrArgLysProGlyValThrLysValCysLysTyValAsp 241
|||
QY 661 TGGATCCAGGAGAGCATGATGAAGAACAT 687
|||
DB 242 TrpLeuGlnLysThrMetLysAsnAsn 250
|||
RESULT 10
ABU66822 standard; Protein: 250 AA.
ID ABU66822;
XX
XX ABU66822;
AC 23-MAY-2003 (first entry)
XX
XX Human PRO polypeptide #253.
DE
XX
XX Human: PRO polypeptide; secreted and transmembrane protein;
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW differentiation; chondrocyte; tumour; genetic disorder;
KW cytosolic.
XX
XX Homo sapiens.
OS
XX
XX US2003036180-A1.
PN
XX
XX 20-FEB-2003.
PD
XX
XX 09-MAY-2002; 2002US-0143114.
PF
XX
XX 31-MAR-1997; 97WO-US05230.
PR
XX 12-JUN-1998; 98WO-US12456.
PR
XX 14-JUL-1998; 98WO-US14552.
PR
XX 28-AUG-1998; 98WO-US17888.
PR
XX 10-SEP-1998; 98WO-US18824.
PR
XX 14-SEP-1998; 98WO-US19093.
PR
XX 14-SEP-1998; 98WO-US19094.

```


Db 42 LysThrIhrGleuLeuCysGlyAlaThrIleLeuIleAlaProArgTrpLeuThrAlaIa 61
QY 121 CACTGCTCAAGCCCGCTACATAGTTACCTGGGGGAGCAGCAACCTCCAGAGAGAG 180
Db 62 HisCysLeuIysProArgTrpIleValHisLeuIyGlnHisAsnLeuGlnGlyGlu 81
QY 181 GGCCTGAGCAGACCCGAGCAGCCAGTACGTCTCCCGCCCGGCTTCAACAGC 240
Db 82 GlySerGluGlnThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 101
QY 241 CTCCCAAGAGAGCAGCCGATGACATGCTGGGAGAGATGGAGTCCAGTCC 300
Db 102 LeuProAsnIysAspHisAlaGlnAspIleMetLeuValIysMetAlaSerProValSer 121
QY 301 ATCACTGGGCTGTGAGACCCCTGACCTCTCTCAAGCTGTCTCACTGTGAGCAGC 360
Db 122 IlleThrTrpAlaValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 141
QY 361 TGCTTCATTTCCGCTGGGCGAGCAGCTCCAGCCCGAGTTACGCTGCTCAGACCTTG 420
Db 142 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 161
QY 421 CGATGCGGCAACATCACCATCATGAGACAGAGAGTGTGAGAGCGCTACCCGCGGAGC 480
Db 162 ArgCysAlaAsnIleThrIleThrIleGlnHisGlnIlyscysGlnAsnAlaTrpGlyAsn 181
QY 481 ATCAAGAGACCATGATGTGTGCGCAGCTGCGAGAGAGGAGGAGCAGTCTGCGCAGGT 540
Db 182 IlleThrAspThrMetValCysAlaSerValGlnGlnGlyIysAspSerCysGlnGly 201
QY 541 GACGCCGGGGCCCTCGGTGTGTACCAAGTCTTCAAGCATTAATCTCTGGGCGCAG 600
Db 202 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 221
QY 601 GATCCGATGGGATCAGCCCGAAGCCTGCTGTACAGGAAGTCTGCAATATGTGGAC 660
Db 222 AspProCysAlaIleThrIleArgIysProGlyValIleThrIysValCysIysTrpValAsp 241
QY 661 TGGATCCAGGAGCAGATGAGAACAT 687
Db 242 TrpIleGlnIleThrMetIysAsnAsn 250
RESULT 11
ABU67098
ID ABU67098 standard; Protein: 250 AA.
XX
AC ABU67098;
XX
DT 27-MAY-2003 (first entry)
XX
DE Human secreted/transmembrane, PRO, protein SEQ ID 506.
XX
KW Human, secreted protein; transmembrane protein; PRO;
inflammatory disease; organ failure; atherosclerosis; cardiac injury;
infertility; birth defects; premature aging; AIDS; biosensor;
acquired immunodeficiency syndrome; cancer; diabetic complication;
bioreactor; tumour.
XX
OS Homo sapiens.
XX
PN US2003032155-A1.
PD 13-FEB-2003.
XX
PF 03-MAY-2002; 2002US-0137865.
XX
PR 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1998; 98WO-US12456.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.

PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 98WO-US25106.
PR 08-MAR-1999; 98WO-US05028.
PR 10-MAR-1999; 98WO-US05190.
PR 20-APR-1999; 98WO-US08615.
PR 14-MAY-1999; 98WO-US10733.
PR 02-JUN-1999; 98WO-US12252.
PR 01-SEP-1999; 98WO-US20111.
PR 08-SEP-1999; 98WO-US20594.
PR 13-SEP-1999; 98WO-US20944.
PR 15-SEP-1999; 98WO-US21090.
PR 15-SEP-1999; 98WO-US21547.
PR 05-OCT-1999; 98WO-US23089.
PR 29-NOV-1999; 98WO-US28214.
PR 30-NOV-1999; 98WO-US28313.
PR 30-NOV-1999; 98WO-US28409.
PR 01-DEC-1999; 98WO-US28301.
PR 01-DEC-1999; 98WO-US28634.
PR 02-DEC-1999; 98WO-US28551.
PR 02-DEC-1999; 98WO-US28564.
PR 02-DEC-1999; 98WO-US28565.
PR 16-DEC-1999; 98WO-US30095.
PR 20-DEC-1999; 98WO-US30911.
PR 20-DEC-1999; 98WO-US30999.
PR 22-DEC-1999; 98WO-US30720.
PR 30-DEC-1999; 98WO-US31243.
PR 30-DEC-1999; 98WO-US31274.
PR 05-JAN-2000; 98WO-US00219.
PR 06-JAN-2000; 98WO-US00277.
PR 11-FEB-2000; 98WO-US00376.
PR 11-FEB-2000; 98WO-US03565.
PR 18-FEB-2000; 98WO-US04341.
PR 18-FEB-2000; 98WO-US04342.
PR 22-FEB-2000; 98WO-US04414.
PR 24-FEB-2000; 98WO-US04914.
PR 24-FEB-2000; 98WO-US05004.
PR 01-MAR-2000; 98WO-US05601.
PR 02-MAR-2000; 98WO-US05746.
PR 02-MAR-2000; 98WO-US05841.
PR 10-MAR-2000; 98WO-US06319.
PR 15-MAR-2000; 98WO-US06884.
PR 20-MAR-2000; 98WO-US07377.
PR 21-MAR-2000; 98WO-US07532.
PR 30-MAR-2000; 98WO-US08439.
PR 17-MAY-2000; 98WO-US13705.
PR 22-MAY-2000; 98WO-US14042.
PR 30-MAY-2000; 98WO-US14941.
PR 02-JUN-2000; 98WO-US15264.
PR 28-JUL-2000; 98WO-US20710.
PR 11-AUG-2000; 98WO-US22031.
PR 23-AUG-2000; 98WO-US23522.
PR 24-AUG-2000; 98WO-US23378.
PR 08-NOV-2000; 98WO-US30952.
PR 10-NOV-2000; 98WO-US30873.
PR 01-DEC-2000; 98WO-US32678.
PR 20-DEC-2000; 98WO-US34956.
PR 28-FEB-2001; 98WO-US06520.
PR 01-MAR-2001; 98WO-US06566.
PR 25-MAY-2001; 98WO-US17082.
PR 01-JUN-2001; 98WO-US17800.
PR 20-JUN-2001; 98WO-US19692.
PR 22-JUN-2001; 98WO-US20116.
PR 29-JUN-2001; 98WO-US21066.
PR 09-JUL-2001; 98WO-US21735.
PR 20-DEC-2000; 98WO-US21735.
PR 20-DEC-2000; 98WO-US21735.

PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001US-0866034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 XX (GENET) GENENTECH INC.
 PA Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR N-PSDB: ACN04276.
 PI WPI: 2003-331925/31.
 PT New secreted and transmembrane nucleic acids and polypeptides,
 PT designated as PRO, useful for treating inflammation, organ failure,
 PT atherosclerosis, cardiac injury, infertility, birth defects, premature
 PT aging, AIDS, or cancer -
 XX
 PS Claim 12; Fig 506; 659pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising, or which is
 CC at least 80% identical to, or the full-length coding sequence of, any of
 CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid
 CC further comprises the full-length coding sequence of the DNA deposited
 CC under American Type Culture Collection (ATCC) accession number in a list
 CC given in the specification. Also included are vectors and host
 CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO
 CC antibodies, PRO extracellular domains and mature sequences, methods
 CC of detecting PRO proteins, methods for stimulating the release of
 CC TNF-alpha (tumour necrosis factor alpha) from human blood,
 CC (and the proliferation of differentiation of chondrocyte cells, the
 CC proliferation of, or gene expression in pericyte cells, the release or
 CC proteoglycans from cartilage, proliferation of inner ear utricular
 CC supporting cells, the proliferation of T-lymphocyte cells, the release
 CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the
 CC proliferation of endothelial cells), a method for modulating the uptake
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
 CC a method for inhibiting the binding of A-peptide to factor VIIA,
 CC or the differentiation of adipocyte cells, a method for detecting the
 CC presence of a tumour in a mammal and an oligonucleotide probe derived
 CC from any of the nucleotide sequences cited above. The nucleic acids and
 CC polypeptides are useful for treating inflammatory diseases, organ
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
 CC diabetic complications. The nucleic acids are useful as hybridisation
 CC probes, in chromosome and gene mapping, and in generating antisense RNA
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
 CC biosensors or bioreactors. Both are useful in tissue typing.
 CC The present sequence represents a PRO protein of the invention.
 XX
 SQ Sequence 250 AA:
 Alignment Scores: 1.4e-94 Length: 250
 Pred. No.: 1258.00 Matches: 229
 Score:

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 98.67% Indels: 0
 DB: 24 Gaps: 0
 US-09-856-320a-1_copy_272_958 (1-687) x ABU67098 (1-250)
 QY 1 ATCATCAAGGGGTGAGTGCAGACCTGACCTCCAGCCGAGGACGCTGTGAG 60
 DB 22 IIEIIEIYSGLYPHEILUCYLSYSPROHISSEGINPTITPGLINIAIALEUPHEG 41
 QY 61 AAGAGCGGCTACTGTGTGGGCGAGCTCATGCGCCCGAGATGCGCTGTGACAGCC 120
 DB 42 LYSTHRTARGLEUCYLSGLYALATHRTLEUIEALPRARGTTPREULEUTHRTAIA 61
 QY 121 CAGTGGCTCAAGCCCGGTACATAGTTCACCGGGGACACAACTCCAGAAAGAGAG 180
 DB 62 HISCYLSLEUYSPTGRTYRTILEVALHISLEUGLYGHNHISASNLEUINLSGLIN 81
 QY 181 GGCTGTGACAGACCCGAGACCCACTGATGCTCCCTCCCGGCTTCAACAGAC 240
 DB 82 GLYCSGLUGINTHTARGHRTALATHRTGUSERPHEPHOHISPTGELYHEASNSER 101
 QY 241 CTCGCCAACAAAGACCCGCAATGACATCATGTGTGAGATGGCATGCCAGTCC 300
 DB 102 LEUPROASNLYASPHISATGASNSPIEMETLEUVALYMETALASERPROVALSER 121
 QY 301 ATCACCCTGGGCTGTGCGACCCCTCACCCCTCTACGCTGTGTACTCTGGCACAC 360
 DB 122 IIEHTTTPALAVATARGPROLEUTHRTLEUSERSERATGYSVALTHRTAGLYTHRSER 141
 QY 361 TGCCTCATTTCCGGCTGGGCGACAGCTCACCCCGCATGTCGCTGCACACCTTG 420
 DB 142 CYSLIEILIESERGLYTPRIPLYSERTHRSESRPROGINLEUARGLEUPROHISTHLEU 161
 QY 421 CGATCGCCCAATCATCATCATGAGCACCGAAGTGTGAGAACGCTTACCCGCGCAAC 480
 DB 162 ARGYSALIASNIETHTRTLEILEGLIHISGLINLYCSGLIASNALATYRPROGLYASN 181
 QY 481 ATCAGACACCATGATGTGTGCCAGCGGACGAGAAAGGGGCAAGACATCTCCAGGT 540
 DB 182 IIEHTASPTHTMETVALCYLSASERVALGINGUGLYLYASPERYSGLINGLY 201
 QY 541 GACTCGGGGGGCGCTGTGCTGTGTAACAGTCTTCAAGGATATCTCTGGGGCCAG 600
 DB 202 ASPSERGLYGLYPROLEUVALCYLSNSNGINSELTGUNGILYILEISERTTPGLGIN 221
 QY 601 GATCGGTGTGATCATCCGGAAGCTGTGTACAGAAAGTGTGCAATATGTGGAC 660
 DB 222 ASPROCYSALAIETHTARGYSPTROGLYVALTYRTHTLYSVALCYLSYSTYVALASP 241
 QY 661 TGGATCCGAGAGCATGAGAACAT 687
 DB 242 TTPLEGLINGLUTHTMETLYSASN 250
 RESULT 12
 ABU59903
 ID ABU59903 standard; Protein: 250 AA.
 XX
 AC ABU59903;
 XX
 DT 13-MAY-2003 (first entry)
 XX
 DE Novel secreted and transmembrane protein PRO1279.
 XX
 KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
 KW cardiac insufficiency disorder; cancer; tumour; immune response;
 KW adrenal cortical capillary endothelial growth; c-fos induction;
 KW vascular endothelial growth factor inhibition; VEGF inhibition;
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
 KW retinal neurons cell survival; rod photoreceptor cell survival;
 KW retinal disorder; retinitis pigmentosa; kidney disorder;
 KW mammalian kidney mesangial cell proliferation; Berger disease;

KW	dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW	chondrocyte redifferentiation; sports injury; arthritis.
XX	
OS	Homo sapiens.
PN	US2003017563-A1.
XX	
PD	23-JAN-2003.
XX	
PF	07-MAY-2002; 2002US-0140808.
XX	
PR	31-MAR-1997; 97MO-US05230.
PR	12-JUN-1998; 98MO-US12456.
PR	14-JUL-1998; 98MO-US14552.
PR	28-AUG-1998; 98MO-US17888.
PR	10-SEP-1998; 98MO-US18824.
PR	14-SEP-1998; 98MO-US19093.
PR	14-SEP-1998; 98MO-US19094.
PR	14-SEP-1998; 98MO-US19177.
PR	16-SEP-1998; 98MO-US19330.
PR	17-SEP-1998; 98MO-US19437.
PR	07-OCT-1998; 98MO-US21141.
PR	29-OCT-1998; 98MO-US22991.
PR	29-OCT-1998; 98MO-US22992.
PR	20-NOV-1998; 98MO-US24855.
PR	01-DEC-1998; 98MO-US25108.
PR	05-JAN-1999; 99MO-US25106.
PR	08-MAR-1999; 99MO-US05028.
PR	10-MAR-1999; 99MO-US05190.
PR	20-APR-1999; 99MO-US06615.
PR	14-MAY-1999; 99MO-US10733.
PR	02-JUN-1999; 99MO-US12252.
PR	01-SEP-1999; 99MO-US20111.
PR	08-SEP-1999; 99MO-US20594.
PR	13-SEP-1999; 99MO-US20944.
PR	15-SEP-1999; 99MO-US21090.
PR	15-SEP-1999; 99MO-US21447.
PR	05-OCT-1999; 99MO-US23089.
PR	29-NOV-1999; 99MO-US28214.
PR	30-NOV-1999; 99MO-US28313.
PR	30-NOV-1999; 99MO-US28409.
PR	01-DEC-1999; 99MO-US28301.
PR	01-DEC-1999; 99MO-US28634.
PR	02-DEC-1999; 99MO-US28551.
PR	02-DEC-1999; 99MO-US28654.
PR	02-DEC-1999; 99MO-US28655.
PR	16-DEC-1999; 99MO-US30095.
PR	20-DEC-1999; 99MO-US30911.
PR	20-DEC-1999; 99MO-US30999.
PR	22-DEC-1999; 99MO-US30720.
PR	30-DEC-1999; 99MO-US31243.
PR	30-DEC-1999; 99MO-US31274.
PR	05-JAN-2000; 2000MO-US00219.
PR	06-JAN-2000; 2000MO-US00277.
PR	06-JAN-2000; 2000MO-US00376.
PR	11-FEB-2000; 2000MO-US03565.
PR	18-FEB-2000; 2000MO-US04341.
PR	18-FEB-2000; 2000MO-US04342.
PR	22-FEB-2000; 2000MO-US04414.
PR	24-FEB-2000; 2000MO-US04414.
PR	24-FEB-2000; 2000MO-US05004.
PR	01-MAR-2000; 2000MO-US05601.
PR	02-MAR-2000; 2000MO-US05746.
PR	02-MAR-2000; 2000MO-US05841.
PR	10-MAR-2000; 2000MO-US06319.
PR	15-MAR-2000; 2000MO-US06884.
PR	20-MAR-2000; 2000MO-US07377.
PR	21-MAR-2000; 2000MO-US07532.
PR	30-MAR-2000; 2000MO-US08439.
PR	17-MAY-2000; 2000MO-US13705.
PR	22-MAY-2000; 2000MO-US14042.
PR	30-MAY-2000; 2000MO-US14941.
PR	02-JUN-2000; 2000MO-US15264.

PR 28-JUL-2000; 2000WO-US02710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06656.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882536.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.

XX
PA (GETH) GENENTECH INC.
XX

PI Baker KP, Bersini M, DeForge L, Desnoyers L, Flivaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gunney AL, Sherwood S;
PI Smith V, Stewart FA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX

DR WPI: 2003-148238/14.
DR N-PSDB: ABX89393.
XX

PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments -
XX

PS Claim 12; Fig 506; 659pp; English.
PS XX

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186 stimulate adrenal cortical capillary endothelial growth, and PRO536, PRO943, PRO828, PRO826 or PRO535, PRO826, PRO819, PRO1126, PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating cancers tumors. PRO812 inhibits vascular endothelial growth factor (VEGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth in mammals which would be beneficial in inhibiting tumour growth. PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune response. PRO828, PRO826, PRO1068 or PRO1312 enhance survival of retinal neurons cells (PRO1312 is also enhances survival/proliferation of

rod photoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinitis pigmentosum, AMD, PRO819, PRO813 and PRO1066 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpeticiformis or Crohn's disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This is the amino acid sequence of a novel human PRO protein.

Sequence 250 AA:

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score: 1.4e-94	250	1258, 00	229	0	0	0
Percent Similarity: 100.00%						
Best Local Similarity: 100.00%						
Query Match: 98.67%						
DB: 24						

US-09-856-320A-1_COPY_272_958 (1-687) x ABUS59903 (1-250)

```

QY 1 ATCATCAGAGGGGTTCGAGTGCAGAGCCTCCTCCAGCCCTGGCAGGACCCCTGTTCCAG 60
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 22 ILEILEYSGLYPHEGLUCYSYSPRONHISSEKINPRTGRLALALALEUPHEGLN 41
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 AAGACGGCGCTACTGTGGGCGAGCGCTCATCGGCCAGATGGCTGCTGCAGAGGCC 120
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 42 LYSTHRAGLLEULEUCSGLYALATHRIEULLEIALAPROALGTRPLEULATHRIALALA 61
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 CACTGCTCAGAGCCCGCTACATAGTCACTGGGCGAGCAGACACCTCCAGAGAGAG 180
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 62 HISCYSLEULYSPROALGTYRILEVALHISLEUGLHNHISASLEULNLSYSGULGN 81
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 181 GGCTGTGAGCAGACCCGGGAGCAGCTGAGTCTCCCGCCCGGGCTCAACAAGAC 240
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 82 GLYCSGLGNLTHRAHTRHATHRGLUSERPHEPRONHISPRGILYPHENASNSER 101
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 241 CTCGCCAACAAGACACCCGCAATGACATCATGTGTGTGAGATGGCATCGCCAGTCTCC 300
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 102 LEUPROANLYASPHISARGSNASPRILEMELLEVALLYMETALASERPROVALSER 121
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 301 ATCATCCTGGGCTGTCGACCCCTCACCCTCTCTACAGCTGTGTCTACATGCTGGCAGCAGC 360
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 122 ILEHTRTPALAVALAARGPROLEUTHRIEUSERSERATGYSVALTHRALAGLYHTRSER 141
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 361 TGCCCATTTCCGGCTGGGGGAGCAGCTGCCAGCCCGGTTACGCTGCTTCACACCTTG 420
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 142 CYSLEULLESERGLYTRPGLYSERHTRSERPROGLNLEUARYLEUPROHISTHRIEU 161
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 421 CGATCGGCCAATCATCATCATCATGAGCAGCAGAGTGTGAGAAAGCCATCCCGGCAAC 480
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 152 ARGYSALASANLLEHTRILELEGLHNHISGLNLSYSGILNASHALATYRPROGLYSN 181
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 481 ATCAGACAGACCCAGTGTGTGCCAGCTGCGAGAGAGGGGGGAGAGACTCTGCCAGGGT 540
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 182 ILEHTRASPETHMETVALCYSALASERVALINGLNGLYGLYASPERCYSGINGLY 201
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 541 GACCTCGGGGGGCGCTGTGTGTGTAACAGATCTCTTCAAGGATATATCTCCGGGGCCAG 600
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 202 ASPSERGLYGLYPROLEUVALCYSASNGLNLSERLEUNGINGLYILELESERTPRGLYN 221
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 601 GATCGGTGTGCATACCCGGAAGCCTGTCTACAGAGAGTGTGCAATATGAGGAG 660
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 222 ASPPROCYSAIAIILEHTRARGLYSPROGLYVALITYRTHLYSVALCYALSYSTYRVALASP 241
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 661 TGGATTCAGGAGACGATGAAGAACAAT 687
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 242 TRPILEGINGLUTHRMETYLSASNASN 250
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 13
ABUS6739

ID ABUS6739 standard; Protein; 250 AA.
XX
AC ABUS6739;
XX
DT 02-APR-2003 (first entry)
XX
XX Lung cancer-associated polypeptide #332.
XX
DE Lung cancer-associated polypeptide; cytosolic; emphysema;
XX
XX anti-inflammatory; antiasthmatic; non-small cell lung cancer;
XX
XX small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
XX
XX chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
XX
XX interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
XX Unidentified.
XX
OS WO200286443-A2.
XX
PN 31-OCT-2002.
XX
PD 18-APR-2002; 2002WC-US12476.
XX
PF 10-MAY-2001; 2001US-284770P.
XX
PR 09-NOV-2001; 2001US-390492P.
XX
PR 13-NOV-2001; 2001US-339245P.
XX
PR 29-NOV-2001; 2001US-350666P.
XX
PR 12-APR-2002; 2002US-372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Aziz N, Murray R;
XX
DR WPI: 2003-093161/08.
XX
DR N-PSDB; ABX76468.
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
XX
PT for treating lung cancer, by contacting a biological sample from the
XX
PT patient with a polynucleotide that exhibits increased or decreased
XX
XX expression in lung cancer -
XX
PS Claim 27; Page 443-444; 453pp; English.
XX
XX The invention relates to a method for detecting a lung cancer-associated
XX
XX transcript in a cell from a patient, comprising contacting a biological
XX
XX sample from the patient with a polynucleotide that selectively hybridises
XX
XX to a sequence that is at least 80 % identical to a gene that exhibits
XX
XX increased or decreased expression in lung cancer samples. Lung
XX
XX cancer-associated polynucleotides and polypeptides are used for
XX
XX identifying a compound that modulates a lung cancer-associated
XX
XX polypeptide, for inhibiting proliferation of a lung cancer-associated
XX
XX cell to treat lung cancer in a patient and for treating a mammal having
XX
XX lung cancer by administering a modulatory compound identified. The
XX
XX methods are useful for treating lung cancer, such as small cell lung
XX
XX cancer, non-small cell lung cancer or other benign or precancerous
XX
XX lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
XX
XX pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
XX
XX pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides
XX
XX and polypeptides are useful for diagnostic purposes and as targets for
XX
XX screening for therapeutic compounds that modulate lung cancer, such as
XX
XX antibodies. Sequences ABUS6408-ABUS6745 represent lung cancer-associated
XX
XX polypeptides of the invention.

SO Sequence 250 AA:

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
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Best Local Similarity: 100.00%						
Query Match: 98.67%						
DB: 24						

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QY 61 AAGACGGGGCTACTCTGTGGGGGACGCTATGCCGCCCAAGATGGCTCTGACAGCACC 120
Db 42 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThrAlaAla 61
QY 121 CACTGCTCAAGCCCGCTACATGATTCACCTGGGGGACGACCACTCCAGAGAGAG 180
Db 62 HisCysLeuLeuysProArgTrpIleValHisLeuIleGlnHisAsnLeuGlnlysglu 81
QY 181 GCGTGTAGCAGACAGCCCGGACAGCCAGTCACTCTCCGCCCAAGCCGCTTCAACAGC 240
Db 82 GlyysgluglnThrArgThrAlaThrGlySerPheProhIsProGlyPheAsnAsnSer 101
QY 241 CTCCCAACAAAGACCCGCAATGACATGATGCTGTGGAAGATGGGATGCCAGTCTCC 300
Db 102 LeuProAsnlysaSPHIsArgAsnAspIleMetLeuVallysaMetAlaSerProValSer 121
QY 301 ATCACTGGGCTGTGCAGCCCTCACTCCCTGCTGACGCTGTGACGCTGGCAGCAGC 360
Db 122 IleThrTrpAlaValAlaGProleuThrLeuSerSerArgCysValThrAlaGlyThrSer 141
QY 361 TGCCCTCAATTCGCGCTGGGGGACAGCAGTCCAGCCCGAGTTACGCTGTCCACACCTTG 420
Db 142 CysleuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProhIsThrLeu 161
QY 421 CGATGCGCCCAACATCACCATTGAGCACCAGCAAGTGTGGAAGCGCTACCCCGGCAC 480
Db 162 ArgCysAlaAsnIleThrIleLeuGlnHisGlnlysaAsnAlaTyProGlyAsn 181
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Db 182 IleThrAspThrMetValCysAlaSerValGlnIleGlylysaSPserCysGlnly 201
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QY 661 TGGATCCAGAGAGAGATGAAGAACAT 687
Db 242 TrpIleGlnIlyThrMetlysaAsnAsn 250
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AC AAV42439;
XX
DT 08-DEC-1999 (first entry)
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DE CASB12 amino acid sequence.
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KM neuropsin; cancer; assay; inhibitor; serine protease; immunogenic;
KM autoimmune disease.
XX
OS Homo sapiens.
XX
PN M09949055-A1.
XX
PD 30-SEP-1999.
XX
PF 17-MAR-1999; 99W0-EP01894.
XX
PR 20-MAR-1998; 98GB-0006095.
XX

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PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Bruck CEM, Cassart J, Coche T, Vinals-bassols C;
XX
DR WPI: 1999-580450/49.
XX
DR N-PSDB: AAZ22638.
XX
FT New human serine protease CASB12, for treatment, prevention and
PT diagnosis of cancer and autoimmune diseases
XX
PS Claim 3; Page 48; 58pp; English.
XX
CC This is the amino acid sequence of the CASB12 protein. The nucleotide
CC sequence of AAZ22638 shows homology with neuropsin and the encoded
CC protein AAV42439 is structurally related to other proteins of the
CC serine protease family, having homology and/or structural similarity
CC with neuropsin. It is expected that as well as similar structure, these
CC proteins will also share similar biological functions and properties.
CC The CASB12 polypeptides and polynucleotides can be used to develop
CC methods for identifying agonists and antagonists/inhibitors of these
CC molecules, and thereby treating conditions associated with CASB12
CC polypeptide imbalance. The invention also provides for diagnostic assays
CC for detecting diseases associated with inappropriate CASB12 polypeptide
CC activity or levels.
CC Since CASB12 is either specifically expressed or highly over-expressed
CC in tumors compared to normal cells, the polypeptides and polynucleotides
CC of the invention are believed to be important immunogens for specific
CC prophylactic or therapeutic immunization against tumors. The
CC polypeptides and polynucleotides can therefore be targeted by antigen
CC specific immune reactions (which result in the destruction of the tumor
CC cell) or they can be used to diagnose the occurrence of tumor cells
XX
SQ Sequence 282 AA;
XX
Alignment Scores:
Pred. No.: 1,43e-94 Length: 282
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.67% Indels: 0
DB: Gaps: 0
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QY 61 AAGACGGGGCTACTCTGTGGGGGACGCTATGCCGCCCAAGATGGCTCTGACAGCACC 120
Db 74 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThrAlaAla 93
QY 121 CACTGCTCAAGCCCGCTACATGATTCACCTGGGGGACGACCACTCCAGAGAGAG 180
Db 94 HisCysLeuLeuysProArgTrpIleValHisLeuIleGlnHisAsnLeuGlnlysglu 113
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QY 421 CGATGCGCCCAACATCACCATTGAGCACCAGCAAGTGTGGAAGCGCTACCCCGGCAC 480

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QY 661 TGGATCCAGAGACGATGAAGAACAT 687
Db 274 TrpIleGlnGluThrMetIysAsnAsn 282

RESULT 15
AAB11712
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XX
AC AAB11712;
XX
DT 23-OCT-2000 (first entry)
XX
DE Human serine protease BSSP6 (hbSSP6) SEQ ID NO:2.
XX
KW BSSP6; serine protease; human; hbSSP6; mouse; mBSSP6; brain;
KW diagnostic marker; antibody; transgenic animal; Alzheimer's disease;
KW epilepsy; cancer; inflammation; infertility; pancreatitis;
KW prostatic hypertrophy.
XX
OS Homo sapiens.
XX
PN WO200031257-A1.
PD 02-JUN-2000.
XX
PF 19-NOV-1999; 99WO-JP06476.
XX
PR 20-NOV-1998; 98JP-0347802.
XX
PA (FUSO ) FUSO PHARM IND LTD.
XX
PI Uemura H, Okui A, Komihama K, Yamaguchi N, Mitsui S;
XX
DR MPI: 2000-400067/34.
DR N-PSDB: AAA61763.
XX
XX
PT Serine protease BSSP6, useful in detecting homologs, mutants and
PT polymorphic variants as markers for diagnosis of Alzheimer's disease,
PT epilepsy, cancer, inflammation, infertility and prostate hypertrophy,
PT using blood or other tissues.
XX
PS Claim 1; Page 69-70; 94pp; Japanese.
XX
XX
CC The invention relates to novel serine proteases designated BSSP6
CC (AAB11712-111714), and to nucleic acids encoding them (AAA61763-61765).
CC The invention also relates to vectors and transformants comprising BSSP6
CC nucleic acids; transgenic animals in which the expression level of BSSP6
CC can be varied; and an mBSSP6 knockout mouse. The invention additionally
CC encompasses anti-BSSP6 antibodies and methods of production of such
CC antibodies, methods of BSSP6 detection using the antibodies, and the
CC use of BSSP6 proteins or fragments as diagnostic markers for certain
CC medical conditions. Nucleotides encoding BSSP6 were initially
CC isolated in a human brain cDNA library using degenerate PCR primers
CC (AAA61795-61796) based on conserved regions of serine proteases. The
CC BSSP6 serine proteases and nucleotides encoding them are useful in
CC detecting homologues, mutants and polymorphic variants in biological
CC samples (e.g., blood, urine, brain, prostate gland, placenta, testis
CC and spleen) as diagnostic markers for conditions such as Alzheimer's

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CC disease, epilepsy, cancer, inflammation, infertility and prostatic
CC hypertrophy. Sequences AAB11712 and AAB11714 represent human BSSP6
CC variants (hbSSP6), and sequence AAB11713 represents murine BSSP6
CC (mBSSP6).
XX
SQ Sequence 282 AA;
XX
Alignment Scores:
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Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Db 74 LysThrArgLeuLeuGlyAlaThrIleIleIleIleIleIleIleIleIleIleIleIleIle 93
QY 121 CACTGCTCAAGCCCGCTACATATGTTCACTTGGGGGAGCAGCAACCTCCAGAGAGAG 180
Db 94 HIsCysLeuIysProArgTrgIleValHISleuGlyGlnHISAsnleuGlnIysGluGln 113
QY 181 GGCTGTGAGCAGACCCGGAGACGCACTAGTCTTCCCGCCCGGCTTCAACAACAGC 240
Db 114 GlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHISProGlyPheAsnAsnSer 133
QY 241 CTCGCCCAACAAGACACCGCAATGACATCATGCTGTGAAGATGGCATCGCCAGTCTCC 300
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QY 601 GATCCGTGTGCATCACCAGAAAGCTGTGTACAGCAAAAGTCTGCAAAATGTGGAC 660
Db 254 AspProCysAlaIleThrArgIysProGlyValIlyThrIlyValCysIlystyValAsp 273
QY 661 TGGATCCAGAGACGATGAAGAACAT 687
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

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and is derived by analysis of the total score distribution.

SUMMARIES

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4	1219.5	95.6	289	4	US-09-386-642-14
5	1182	92.7	228	4	US-09-205-258-1150
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7	884	53.6	260	3	US-09-025-059-3
8	681	53.4	260	3	US-09-070-526-2
9	673	52.8	260	3	US-09-008-271A-7
10	674.5	52.7	288	4	US-09-386-642-13
11	644.5	50.5	293	4	US-09-996-243-309
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17	591.5	46.4	263	3	US-08-807-151-5	Sequence 5, Appl1
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23	577.5	45.3	237	3	US-08-767-820A-16	Sequence 16, Appl1
24	577.5	45.3	237	3	US-08-622-046B-12	Sequence 12, Appl1
25	577.5	45.3	237	3	US-08-944-483-37	Sequence 37, Appl1
26	577.5	45.3	237	3	US-09-100-264-1	Sequence 1, Appl1
27	577.5	45.3	237	4	US-08-843-076D-1	Sequence 1, Appl1
28	577.5	45.3	238	4	US-08-768-859A-8	Sequence 8, Appl1
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ALIGNMENTS

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Patent No. 6525174
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APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
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EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
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ORGANISM: Homo sapiens
US-09-205-258-427

Alignment Scores:
Pred. No.: 2,82e-105 Length: 250
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.67% Indels: 0
DB: 4 Gaps: 0

US-09-856-320a-1_copy_272_958 (1-687) x US-09-205-258-427 (1-250)
QY 1 ATCATCAAGGGGCTCGAGTGCACGCTCCAGCCCTGCGAGGAGCCCTGTTCGAG 60

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Db 22 IleIleIysgIyPhegIuCySAlYsPProHIsSerInPProIrgInAlaAlaLeuPheglu 41
QY 61 AAGAGCGGCTACTCTGTGGGGCGACGCTCTCCGCCAGATGGCTCTGCAGCAGCC 120
|||||
Db 42 LysThrArgLeuLeuCySgIyAlaThrLeuIleAlaProArgIyPheLeuThrAlaAla 61
QY 121 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGCGACCAACTCTCCAGAGAGAG 180
Db 62 HisCySLeuIySProArgIyTlleValHisLeuGlyInHisAsnLeuGlnIySglu 81
QY 181 GCGTGTAGCAGACCCGCGACGACGCTAGTCTTCCGCCACCCCGGCTTAACAACAGC 240
Db 82 GlyCySgluGlnThrAlaThrAlaThrLeuSerPheProHisProGlyPheAsnAsnSer 101
QY 241 CTCCCAACAAGACACACCCGATGACATCTGCTGGTGAAGATGGCATGCCAGTCC 300
Db 102 LeuProAsnIySAspHisArgAsnAspIleMetLeuValIySMeAlaIaSerProValSer 121
QY 301 ATCACTGGGCTGTGCGACCCCTCACCCTCTCCACGCTGTCTACTGTGCGACGAGC 360
Db 122 IlleThrTrpAlaValAlaArgProLeuThrLeuSerSerArgCySValThrAlaGlyThrSer 141
QY 361 TGCCTCATTTCCGGCTGGGGCGACGCTCCAGCCGCCAGTACGCTCTGCACACTTG 420
Db 142 CySLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 161
QY 421 CGATGCGGCAATCACCACCATTCATGACGACGACGAGAGTGTGAGACGCTACCCGCGAGC 480
Db 162 ArgCySAlaAsnIleThrIleIleGlnHisGlnIySgIuAsnAlaIyTrpGlyAsn 181
QY 481 ATCAACAGACACCATGTGTGTGTGCCAGGTGCGAGAGAGGGGGCGACACTCTGCCAGGT 540
Db 182 IlleThrAspThrMetValCySAlaSerValGlnGlnIyGlyIySAspSerCySglnGly 201
QY 541 GACTCGGGGGCGCTGTGCTGTACACAGCTCTTAAGGCAATATCTCTGGGGCGAG 600
Db 202 AsperGlyGlyProLeuValCySAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 221
QY 601 GATCCGTGTGCGATCACCCGAAAGCTGTGTCTACAGAAAGTCTGCAATATGTGGAG 660
Db 222 AspProCySAlaIleThrArgIySProGlyValIyThrIySValCySlySlyValAsp 241
QY 661 TGGATCCAGGAGACGATGAGACAAAT 687
Db 242 TrpIleGlnIyThrMetIySAsnAsn 250

RESULT 2
US-09-025-059-1
Sequence 1, Application US/09025059
Patent No. 6075136
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,059
FILING DATE:
CLASSIFICATION:

QY 61 AAGAGGGGCTACTCTGTGGGGGAGCGCTCATCCGCCAGATGGCTTCAGACAGACC 120
DB 40 LysThrArgLeuLeuCysGlyAlaThrLeuLeaLProArgTrpLeuLeuThrAlaIa 59
QY 121 CACTGCGCTCAAGCCCCGCTACATAGTTCACCTGGGGGAGCAGCAACCTCCAGAGAGAG 180
DB 60 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGln 79
QY 181 GCGTGTAGAGCAGACCCGAGCAGCCAGCTAGTCTCCGCCAGCCGCGCTTCAACAGAGC 240
DB 80 GlyArgGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 99
QY 241 CTCCCAACAAGACACACCGCAATGACATCATGCTGGTGAAGATGGAGCGCCAGTCTCC 300
DB 100 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 119
QY 301 ATCCAGTGGGCTGGGAGCCGCTACGCTCCCTCAGCTGTGTCATGCTGGGAGCAGC 360
DB 120 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 139
QY 361 TGCCCTCATTTCCGGCTGGGGAGCAGCGTCCAGCCCGATACGCTGCTCAGACCGTGG 420
DB 140 CysLeuLeuSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 159
QY 421 CGATGGCCCAACATCACCATCATGAGCACCAGAAAGTGTGAAAGCCCTACCCGCGAAC 480
DB 160 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTrpProGlyAsn 179
QY 481 ATCCAGACACCATGAGTGTGGTGGAGCGTGGAGAGAGGGGAGGAGTCTGGCAGAGT 540
DB 180 IleThrAspThrMetValCysAlaSerValGlnGlyLysAspSerCysGlnGly 199
QY 541 GACTCCGGGGCCCTGTGCTGTACACAGTCTCTCAAGGCAATATCTCTGGGGGAGC 600
DB 200 AsperGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 219
QY 601 GATCCGTGTGCGATCACCAGGAGCTGGTGTCTACAGAAAGTCTGCAATATGTGAC 660
DB 220 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTyValAsp 239
QY 661 TGGATCCAGAGACGATGAGAAACAAT 687
DB 240 TrpIleGlnGlnThrMetLysAsnAsn 248
RESULT 4
US-09-386-642-14
Sequence 14, Application US/09386642
Patent No. 6420157
GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jensen
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 289
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
US-09-386-642-14
Alignment Scores:
Pred. No.: 8,42e-102 Length: 289
Score: 1219.50 Matches: 223
Percent Similarity: 98.26% Conservative: 3
Best Local Similarity: 96.96% Mismatches: 3

Query Match: 95.65% Indels: 1
DB: 4 Gaps: 1
US-09-856-320a-1_copy_272_958 (1-687) x US-09-386-642-14 (1-289)
QY 1 ATCATCAAGGGGTTTCAGATGC--AAGCTTACTCCAGCCCTGGAGGAGCCCTTTC 57
DB 52 ILeValGlyGlyTrpAlaCysLeuGlnLysHisSerGlnProTrpGlnAlaIleAlaPhe 71
QY 58 GAGAGAGAGCGGCTACTGTGGGGGAGCGCTACGCGCCAGATGGCTTCAGACGA 117
DB 72 GlnLysThrArgLeuLeuCysGlyAlaThrLeuLeaLProArgTrpLeuLeuThrAla 91
QY 118 GCCCATGCTCTCAAGCCCCGCTACATAGTTCACCTGGGGGAGCAGCAACCTCCAGAGAG 177
DB 92 AlaHisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGln 111
QY 178 GAGGGCTGTAGAGCAGACCCGAGCAGCCAGCTAGTTCCTCCCGCCGCTTACACAC 237
DB 112 GlnLysCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsn 131
QY 238 AGCCTCCCAACAAGACACACCGCAATGACATCATGCTGGTGAAGATGGAGTGGCAGTC 297
DB 132 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 151
QY 298 TCCATCAGCTGGGCTGTGCGACCCCTCAGCTCTCTCAGCTGTGTCATGCTGGCAGC 357
DB 152 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 171
QY 358 AGCTGCTCATTTCCGGCTGGGGAGCAGACGTCACAGCCCGCAATGAGCTGCTCAGACC 417
DB 172 SerCysLeuLeuSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 191
QY 418 TTGGAGTGGCGCAACATCACCATCATGAGCAGCAGAAAGTGTGAAAGCCCTACCCGAGC 477
DB 192 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTrpProGly 211
QY 478 AACATCAGACACCATGAGTGTGTGCGACGCTGCGAGAGAGGGGAGGAGCAAGCTCTGCGAC 537
DB 212 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 231
QY 538 GGTGATCCGGGGCCCTGTGCTGTACACAGTCTCTCAAGGCAATATCTCTGGGGC 597
DB 232 GlnAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 251
QY 598 CAGATCCGTGTGCGATCACCAGGAGCTGGTGTCTACAGAAAGTCTGCAATATGTG 657
DB 252 GlnAspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTyVal 271
QY 658 GACTGATCCAGAGACGATGAGAAACAAT 687
DB 272 AspTrpIleGlnGlnThrMetLysAsnAsn 281
RESULT 5
US-09-205-258-1150
Sequence 1150, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
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EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1150

LENGTH: 228
TYPE: PRT
ORGANISM: Homo sapiens
US-09-205-258-1150
Alignment Scores:
Pred. No.: 1,89e-98
Score: 1182.00
Percent Similarity: 98.67%
Best Local Similarity: 98.67%
Query Match: 92.71%
DB: 4
Gaps: 0
US-09-856-320a-1_copy_272_958 (1-687) x US-09-205-258-1150 (1-228)
QY 1 ATCATCAAGGGGTTGAGTGCAGACCTCACTCCAGCCCTGGAGGAGCCCTGTTGAG 60
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DB 4 TlelllellySGlypnelelucylslylsleuHlsSerGlnProtpRlnlaaleupneglu 23
QY 61 AAGACGGGCTACTCTGTGGGGGAGCCGTCATCGCCAGATGCTCTGACGACGCC 120
|||||
DB 24 LysThrArgLeuLeucylsGlyAlaThrIleuIleAlaProAlgrTrpLeuThrAlaAla 43
QY 121 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGCGAGACACAACTCCAGAGAGAG 180
|||||
DB 44 HlscylleuHlsProAlgrTylrIleValHlsleuGlyGlnHlsasneleuGlnslglu 63
QY 181 GGCTGTGACAGACCCGAGCCGAGCCACTGAGTCTTCCGCCCGGCTTCACACAGC 240
|||||
DB 64 GlycylslgluHlnThrAlgrThrAlaThrGlnSerPheProHlsProAlgrPheasnsSer 83
QY 241 CTCGCCCAAGACCCAGCCGCAATGACATCATCTGTGAAGATGCGATCGCAGTCTCC 300
|||||
DB 84 LeuProAsnHlsAspHlsArgAsnAspIleMetLeuValHlsMetAlaSerProValSer 103
QY 301 ATCACTGGGCTGTGCGACCCCTCACCTCTCTCAAGCTGTGTCACTGCGACACAGC 360
|||||
DB 104 lletHrTrpAlaValArProleuThrLeuSerSerArgCysValThrAlaGlyThrSer 123
QY 361 TGCCCTCATTCGCGGCTGGGGGAGACAGCTCAGCCCGCCAGCTGCTGCTCACACTTG 420
|||||
DB 124 Cys-SerPheProAlaGlyAlaAlaArgProAspProSerTyrAlaCysleuThrProC 143
QY 421 CGATGCGCAACATCAATCATATGAGCAGCAAGATGTGAGAAAGCCCTACCCGGGCAAC 480
|||||
DB 143 sasAlaProHlnSerProSerleuSerThrArgSerValArgThrProHlnProAlaH 163
QY 481 ATCAGAGACACATGCTGTGTGCGACGCTGCGAGAGAGGGGCGAAGGACTCTGCCAGGCT 540
|||||
DB 163 rSerGlnHlnProTrpCysValProAlaCysArgIlyslAlaArgThrProAlaArgVa 183
QY 541 GACTCGGGGGGCGCTGTGTGTATACAGTCTCTCAAGGATTTCTCGGGGGCCAG 600
|||||
DB 183 llnHrProGlyAlaIleuTrpSerValThrSerleuPheHlsAlaIleuSerProGlyAlaAr 203
QY 601 GATCGCTGTGCGATCACCCGAAAGCCTGTGTCTACACCAAGTCTGCAATATGTGAGC 660
|||||
DB 203 glleArGValArgSerProGlnSerleuValSerThrArgIlysserAlaAsnMetTrpH 223
QY 661 TGGATCCAGAGACCA 676
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DB 223 rGlySerArgArgArg 228
RESULT 6
US-09-205-258-1149
Sequence 1149, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04

EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
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EARLIER APPLICATION NUMBER: 60/048,896
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EARLIER APPLICATION NUMBER: 60/049,020
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EARLIER APPLICATION NUMBER: 60/048,876
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EARLIER APPLICATION NUMBER: 60/048,892
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EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
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EARLIER APPLICATION NUMBER: 60/048,963
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EARLIER APPLICATION NUMBER: 60/048,877
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EARLIER APPLICATION NUMBER: 60/048,878

EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1149
LENGTH: 246
TYPE: PRF
ORGANISM: Homo sapiens
US-09-205-258-1149
Alignment Scores:
Pred. No.: 1,92e-98 Length: 246
Score: 1182.00 Matches: 223
Percent Similarity: 98.67% Conservative: 0
Best Local Similarity: 98.67% Mismatches: 2
Query Match: 92.71% Indels: 1
DB: 4 Gaps: 0
US-09-856-320a-1_COPY_272_958 (1-687) x US-09-205-258-1149 (1-246)
QY 1 ATCATCAGGGGGTTCGAGTGCAGAGCTCCAGCCCTGGAGGAGCCCTGTCGAG 60
DB 22 IletlleysglypnehlucyslyleuhsierglnprptgrlnalalaLeupheglu 41
QY 61 AAGAGGGGGTACCTGTGGGGGAGGAGCTGACCCCAAGATGGCTTCAGAGAGCC 120
DB 42 Lysthrtrglyleuucysglyalathrlleuilelproalgrtprleuethrlala 61
QY 121 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGAGAGCACAACCTCCAGAGAG 180
DB 62 Hiscysleuysproalgrtyrllevalhlsleuclglnhlsanleuclnglucgu 81
QY 181 GCGTGTGAGCAGACCCGAGCAGCCAGTGAAGTCTTCCCCACCCGGCTTACACAGC 240
DB 82 Glycysgluglntrargthralathrlgluserphepromlsprogllypheasnnsr 101
QY 241 CTCCCAAGAACCCGCAATGACATGATGCTGGTGAAGATGGATGCCAGTCTCC 300
DB 102 LeuproasnlysaBPhlsargasnaspIleleuvallyskelalaserprovalser 121
QY 301 ATCAGCTGGGCTGTGCACCCCTGCACCTCTCTCAGCTGTGTACCTGTGCAGCAGC 360
DB 122 IletthrtrpalaValargproleuthrlleuserserargysvalthrAlaglythSer 141
QY 361 TGCTCATTTCCGGCTGGGGCAGCAGCTCCAGCCCAAGTTAGCCTGCTCAGACCTG 420
DB 142 Cys-SerpheprolaaglyalaalaargproaspProserlyralCysleuethrProcy 161
QY 421 CGATGGCGCAACATCATCATGAGCAGCAGAGTGTGAGAGCGCTACCCGGGCAAC 480
DB 161 sasAlaProthrserProserleuserthrlargsetValargthrProthrProalath 181
QY 481 ATCAGACACCATGTGTGTGCCAGCTGCAGAGAGGGGGCAAGAGCTCTGCCAGGT 540
DB 181 rserglnthrProthrpyValproalacysarglyglYalargthrProalargva 201
QY 541 GACTCCGGGGCCCTGTGGTCTGTAAACAGTCTTTCAAGGCATTATCTCTGGGGCAG 600
DB 201 lThrProglyAlaleuThrpservalThrSerleuPhelyslaleuSerProglyAlaar 221
QY 601 GATCCGTGGTGGATCACCCGAAAGCTGTGTCTACAGGAAGCTCAATATGTGAGC 660
DB 221 gllargValargserProgluserleuValserThrarglyseralasnethrpin 241
QY 661 TGGATCCAGAGAGCA 676
DB 241 rglYSerargArgarg 246


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-070-526-2

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Alignment Scores:
Pred. No.: 2,19e-53 Length: 260
Score: 681.00 Matches: 116
Percent Similarity: 70.54% Conservative: 42
Best Local Similarity: 51.79% Mismatches: 64
Query Match: 53.41% Indels: 2
DB: Gaps: 2

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US-09-856-320A-1_COPY_272_958 (1-687) x US-09-070-526-2 (1-260)

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DB 33 ValIeuD1yL1nH1sG1uCySg1nPr0H1sSerG1nPr0TrpG1nAla1aLeuPhg1n 52
    :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 61 AAGACGGGCTACTCTGTGGGGGAGCGCTCATCGCCCGCCAGATGGCTTCGACAGACC 120
    :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB 53 G1yG1nG1nLeuEuCySg1yG1yValLeuValG1yG1yAsnTrpValLeuThrAla1a 72
    :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 121 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGCAGCACAACCTCCAGAGAGAG 180
    ||||| |||||:::|||||:::|||||:::|||||:::|||||:::
DB 73 H1sCyS1yS1ySPr0LyS1yTrH1ValArgLeuG1yAspH1sSerLeuG1nAsnLySAsp 92
    ||||| |||||:::|||||:::|||||:::|||||:::|||||:::
QY 181 GGCTGTAGCAGACCCGAGACGACCATGAGTCTTCCCGCCCGGCTTCACACAGC 240
    ||| |||||:::|||||:::|||||:::|||||:::|||||:::
DB 93 G1yPr0G1nG1nLeu1n1ePr0Val1aG1nSer1ePr0H1sPr0CyS1yAsnSer 112
    ||| |||||:::|||||:::|||||:::|||||:::|||||:::
QY 241 CTCGCCAACAAGACACGCAATGACATCATGCTGTGAAGATGCATGCCAGTCTCC 300
    :::|||||:::|||||:::|||||:::|||||:::|||||:::
DB 113 ---AspValG1uAspH1sAsnH1sAspLeuMetLeuG1nLeuArgAspG1nAla1Ser 131
    :::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 301 ATCACTGGGCTGTGCACCCCTCACCCTCTCTCAGCGTGTCTACTGTGCAGCAGC 360
    :::|||||:::|||||:::|||||:::|||||:::|||||:::
DB 132 LeuG1ySer1yVal1yS1ySPr0L1eSer1eLeuAlaAspH1sCyS1yTrH1nPr0G1yG1n 151
    :::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 361 TGGCTGCTTTCGGGGGGGAGCAGAGCTGACGCCCCAGTTAGCCCTCCAGACCTTG 420
    ||| :::|||||:::|||||:::|||||:::|||||:::|||||:::
DB 152 CysThrValSerG1yTrpG1yTrH1ValTrH1SerPr0Arg1uAsnPr0AspTrH1Leu 171
    :::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 421 CGATGGCCCAACATCACCATATTGAGACCAACAGAGTGTGAAGCGCTCAGCCGAGC 480
    ||||| :::|||||:::|||||:::|||||:::|||||:::|||||:::
DB 172 AsnCyS1aG1uVal1yS1yTrH1ePr0G1nLyS1ySg1uAspAla1yTrp0G1yG1n 191
    :::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 481 ATCAGACACACATGTGTGTGCCAGCGTGCAGAGAGGGGCAAGACCTCTGCCAGG 540
    ||||| |||||:::|||||:::|||||:::|||||:::|||||:::
DB 192 I1eThrAsp1yMetVal1CyS1aG1ySer1eSer1yG1yAla1---AspTrH1CyS1nG1y 210
    ||||| |||||:::|||||:::|||||:::|||||:::|||||:::
QY 541 GACTCGGGGGGCGCTGTGTGTGAACGATCTTCTTAAGCATTTATCTCTGGGGCAG 600
    ||||| |||||:::|||||:::|||||:::|||||:::|||||:::
DB 211 AspSerG1yG1yPr0LeuVal1CySAspG1yAlaLeuG1nG1yI1eThrSer1ePr0G1ySer 230
    :::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 601 GATCGCTGTGCATGACCCGAGAGCCGTGTGTATACAGAAAGTCTCAATATGTGGAC 660
    ||||| :::|||||:::|||||:::|||||:::|||||:::|||||:::
DB 231 AspPr0CySg1yArgSerAsp1ySPr0G1yVal1yTrH1Asn1eCySAla1yTrLeuAsp 250
    :::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 661 TGGATCCAGGAG 672
    |||||:::
DB 251 Trp1eLeu1yS1yS 254
    |||||:::

```

```

RESULT 9
US-09-008-271A-7
; Sequence 7, Application US/09008271A
; Patent No. 6203979
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.

```

```

; Yue, Henry
; Guegler, Karl J.
; Corley, Neil C.
; Tang, Tom Y.
; Shah, Purvi
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,271A
; FILING DATE: 16-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohan-Peterson, Sheela
; REGISTRATION NUMBER: 41,201
; REFERENCE/DOCKET NUMBER: PF-0458 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: COLNOT27
; CLONE: 1798496
; SEQUENCE DESCRIPTION: SEQ ID NO: 7 :
US-09-008-271A-7
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 7 :
Alignment Scores:
Pred. No.: 1,15e-52 Length: 260
Score: 673.00 Matches: 115
Percent Similarity: 70.09% Conservative: 42
Best Local Similarity: 51.34% Mismatches: 65
Query Match: 52.78% Indels: 2
DB: Gaps: 2
US-09-856-320A-1_COPY_272_958 (1-687) x US-09-008-271A-7 (1-260)
QY 1 ATCATCAAGGGGTTCCAGTGCAGCCCTCCAGCCCTGGCAGGAGCCCTTTCGAG 60
    ::::: ||| |||||:::|||||:::|||||:::|||||:::|||||:::
DB 33 ValIeuD1yL1nH1sG1uCySg1nPr0H1sSerG1nPr0TrpG1nAla1aLeuPhg1n 52
    :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 61 AAGACGGGCTACTCTGTGGGGGAGCGCTCATCGCCCGCCAGATGGCTTCGACAGACC 120
    :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB 53 G1yG1nG1nLeuEuCySg1yG1yValLeuValG1yG1yAsnTrpValLeuThrAla1a 72
    :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 121 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGCAGCACAACCTCCAGAGAGAG 180
    ||||| |||||:::|||||:::|||||:::|||||:::|||||:::
DB 73 H1sCyS1yS1ySPr0LyS1yTrH1ValArgLeuG1yAspH1sSerLeuG1nAsnLySAsp 92
    ||||| |||||:::|||||:::|||||:::|||||:::|||||:::
QY 181 GGCTGTAGCAGACCCGAGACGACCATGAGTCTTCCCGCCCGGCTTCACACAGC 240
    ||| |||||:::|||||:::|||||:::|||||:::|||||:::
DB 93 G1yPr0G1nG1nLeu1n1ePr0Val1aG1nSer1ePr0H1sPr0CyS1yAsnSer 112
    ||| |||||:::|||||:::|||||:::|||||:::|||||:::
QY 241 CTCGCCAACAAGACACGCAATGACATCATGCTGTGAAGATGCATGCCAGTCTCC 300
    :::|||||:::|||||:::|||||:::|||||:::|||||:::
DB 113 ---AspValG1uAspH1sAsnH1sAspLeuMetLeuG1nLeuArgAspG1nAla1Ser 131
    :::|||||:::|||||:::|||||:::|||||:::|||||:::

```

```
QY 301 ATCACTGGGCTGTGGAGCCCTCACCCCTCTCTACGCTGTGTACTCTGTGGACAC 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 132 LeuGlySerLysValLysProIleSerIleuAlaAspHisCysThrGlnProGlyGln 151
QY 361 TGGCTCATTTCCGGGGGGGAGCAGCAGCTCCAGCCCAATTACGCTGTGTACACCTTG 420
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 152 CysThrValSerGlyTrpGlyThrValThrSerProAlaGlnAspIleu 171
QY 421 CGATGGCCCAATCATCACTATTTGAGCACAGAAAGTGTGAGAACGCTTACCCGGCAAC 480
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 172 AsnCysAlaGlnValLysIlePheProGlnLysCysGlnAspAlaIleTrpProGlyGln 191
QY 481 ATCAACAGACACCATGTGTGTGTGCGACGCTGACAGAAAGGGGCGCAAGCATCTGCCAGGT 540
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 192 IleThrAspGlyMetValCysAlaGlnSerSerLysGlyAla--AspThrCysGlnGly 210
QY 541 GACTCGGGGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 211 AspSerGlyGlyProLeuValCysAspGlyAlaLeuGlnGlyIleThrSerTrpGlySer 230
QY 601 GATCCGTGTGCATCAACCCGAAAGCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 231 AspProCysGlyArgSerAspLysProGlyValIleThrAsnIleCysArgTrpIleuAsp 250
QY 661 TGGATCCAGGAG 672
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 251 TrpIleLysLys 254
```

RESULT 10

```
US-09-386-642-13
; Sequence 13, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Ol, Jensen
; APPLICANT: Andrade-Cordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-13
```

Alignment Scores:

```
Pred. No.: 1,6e-52 Length: 288
Score: 671.50 Matches: 116
Percent Similarity: 70.228 Conservative: 42
Best Local Similarity: 51.56% Mismatches: 64
Query Match: 52.67% Indels: 3
DB: 4 Gaps: 3
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US-09-856-320a-1_COPY_272_958 (1-687) * US-09-386-642-13 (1-288)

```
QY 1 ATCATCAAGGGGTGAGTGC--AAGCTCATCTCCAGCCCTGGAGCAGACCTGTTC 57
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 52 IleValGlyLysValAsnCysLeuGlnProHisSerGlnProTrpGlnAlaIleuPhe 71
QY 58 GAGAAGACGGCGCTCTGTGTGGGCGAGCGCTCATCGCCCGCCAGATGGCTCTGACAGCA 117
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 72 GlnGlyGlnGlnLeuGlnCysGlnValLeuValGlyLysAsnTrpAlaIleuThrAla 91
QY 118 GCCCACTGCTCAACCCCGCTACATAGTTCACCTGGGGGAGCAACAACCTCCAGAGAG 177
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 92 AlaHisCysLysLysProLysTrpThrValArgLeuGlyAspHisSerLeuGlnAsnLys 111
```

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QY 178 GAGGCGTGTGACAGACCCGAGACAGCCACTGAGTCCCTTCCACCCCGGCTTCAACAAC 237
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 112 AspGlyProGlnGlnIleuIleProValValGlnSerIleProHisProCysTrpIleuSer 131
QY 238 AGCTTCCCAACAAGACACCGCAATGACATCATGCTGTGTGTGTGTGTGTGTGTGTGTGT 297
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 132 Ser---AspValGlnAspHisAsnHisAspLeuMetLeuGlnIleuArgAspGlnAla 150
QY 298 TCCATCACTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 357
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 151 SerLeuGlySerLysValLysProIleSerIleuAlaAspHisCysThrGlnProGlyGln 170
QY 358 AGCTGCTCATTTCCGGCTGTGGGAGCAGCAGCTCCAGCCCAATTACGCTGTGTACAC 417
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 171 LysCysThrValSerGlyTrpGlyThrValThrSerProArgGlnAspIleuProAspThr 190
QY 418 TTGGCATGGCCCAATCATCACTATTTGAGCACAGAAAGTGTGTGAGAACGCTTACCCGGC 477
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 191 LeuAsnCysAlaGlnValLysIlePheProGlnLysLysCysGlnAspAlaIleTrpProGly 210
QY 478 AACATCAACAGACACCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 537
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 211 GlnIleThrAspGlyMetValCysAlaGlnSerSerLysGlyAla---AspThrCysGln 229
QY 538 GGTGACTCCGGGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 597
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 230 GlyAspSerGlyGlyProLeuValCysAspGlyAlaLeuGlnGlyIleThrSerTrpGly 249
QY 598 CAGGATCCGTGTGCATCAACCCGAAAGCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 657
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 250 SerAspProCysGlyArgSerAspLysProGlyValIleThrAsnIleCysArgTrpIleu 269
QY 658 GACTGGATCCAGGAG 672
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 270 AspTrpIleLysLys 274
```

RESULT 11

```
US-09-996-243-309
; Sequence 309, Application US/09996243
; Patent No. 6478825
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C13
; CURRENT APPLICATION NUMBER: US/09/996,243
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
```



```

QY 196 CGGACGACCACTGATGCTTCCCGCCAGCCGCTTCAACAACACCTCCCGCAACAAGAC 255
D 109 PheGlnGlyValLysSerIleProH1sProGlyTyrSer-----HisProGly 124
QY 256 CACCGCAATGATCATGCTGTGAGATGGCATCGGACGATCCATACACCTGGGCTGTG 315
D 125 HisSerAsnAspMetLeuIleLysLeuAsnArgArgIleArgProThrLysAspVal 144
QY 316 CGACCCCTCAACCTCTCTCTCAAGCTGTGATGCTGCGACACAGCTGCTCATTTCCGCG 375
D 145 ArgProIleAsnValSerSerHisCysProSerIleGlyThrLysCysLeuValSerGly 164
QY 376 TGGGGCAGCAGCTGCTGACCCCGCATTTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 435
D 165 TrpIleThrThrLysSerProGlnValHisPheProLysValLeuGlnCysLeuAsnIle 184
QY 436 ACCATCATATGAGCAGCAAGTGTGAGACAGCCGACCCGCGGACATCAACAGACCATG 495
D 185 SerValLeuSerGlnLysArgCysGlnAspAlaTyrProArgGlnIleAspAspThrMet 204
QY 496 GTGTGTCCAGCAGCTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 555
D 205 PheCysAlaGly--AspLysAlaGlyArgAspSerCysGlnGlyAspSerGlyGlyPro 223
QY 556 CTGGTCTGTACACGATCTCTTCAAGGATTAATCTCTGGGGCCAGGATCCGTGTGCATC 615
D 224 ValValCysAsnGlySerLeuGlnGlyLeuValSerTrpLysAspTyrProCysAlaArg 243
QY 616 ACCCGAAGCCTGTGTCTACACGAAAGTGTGCAAAATATGAGCATGATCCAGAGAGCG 675
D 244 ProAsnArgProGlyValTyrThrAsnLeuCysLysSerThrLysTrpIleGlnIuThr 263
QY 676 ATGAGAACAT 687
D 264 IleGlnAlaAsn 267

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RESULT 13

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US-09-210-084-1
; Sequence 1, Application US/09210084
; Patent No. 6197511
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTED for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,084
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,874
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:

```

SEQUENCE CHARACTERISTICS:

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; LENGTH: 268 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KERN0702
; CLONE: 820694

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US-09-210-084-1

Alignment Scores:

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Pred. No.: 7, 11e-46
Score: 597.50
Percent Similarity: 66.52%
Best Local Similarity: 49.11%
Query Match: 46.86%
Gaps: 3
Matches: 110
Conservative: 39
Mismatches: 68
Indels: 7

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US-09-856-320a-1_COPY_272_958 (1-687) x US-09-210-084-1 (1-268)

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QY 19 TGCAGGCTCACTCCAGCCCTGGGACGACCCCTGTTCGAGAAAGACGCGCTACTGTG 78
D 50 CysThrPro--SerArgGlyGlnAlaIleLeuLeuArgProAsnGlnLeuTyrCys 68
QY 79 GGGGACGCTCATCCGCCCCAGATGCGCTCTGACAGCAGCCCATGCTCAAGCCCGC 138
D 69 GlyAlaValAlaValHisPheProGlnTrpLeuThrAlaIleHisCysArgLysVal 88
QY 139 TACATAGTCACTGCGGGGACAGCAGCAACCTCCAGAG--GAGGAGGCTGTGAGCAGAC 195
D 89 PheArgValArgLeuGlnIleTyrSerLeuSerProValTyrGlnSerGlyGlnMet 108
QY 196 CGGACGACCACTGATGCTTCCCGCCAGCCGCTTCAACAACACCTCCCGCAACAAGAC 255
D 109 PheGlnGlyValLysSerIleProH1sProGlyTyrSer-----HisProGly 124
QY 256 CACCGCAATGATCATGCTGTGAGATGGCATCGGACGATCCGATCTCATACCTGGGCTGTG 315
D 125 HisSerAsnAspMetLeuIleLysLeuAsnArgArgIleArgProThrLysAspVal 144
QY 316 CGACCCCTCAACCTCTCTCTCAAGCTGTGATGCTGCGACACAGCTGCTCATTTCCGCG 375
D 145 ArgProIleAsnValSerSerHisCysProSerIleGlyThrLysCysLeuValSerGly 164
QY 376 TGGGGCAGCAGCTGCTGACCCCGCATTTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 435
D 165 TrpIleThrThrLysSerProGlnValHisPheProLysValLeuGlnCysLeuAsnIle 184
QY 436 ACCATCATATGAGCAGCAAGTGTGAGACAGCCGATCCCGGCAACATCAGACACCATG 495
D 185 SerValLeuSerGlnLysArgCysGlnAspAlaTyrProArgGlnIleAspAspThrMet 204
QY 496 GTGTGTCCAGCAGCTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 555
D 205 PheCysAlaGly--AspLysAlaGlyArgAspSerCysGlnGlyAspSerGlyGlyPro 223
QY 556 CTGGTCTGTACACGATCTCTTCAAGGATTAATCTCTGGGGCCAGGATCCGTGTGCATC 615
D 224 ValValCysAsnGlySerLeuGlnGlyLeuValSerTrpLysAspTyrProCysAlaArg 243
QY 616 ACCCGAAGCCTGTGTCTACACGAAAGTGTGCAAAATATGAGCATGATCCAGAGAGCG 675
D 244 ProAsnArgProGlyValTyrThrAsnLeuCysLysSerThrLysTrpIleGlnIuThr 263
QY 676 ATGAGAACAT 687
D 264 IleGlnAlaAsn 267

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RESULT 14

```

US-09-764-762-1
; Sequence 1, Application US/09764762
; Patent No. 6472195
; GENERAL INFORMATION:

```

```

1 APPLICANT: Hillman, Jennifer L.
2
3 TITLE OF INVENTION: NOVEL KALLIKREIN
4
5 NUMBER OF SEQUENCES: 5
6
7 CORRESPONDENCE ADDRESS:
8
9 ADDRESSEE: Incyte Pharmaceuticals, Inc.
10
11 STREET: 3174 Porter Drive
12
13 City: Palo Alto
14
15 STATE: CA
16
17 COUNTRY: USA
18
19 ZIP: 94304
20
21 COMPUTER READABLE FORM:
22
23 MEDIUM TYPE: Diskette
24
25 COMPUTER: IBM Compatible
26
27 OPERATING SYSTEM: DOS
28
29 SOFTWARE: FastSeq for Windows Version 2.0
30
31 CURRENT APPLICATION DATA:
32
33 APPLICATION NUMBER: US/09/764,762
34
35 FILING DATE: 16-Jan-2001
36
37 CLASSIFICATION: <unknown>
38
39 PRIOR APPLICATION DATA:
40
41 APPLICATION NUMBER: 09/210,084
42
43 FILING DATE: <unknown>
44
45 ATTORNEY/AGENT INFORMATION:
46
47 NAME: Billings, Lucy J.
48
49 REGISTRATION NUMBER: 36,749
50
51 REFERENCE/DOCKET NUMBER: P#-0252 US
52
53 TELECOMMUNICATION INFORMATION:
54
55 TELEPHONE: 415-855-0555
56
57 TELEFAX: 415-845-4166
58
59 INFORMATION FOR SEQ ID NO: 1:
60
61 SEQUENCE CHARACTERISTICS:
62
63 LENGTH: 268 amino acids
64
65 TYPE: amino acid
66
67 STRANDEDNESS: single
68
69 TOPOLOGY: linear
70
71 IMMEDIATE SOURCE:
72
73 LIBRARY: KERNOT02
74
75 CLONE: 820694
76
77
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[illegible]

Alignment Scores:

Pred. No.:	2,45e-45	Length:	263
Score:	591.50	Matches:	106
Percent Similarity:	63.03%	Conservative:	44
Best Local Similarity:	44.54%	Mismatches:	79
Query Match:	46.39%	Indels:	9
DB:	2	Gaps:	2

US-09-856-320a-1_COPY_272_958 (1-687) x US-08-790-137-4 (1-263)

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OY 1 ATCATCAAGGGGTTGAGTGCAGGCTTCACCTCCAGCCCTGGACAGGACCCCTGTTCAG 60
    ||||| ||||| |||:: ::||| ||||| |||:::
Db 25 IleIleGIyGlyPheAsnCysGluLysAsnSerGlnProTrpHisValAlaValTyrArg 44
    |||
OY 61 AAGACGGGCTACTCTGTGGGCGACGCTCATGCCGCCAGATGGCTCTGACAGCAGCC 120
    ||| ||||| |||::: |||::: ||||| |||||
Db 45 PheAlaTrgTyrGlnCysGlyValLeuLeuAsnPalAsnTrpValLeuThrAlaAla 64
    |||
OY 121 CACTGCCCTCAAGCCCCGCTACATAGTTCACCTGGGGCGACACAACTCCAGAGAGAGAG 180
    ||||| ::||| ||| ||||| ::|||
Db 65 HisCysTyrAsnAspLysTyrGlnValTrpLeuGlyLysAsnAsnArgPheGluAspGlu 84
    |||
OY 181 GCGTGTGAGACAGCCCGACAGCCAGCTGAGTCTTCCCCACCCCGGCTTCACACACAGC 240
    ||| ::| ::| ::| ::| ::| ::| ::| ::|
Db 85 ProSerAlaGlnHisGlnLeuIleSerLysAlaIleProHisProGlyPheAsnMetSer 104
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OY 241 CTCCCAACAAGACAC-----CGCATGACATCATGCTG 276
    ||| ||||| |||||
Db 105 LeuLeuAsnLysAspHisThrProHisProGluAspArgTyrSerAsnAspLeuMetLeu 124
    |||
OY 277 GTGAAGATGCGATCGCCAGTCCATCCATCGCTGGGCTGGCAGCCCTCACCTCTCTCA 336
    |||::: ||| ||||| |||::: ||| ::|
Db 125 ValArgLeuLysLysProAlaGluIleThrAspValValLysProIleAspLeuProThr 144
    |||
OY 337 CGCTGTGCTACTGCTGGACACCGCTCATTTCCGGCTGGGGCAGCAGCTCC--AGC 393
    || |||::: ||||| ||||| ||||| ||||| ::|
Db 145 GluGluProThrValGlySerArgCysLeuAlaSerGlyTrpGlySerThrThrProThr 164
    |||
OY 394 CCCAGTTACGCTGCTGCACACCTTGCGATCGCCAAACATCACCATCATTTGAGCACCAG 453
    ::| ::| ::| ::| ::| ::| ::| ::|
Db 165 GluGluPheGluTyrSerHisAspLeuGlnCysValTyrLeuGluLeuLeuSerAsnGlu 184
    |||
OY 454 AAGTGTGAGAACGGCTACCCCGGCAACATCACAGACCAATGCTGTGCTGCCAGCGTGCAG 513
    ||| ||||| ||||| ::| ||||| |||||
Db 185 ValCysAlaLysAlaHisThrGluLysValThrAspThrMetLeuCysAlaGlyGluMet 204
    |||
OY 514 GAAGGGGGCAAGACTCCTGCCAGGTGACTCCGGGGCCCTGTGCTGTAAACAGTCT 573
    ::| ||||| ::||| ||||| ||||| ||||| ::|
Db 205 AspGlyGlyLysAspThrCysValGlyAspSerGlyGlyProLeuIleCysAspGlyVal 224
    |||
OY 574 CTTCAAGGCAATTATCTCTGGGGCCAGAGTCCGTGCGATCACCCGAAAGCCTGTGTCT 633
    ||||| ||||| ||||| ||||| |||||
Db 225 LeuGlnGlyIleThrSerTrpGlyProThrProCysAlaLeuProAsnValProGlyIle 244
    |||
OY 634 TACACGAAGCTCCTCAATATGTGACTGGATCCAGAGACAGATGAAGACAAT 687
    ||||| ||||| ::||| ||||| ::|||
Db 245 TyrThrLysLeuIleGluTyrArgSerTrpIleLysAspValMetAlaAsnAsn 262
    ||||| ||||| ::||| ||||| ::|||
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Search completed: October 15, 2003, 20:29:02
Job time : 16.2679 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleole - protein search, using frame_plus_n2p model

Run on: October 15, 2003, 19:44:50 ; Search time 89.3292 Seconds
(without alignments)
7516.609 Million cells updates/sec

Title: US-09-856-320A-1
Perfect score: 2370
Sequence: 1 ctcgctgtctccacacctgg.....aaaaaaaaaaaaaaaaaaaaa 1301

Scoring table:
BLOSUMP62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 1661050

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame_n2p.model -DEV=xlp
-O/cgn2.1/USPTO.spool.p/US09856320/runat.15102003.105639.8524/app.query.fasta.1.2318
-DB=SPTRMBL.23 -GFWT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPT=0 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCAIIGN=200 -THR.SCORE=pcr -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pcr -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09856320@cgn.1.1.159@runat.15102003.105639.8524 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEOBUDERY -NEG.SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

SPTRMBL.23:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1332.5	56.2	275	4	Q81XD7

2	1187	50.1	276	11	Q9QYN3	Q9qyn3 mus musculus
3	1129	47.6	249	11	Q9QYN4	Q9qyn4 mus musculus
4	692	29.2	260	4	Q81W69	Q81w69 homo sapien
5	685.5	28.9	255	4	Q96R00	Q96r00 homo sapien
6	683.5	28.8	254	11	Q8CGR4	Q8cgr4 mus musculus
7	678	28.6	276	11	Q8CGR6	Q8cgr6 mus musculus
8	665	28.1	251	11	Q9DB08	Q9db08 mus musculus
9	632.5	26.7	293	11	Q9D140	Q9d140 mus musculus
10	626	26.4	250	11	Q8CGR5	Q8cgr5 mus musculus
11	602	25.4	261	11	Q9JW70	Q9jw70 mus musculus
12	600.5	25.3	246	11	Q9Z189	Q9z189 mus musculus
13	599.5	25.3	234	11	Q9CV76	Q9cv76 mus musculus
14	598.5	25.3	246	11	Q9R077	Q9r077 mus musculus
15	597.5	25.2	239	11	Q9J275	Q9j275 mus musculus
16	597	25.2	246	11	Q9QUR9	Q9qu9 mus musculus
17	592.5	25.0	261	6	Q9N1Q1	Q9n1q1 saginus oe
18	591.5	25.0	261	6	Q29474	Q29474 canis faml
19	587.5	24.8	235	11	Q63274	Q63274 rattus norv
20	582	24.6	249	11	Q91VE3	Q91ve3 mus musculus
21	576	24.3	263	11	Q9JW71	Q9jw71 mus musculus
22	575	24.3	244	13	Q8QGW3	Q8qgw3 anguilla ja
23	572.5	24.2	261	11	Q8C232	Q8c232 mus musculus
24	572	24.1	251	11	Q54854	Q54854 rattus norv
25	570.5	24.1	263	11	Q9JW69	Q9jw69 mus musculus
26	570.5	24.1	269	4	Q81U35	Q81u35 homo sapien
27	568.5	24.0	253	11	Q91Y82	Q91y82 mus musculus
28	568	24.0	246	11	Q88301	Q88301 mus musculus
29	567.5	23.9	247	11	Q9CPN7	Q9cpn7 mus musculus
30	567	23.9	240	13	Q98TH0	Q98th0 engraulis j
31	566	23.9	245	13	Q42160	Q42160 petromyzon
32	564.5	23.8	237	13	Q91515	Q91515 fuigu rubrip
33	563	23.8	247	13	Q42158	Q42158 petromyzon
34	562	23.7	247	13	Q42608	Q42608 petromyzon
35	561	23.7	247	11	Q9CPN9	Q9cpn9 mus musculus
36	560.5	23.6	253	4	Q8W5N9	Q8w5n9 mus musculus
37	560	23.6	244	13	Q42159	Q42159 homo sapien
38	559	23.6	242	13	Q92099	Q92099 petromyzon
39	558	23.5	254	6	Q9XSN6	Q9xsn6 sus scrofa
40	556	23.5	238	13	Q9W706	Q9w706 paratichthy
41	555.5	23.4	222	13	Q8AV11	Q8av11 opcorrhynch
42	555.5	23.3	243	13	Q8AV13	Q8av13 brachydanto
43	553	23.3	261	11	Q88309	Q88309 mus musculus
44	552	23.3	242	13	Q9W707	Q9w707 paratichthy
45	551	23.2	247	13	Q9W705	Q9w705 paratichthy

ALIGNMENTS

RESULT 1

ID Q81XD7 PRELIMINARY; PRT; 275 AA.

AC Q81XD7; 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Variant form hippostasin/KIK11.

GN KIK11.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Prostate;

RA Nakamura T., Mitsui S., Miki T., Yamaguchi N.;

RT "Molecular cloning and expression of a variant form of

RL hippostasin/KIK11 in prostate.,"

DR Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

EMBL; AB078780; BACS4105.1; -

SO SEQUENCE 275 AA; 30165 MW; 257A42B28F40E2C4 CRC64;

Alignment Scores:

2.33e-99

Length:

275

Score: 1332.50 Matches: 250
Percent Similarity: 90.81% Conservative: 0
Best Local Similarity: 90.91% Mismatches: 0
Query Match: 56.22% Indels: 25
Gaps: 1

US-09-856-320a-1 (1-1301) x Q81XD7 (1-275)

QY 209 ATGAGAGATTTCGACGTTAAATCCTGCTGCTGCGCAACAGGCGCTTGAAGGGGAGAGACC 268
1 MetArgileuLeuGlnleuIleleuIleuAlaIleuAlaThrGlyLeuValGlyGluThr 20

QY 269 AGCATCATCAAGGGGTTGAGTGCAGAGCTCTACCTCCAGCCCTGGCAGAGCCCTGTTC 328
21 ArgIleleuGlyGlyPheGluCysLysProHisSerGlnProThrGlnAlaIleuPhe 40

QY 329 GAGAGAGCGCGCTCTGTGTGGGCGAGCTCAATCGCCAGATGGCTCTGACAGCA 388
41 GluysThrArgleuLeuGlyAlaThrIleuIleAlaProArgTyrPheLeuThrAla 60

QY 389 GCGCCAGCTGCTCAAGCCC----- 406
61 AlaHisCysleuLysProTyrValSerleuThrSerProThrHisValSerProAspLeu 80

QY 407 -----CGTAAATAGTTCACTGGGCGACAC 433
81 SerSerSerAsnTyrCysLeuSerHisLeuSerArgTyrIleValHisLeuGlyGlnHis 100

QY 434 AACCTCCAGAGAGAGAGGCTGTGACAGACCCGCGAGAGCCAGCTGATCCTTCCCCAC 493
101 AsnleuGlnLysGluGlnGlyCysGlnGlnThrArgThrAlaThrGlnLysPheProHis 120

QY 494 CCGCGCTTCAACAACAGGCTCCCAACAAGACACCGCAATGACATATGCTGGTAG 553
121 ProGlyPheAsnAsnSerleuProAsnLysAspHisArgAsnAspIleMetLeuValLys 140

QY 554 ATGGCATCGCGAGCTCCATCATCCTGGGCTGTGGAGCCCTCACCCTCTCTCCAGCTGT 613
141 MetAlaSerProValSerIleThrTTPAlaValArgProleuThrLeuSerSerArgCys 160

QY 614 GTCACCTGCTGGCAGCAGCTGCTCATTTCCGGCTGGGCGAGCAGCTCAGCCCGCATTA 673
161 ValThrIleGlyThrSerCysleuIleSerGlyTyrPheLysThrHisSerProGlnLeu 180

QY 674 CGCCTGCTCAGACCTTGCATGCGCCGCAACATCACAATCATGAGCAGCAGAGCTGAG 733
181 ArgleuProHisThrIleuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlu 200

QY 734 AAGCCTACCGCGGCAATCAGACAGACAGCATGCTGTGGCAGCGAGGAGGGGGC 793
201 AsnAlaTyrProGlyAsnIleThrAspThrMetValCysAlaSerValGlnGluGly 220

QY 794 AAGGACTCTCCAGAGGTGACTCCGGGGCCCTCTGCTGTAAACAGTCTTCAAGGC 853
221 LysAspSerCysGlnGlyAspSerGlyGlyProleuValCysAsnGlnSerleuGlnGly 240

QY 854 ATATATCTCCGGGGGCGAGATCCCTGTGCCATCACCCGAAAGCTGGTGTCTAACAGAA 913
241 IleIleSerTyrGlyGlnAspProCysAlaIleThrArgLysProGlyValTyrThrLys 260

QY 914 GTCTCAAAATATGTGACTGGATCCAGAGAGCATGAAGAACAAT 958
261 ValCysLysTyrValAspTyrIleGlnGluThrMetLysAsnAsn 275

RESULT 2
ID Q9QYN3 PRELIMINARY; PRT: 276 AA.
AC Q9QYN3;
DT 01-MAY-2000 (TRMBLurel. 13, Created)
DT 01-MAY-2000 (TRMBLurel. 13, Last sequence update)
DT 01-MAR-2003 (TRMBLurel. 23, Last annotation update)
DE Hipostasin prostate type.
GN PRSS20.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Yamaguchi N., Mitsui S.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA MEDLINE=20525460; PubMed=11072088;
RX Mitsui S., Okui A., Komiyama K., Yamaguchi N.;
RT "cDNA cloning and tissue-specific splicing variants of mouse
RT hipostasin/TLSP (PRSS20).";
RL Blochm. Biophys. Acta 1494:206-210(2000).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB016227; BAA36955.1; -.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.257; -.
DR MGD; MGI:1929977; Prss20.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser. protease_Try.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PRO0722; CHYMOTRPSIN.
DR SMART; SM00020; TRYPSIN_SPEC.1.
DR PROSITE; PS0240; TRYPSIN_DOM.1.
DR PROSITE; PS0134; TRYPSIN_HIS.1.
DR PROSITE; PS00135; TRYPSIN_SER.1.
KW Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 276 AA; 30753 MW; 90BDC03ABAB17BD6 CRC64;

Alignment Scores:
Pred. No.: 1,37e-87 Length: 276
Score: 1187.00 Matches: 217
Percent Similarity: 86.88% Conservative: 28
Best Local Similarity: 76.95% Mismatches: 31
Query Match: 50.08% Indels: 6
Gaps: 2

US-09-856-320a-1 (1-1301) x Q9QYN3 (1-276)

QY 113 ATGCAAGAGTTGAGCTGCGCTGCGGAGCTGGAAGTCATCGGGCAGAGCTCTCAGACGACC 172
1 MetArgArgleuLys-----SerAspTyrLysLeuSer-----ThrGluThr 14

QY 173 AAGGAGCTGGGGCGCGCTCTCTCCCTCCAGGCGATGAGGATTTCGAGTTAATCTGTG 232
15 ArgGluProGlyAlaArgProAlaLeuLeuGlnAlaArgMetIleLeuArgleuIleAla 34

QY 233 CTTCCTCTGGCAGAGGCTTGTAGGGGAGAGACAGCATCATCAAGGGGTTGAGTGC 292
35 LeuAlaLeuValThrGlnHisValGlyGlyGluThrArgIleIleLysGlyTyrGlnCys 54

QY 293 AAGCTACTCTCCAGCCCTGGCAGAGCCCTGTGTGAGAAAGACGGCTACTGTGGG 352
55 ArgProHisSerGlnProTyrGlnValAlaLeuPheGlnLysThrArgleuLeuCysGly 74

QY 353 GCGAGCTCATCGCGCCCAATGAGCTCTTACAGACAGCCAGCTGCTCAAGCCCGGTAC 412
75 AlaThrIleuIleAlaProLysTyrPheLeuThrAlaAlaHisCysAlaGlySproHisTyr 94

QY 413 ATAGTTCACCTGGGGCAGACAACTTCAGAGAGAGAGGCTGTGAGACCCGGACA 472
95 ValIleLeuLeuGlyGlnHisAsnLeuGlnLysThrAspLysGlyGlnArgGlnMet 114

QY 473 GCGACGTAGTCTTCCCGCCAGCCCGGCTTAAACAACAGCTCCCAACAAGACAGCCGC 532
115 AlaThrGluSerPheProHisProAspRhsAsnSerleuProAsnLysAspHisArg 134

QY 533 AATGACATCATGCTGGGGAAGATGGCATGCCAGTCTCCATCAGCTGGGTGGCGACC 592
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Db      135 AsnAspIleMetIleuValIysMetSerSerProValPheSerThrArgAlaValGlnPro 154
QY      593 CTCACCCCTCTCTACACGCTGTGTCTACCTGCTGGCACACAGCTGCTCATTTCCGGCTGGGCG 652
Db      155 LeuThrIleuSerProIleuValAlaIleValGlyThrSerCysIleuIleSerGlyTrpGly 174
QY      653 AGACAGCTGACGCCCCAGTACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 712
Db      175 ThrThrSerSerProIleuValIleuValGlyProIleuValSerIleuValGlyAlaValSerIle 194
QY      713 ATTAGACACACAGAGTGTAGAGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 772
Db      195 ILeuGlnHisLysGlnCysGlnValAlaTrpProGlyAlaHisIleThrSphMetIleCys 214
QY      773 GCCAGCTGACAGAGAGGGGCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 832
Db      215 AlaSerValArgGlySerGlnGlyLysAspSerCysGlnGlyLysPserGlyLysProIleuVal 234
QY      833 TGTAAACAGTCTCTTAAAGCATATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 892
Db      235 CysAsnGlySerLeuGlnGlyIleIleSerTrpGlyLysAspProCysAlaValAlaThrArg 254
QY      893 AAGCCTGTGTCTACACGAAAGTCTGCAATATATGTGAGTGGAGTCCAGGAGAGAGATGAG 952
Db      255 LysProGlyValAlaThrThrLysValCysLysTrpPheAsnTrpIleHisGlnValMetArg 274
QY      953 AACCAAT 958
Db      275 AsnAsn 276

RESULT 3
Q90YN4 PRELIMINARY; PRT; 249 AA.
ID      Q90YN4;
AC      01-MAY-2000 (TrEMBLrel. 13, Created)
DT      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      HIPOSTRASIN (2310015108RIK protein).
GN      PRS520 OR 2310015108RIK.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RA      Yamaguchi N., Mitsui S.;
RT      "CDNA cloning of a novel brain serine protease, Hipostasin.";
RL      Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RA      Mitsui S., Yamaguchi N.;
RT      "CDNA cloning of a novel brain serine protease, Hipostasin.";
RL      Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Tongue;
RC      MEDLINE=21085660; PubMed=11217851;
RA      Kawai T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA      Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA      Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamahata T.,
RA      Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA      Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA      Fleischmann W., Gaasterland T., Glass C., King B., Kochiwa H.,
RA      Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA      Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA      Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsi G.,
RA      Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA      Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA      Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA      Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA      Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N.,
RA      Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

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RA      Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA      Wyshnaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA      Hayashizaki Y.;
RT      "Functional annotation of a full-length mouse cDNA collection.";
RL      Nature 409:685-690(2001).
DR      EMBL: AB016226; BAA88825.1; -
DR      EMBL: AK009720; BAB26461.1; -
DR      EMBL: AK009360; BAB26241.1; -
DR      HSSP: P00763; IDPO.
DR      MEROPS: S01.257; -.
DR      MGD: MGI:1929977; Prss20.
DR      InterPro: IPR001254; Ser. protease_Try.
DR      Pfam: PF00089; Trypsin; I.
DR      SMART: SM00020; Tryp_Spc; 1.
DR      PROSITE: PS00240; TRYPSIN_DOM; 1.
DR      PROSITE: PS00134; TRYPSIN_HIS; 1.
DR      PROSITE: PS00135; TRYPSIN_SER; 1.
KW      Hydrolase; Protease; Serine protease.
SQ      SEQUENCE 249 AA; 27604 MW; F9FP9CH457D727D5 CRC64;

Alignment Scores:
Pred. No.: 6,65e-83 Length: 249
Score: 1129.00 Matches: 201
Percent Similarity: 90.738 Conservative: 24
Best Local Similarity: 81.058 Mismatches: 23
Query Match: 47.648 Indels: 0
DB: Gaps: 11

US-09-856-320a-1 (1-1301) x Q90YN4 (1-249)
QY      215 ATTCTGCACTTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 274
Db      2 ILeuValArgIleuIleAlaIleuValIleuValIleuValIleuValIleuValIleuValIleuVal 21
QY      275 ATCAAGGGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 334
Db      22 ILeuValArgIleuIleAlaIleuValIleuValIleuValIleuValIleuValIleuValIleuVal 41
QY      335 AGCGGCTACTGTGTGTGGGAGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 394
Db      42 ThrArgLeuIleuCysGlyLysIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 61
QY      395 TGGCTGACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 454
Db      62 CysArgLysProIleuValIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 81
QY      455 TGTGAGCAGACCCGAGCAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 514
Db      82 CysGlnGlnArgArgMetAlaThrGluSerPheProIleuValAlaIleuValIleuValIleuVal 101
QY      515 CCCAACAAAGACCCAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 574
Db      102 ProAsnLysArgIleuValIleuValIleuValIleuValIleuValIleuValIleuValIleuVal 121
QY      575 ACCTGGGCTGTGAGCCCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 634
Db      122 ThrArgAlaValAlaIleuProIleuThrIleuSerProIleuValAlaIleuValIleuValIleu 141
QY      635 CTCATTTCCGGTGGGAGCAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 694
Db      142 LeuIleSerGlyTrpIleuThrIleuSerProIleuValIleuValIleuValIleuValIleuVal 161
QY      695 TCCGCCAATACATCATCTTGTAGCAGCAGTGTGAGAAAGGAGAGAGTGTGAGAGTGTGAGAGTGTGAG 754
Db      162 CysAlaAsnValSerIleuIleuGlnHisLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 181
QY      755 ACAGACACATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 814
Db      182 ThrAspThrMetIleuValIleuValIleuValIleuValIleuValIleuValIleuValIleuVal 201
QY      815 TCCGGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 874
Db      202 SerGlyLysProIleuValIleuValIleuValIleuValIleuValIleuValIleuValIleuVal 221

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OY 875 CCGTGCATACCCGAAACCGGTGTCTACAGAAAGTCTGCAATATGTGACTGG 934
|||||
Db 222 ProctyalaValTtrArgLysProGlyValTtrThrylsValCysLysTyrPhaSnTrp 241
935 ATCCAGAGACGATGAGAACAAAT 958
|||
Db 242 IlleHsGluValMetArgAsnAsn 249

RESULT 4
O81W69 PRELIMINARY; PRT; 260 AA.
AC O81W69:
DT 01-MAR-2003 (TRMBLrel. 23, Created)
DT 01-MAR-2003 (TRMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC040887; AAI40887.1; -.
KW Hypothetical protein.
SQ SEQUENCE 260 AA; 28090 MW; EF5934EB96295660 CRC64;

Alignment Scores:
Pred. No.: 1.51e-47 Length: 260
Score: 692.00 Matches: 125
Percent Similarity: 66.93% Conservative: 45
Best Local Similarity: 49.21% Mismatches: 80
Query Match: 29.20% Indels: 4
DB: Gaps: 3

US-09-856-320a-1 (1-1301) x O81W69 (1-260)
OY 188 CGGTCTCCCTCCAGCCATGAGATTCTGCAATTAACTGCTT-----GCTCTG 241
|||||
Db 3 ArgProArgProArgAlaAlaLysLThrTrpMetRheuleuleuleuGlyAlaTTrp 22
242 GCACACAGGCTTGTAGGGGAGACAGCATATCAAGGGTTCAGTCAAGCCCTCAC 301
|||||
Db 23 AlaGlyHisSerArgAlaGlnArgLysValLeuLysGlnHisGlyCysGlnProHis 42
302 TCCGAGCCCTGGAGAGAGCCCTGTGAGACAGCGGCTACTCTGTGGGCGAGCCCTC 361
|||||
Db 43 SerGlnProTrpGlnAlaAlaLeuPheGlnGlyGlnLeuLeuLeuGlyValLeu 62
362 ATCGCCCCAGATGGCTCTGTACAGACGACCTGCTCAAGCCCGCTCATAGATTAC 421
|||||
Db 63 ValGlyGlyLysnTrpValLeuThrAlaAlaHisCysLysLysProLysTyrThrValArg 82
422 CTGGGGCAGACAACTCTCAGAAAGAGAGAGGCTGTGACAGACCCGAGACGACATGAG 481
|||||
Db 83 LeuGlyAspHisSerLeuGlnAsnLysAspGlyProGlnGlnGlnLysLeuProValAlaGln 102
482 TCCCTCCCGCCACCCGGCTTCAACACAGCGCTCCCAACAACAACCCCAATGACATC 541
|||||
Db 103 SerTLeuProHisProCysTyrAsnSerSer--AspValGlnAspHisAsnHisAspLeu 121
542 ATGCTGATGAAATGGCATGCGCAGTCTCATCATCACTGGGCTGGGAGCCCTCACCCCTC 601
|||||
Db 122 MetLeuLeuGlnLeuLysArgGlnAlaSerLeuGlySerLysValLysProLysSerLeu 141
602 TCCCTCAGGCTGTGCTGCTGAGCAGACGCTGCTCATTTCCGCTGGGCGACAGCTCC 661
|||||
Db 142 AlaAspHisCysThrGlnProGlnLysCysThrValSerGlyTrpGlyThrValThr 161
662 AGCCCCCAGTAAAGCCCTGCTCAGACCTTGCGGCGCCCAACATCACTCATTTGAGCAC 721
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Db 162 SerProArgGluAsnPheProAspThrLeuAsnCysAlaGluValLysIlePheProGln 181
722 CAGAAAGTGTGAGAGGCTTACCCGGCAACATCAACACACAGGCTGTGCCAGCTG 781
|||||
Db 182 LysLysCysGlnAspAlaLysProGlyGlnLleThrAspAlaMetValCysAlaGlySer 201
782 CAGGAAGCGGCGCAAGACTCCTGCGCAGGTCAGCTCCGGGGCCCTCTGTGTAAACAG 841
|||||
Db 202 SerLysGlyAla--AspThrCysGlnGlyAspSerGlyGlyProLeuValCysAspGly 220
842 TCTCTTCAAGGCATTAATCTCTGGGCGCAGAGATCCGTGTGCGATCACCCGAAACCTGTG 901
|||||
Db 221 AlaLeuGlnGlyIleThrSerTrpGlySerAspProCysGlyArgSerAspLysProGly 240
902 GTCACACGAAAGCTGCAATATGTCAGTACGATCCAGAGG 943
|||||
Db 241 ValTyrThrAsnIleCysArgTyrLeuAspTrpIleLysLys 254

RESULT 5
O96R00 PRELIMINARY; PRT; 255 AA.
AC O96R00:
DT 01-DEC-2001 (TRMBLrel. 19, Created)
DT 01-DEC-2001 (TRMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TRMBLrel. 23, Last annotation update)
DE Prostinogen.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21226193; PubMed=11327827;
RA Takayama T.K., Carter C.A., Deng T.;
RT "Activation of prostate-specific antigen precursor (pro-PSA) by
RT prostin, a novel human prostatic serine protease identified by
RT degenerate PCR."
RL Biochemistry 40:1679-1687(2001).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AF303046; AAK62813.1; -.
DR HSP: P00761; 1ANI.
DR MEROPS; S01.081; -.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser-protease_Try.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_SPEC; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
KW Hydroxylase; Protease; Serine protease.
SQ SEQUENCE 255 AA; 27986 MW; 00D5B79E14B9468F CRC64;

Alignment Scores:
Pred. No.: 5.05e-47 Length: 255
Score: 685.50 Matches: 129
Percent Similarity: 65.00% Conservative: 40
Best Local Similarity: 49.62% Mismatches: 76
Query Match: 28.92% Indels: 15
DB: Gaps: 4

US-09-856-320a-1 (1-1301) x O96R00 (1-255)
OY 209 ATGAGGATCTGAGAGTTAACTCCGTGCTGTGCAACAGGCTTGTAGGGGAGAGACC 268
|||||
Db 1 MetTrpLeuLeuLeuThrLeuSerPheLeuAlaLysSerThrAlaGlnAspGlyAsp--- 19
269 AGCATCATCAAGGGGTTTCAGAGTCAAGCTCACTCCAGCCCTGCGAGCAGCAGCTGTTG 328
|||||
Db 20 LysLeuLeuGlnLysArgLysGlyAlaProHisSerGlnProTrpLysValAlaLysLys 39
329 GAGAAACGCGGCTACTCTGTGGGCGAGCGCTCATGCGCCCGCAGATGCTCTGACAGCA 388
|||||
```


Db		40	GIUARGIYARPhasnscylLylasleuileuileserProhistrVallLeuSerAla	59
QY		389	GGCCATGCGCTCAAGCCCGCTACATTAAGTCACTGGGGGACGCAACCTCCAGAGAG	448
Db		60	AlAniscysglInserlArPhemeIarValArgleuLgylunIshasleuValArg	79
QY		449	GAGGGGTGAGACAGACCCGAGACACCACTGAGCTCCGCCCCCGGGCTCAACAC	508
Db		80	AspGlyProglInleuArGThrThrserArValIleProhIsProAlGyTylu---	98
QY		509	AGCCTCCCAAGAACCCGCAATGATCATATGCTGTGAAGATGGATCGCCAGTC	568
Db		99	-----AlArGserhIsArGsnAspIleMetLeuArGleuValGlnProAla	115
QY		569	TCCATACCTGGGCTGTGGACCCCTCAACCTCTCCATGCTGTGCATCGTGGCCACC	628
Db		116	ArgleuAsnProglInValInProAlaValLeuProhIhArGysProhIsProGlyGlu	135
QY		629	AGCTGCCTCATTTCCGGCTGGGGGACGACGTC-----AGC	664
Db		136	AlAcysValIValserGlyTyrpIlyLeuValserhIsaengIuProGlyIhAlaGlySer	155
QY		665	CCC-----CAPTTACGCTGGCTCACACCTTGGCATCGCCCAACATCACCATTTAG	718
Db		156	ProArGserGlnValSerleuProAspThrLeuhtIsCysAlaAsnIleGlyIleIeser	175
QY		719	CACCAAGTGTAGAGACGCTTACCCCGGCAACATCAAGACACATGATGTGGCCAGC	778
Db		176	AspThrSerCyAspIyseryTyrProGlyArGleuThrAsnIhMetValCysAlaGly	195
QY		779	GTGCAGAGAGGGGCAAGAGATCTCTCCAGGGTGACTCCGGGGCCCTGTGCTGTAC	838
Db		196	AlaGlnGlyArGlyAlaGlnIserCysGlnIuGlyAspserGlyGlyProLeuValCysGly	215
QY		839	CAGTCTCTCAAGGATTAATCTCTGGGGGACGAGATCGGTGGGATCACCCGAAGCCT	898
Db		216	GlyIleLeuGlnGlyIleValserTrpGlyAspValProCysAspAsnThrIhIysPro	235
QY		899	GGTGTATACAGAAAGTCTGCAAAATATGTGACTGATGCCAGAGACGATGAAGACAT	958
Db		236	GlyValIlyTrhIysValCyshtIsYIleuGlnIuTrpIleArGluIhMetIysArgAsn	255

Alignment Scores:	7.33e-47	25
Pred. No.:	683, 50	Matches:
Score:	65.10%	Conservative:
Percent Similarity:		38

Best Local Similarity:	50.20%	Mismatches:	74
Query Match:	28.84%	Indels:	15
DB:	11	Gaps:	4

[illegible]

RESULT	7
OBCCR6	
ID	OBCCR6
AC	OBCCR6;
DT	01-MAR-2003 (TREMBLrel. 23, Created)
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE	Glandular kallikrein KLIK3.
GN	KLIK3.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.


```

Db      25 GlyAlaArgLncCysValAlrGAsnSer***ProTPrGlnAlaGlyLeuDehYrLeuThr 44
QY      338 CGGCTACTGTGTGGGCGAGCTCATGCGCCCGAGATGGCTCTGACAGACCGCACTGC 397
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      45 ATGAGLncCysGlyAlaThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 64
QY      398 ATGAGLncCysGlyAlaThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 457
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      65 ATGlysProTylLeuThrValAlrGLeuGlyGlnHisHisLeuThrPrGTrGlnGlyPro 84
QY      458 GAGCGAGCCCGGAGAGCCGACGCTGCTCTCCCGCCCGGCTCCGAGCAAGACGCGCCG 517
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      85 GlnGlnLeuLeuLeuValThrAspRhePrHePrOnIsProGlyRheAsnProAsnLeuSer 104
QY      518 AACAAAGACCCGACCGCATGACATCATGCTGTGAAGATGGACATCCGCACTCTCCATCAC 577
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      105 AlaAsnAspHisAsnAspAspIleMetLeuIleArgLeuProArgValAlrGLeuThr 124
QY      578 TGGGCTGTGCGAACCCCTCACCCCTCTCCACGCTGTGTACTGTGGACACGAGCTGCTC 637
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      125 ProAlaValAlrProLeuAsnLeuThrGlnSerArgProProValGlyThrGlnCysLeu 144
QY      638 ATTTCGGCTGGCGGACAGCTGACAGCTGACAGCCCGGCTGACAGCTGACAGCTGACAGCTG 697
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      145 IlePheGlyTrpGlySerValSerSerLysLeuGlnTrpGlySerLysLeuGlnCys 164
QY      698 GCGAACATCATCATCTTGTAGACACGACAGTGTGAGACGCGCTACCCCGGCAACATCAC 757
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      165 AlaAsnIleSerIleLeuAspAsnLysPheCysArgTrpAlaTrpProGlyHisIlePhe 184
QY      758 GACACCATGTGTGTGTGACAGCTGACAGAGGGGAGGAGAGAGAGAGAGAGAGAGAGAGAG 817
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      185 LysLysIleLeuCysAlaIleGlyLeuTrpGlnGlyGlyArgGlySerCysGlnGlyAspPhe 204
QY      818 GGGGGCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 877
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      205 GlyGlyTrpLeuValLysGlnGlyLysLeuAlaGlyIleValAlrPheGlyLysPheGlyPro 224
QY      878 TGTGCGATCACCGGAGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 937
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      225 CysSerArgProArgTrpArgProAlaValLysTrpHisValPheAspTrpLeuGlnTrpIle 244
QY      938 CAGGAGACGATGACAGACAT 958
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      245 GlnSerProMetGlnLysAsn 251
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
Q9D140 PRELIMINARY; PRT; 293 AA.
AC 09D140;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 1110030019rik protein.
GN 1110030019rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RA
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=11085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakata I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Kuehl L.M., Lewis S., Matsuo Y., Nakai I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

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RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL: AK003996; BAB23113.1; -.
DR HSSP: P00763; IDPO.
DR MEROPS: S01.017; -.
DR MEROPS: S01.418; -.
DR MGD: MGI:1915918; 1110030019rik.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser-protease_Ltry.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYP-SPC; 1.
DR PROSITE: PS50240; TRYP-SIN_DOM; 1.
DR PROSITE: PS00134; TRYP-SIN_HIS; 1.
DR PROSITE: PS00135; TRYP-SIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 293 AA; 31908 MW; ED1F45D8226FE911 CRC64;

Alignment Scores:
Pred. No.: 1e-42 Length: 293
Score: 632.50 Matches: 118
Percent Similarity: 63.74% Conservative: 49
Best Local Similarity: 45.04% Mismatches: 81
Query Match: 26.69% Indels: 14
DB: Gaps: 5

US-09-856-320a-1 (1-1301) x Q9D140 (1-293)
QY 199 CTTCCAGCCGATGACAGATTCTGCAAGTTACTGCTGCTGTGCAAGAGGCTGTGAG 258
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 38 ProSerGlyThrGlnProSerGlyThrAsnArgAspLeuSerThrAspSerLysSer-G1 57
QY 259 GGGAGAGACC-----AGATCATCAAGGGTGTGAGTGCAGAGCTCA 300
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 57 yglAspTrpArgSerAspSerSerArgLysIleValAsnGlySerAspGlySlnAs 77
QY 301 CTCGAGCCCTGGACGAGCACC--CTGTGAGAGAGAGCCGCTACTGCTGGGGGAG 357
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 77 pAlaGlnProTrpGlnGlyAlaLeuLeuLeuGlyProAsnLysLeuTrpCysGlyAla 97
QY 358 GCTCATGCCCCAGATGGCTCTGTACAGAGCCCACTGCTCAAGCCCGCTACATAGT 417
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 97 lleuIleSerProGlnTrpLeuLeuThrAlaAlaHisCysArgLysProValPheArg11 117
QY 418 TCACSTGGGCGACACACCTCCAGAG--GAGGAGGCTGTGAGCAGACCCGAGAGC 474
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 117 eArgLeuGlnHisHisSerMetSerProValLysGlnGlnGlnGlnGlnGlnGlnGln 137
QY 475 CACTGAGTCTGCTCCCGACCCCGGCTTCAACAAACAGCTCCGCAACAAAGACCGGAA 534
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 137 ylleYSerLlePrGlnHisProGlyLysSer-----HisProGlyHisSerAs 153
QY 535 TGACATCATGCTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 594
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 153 nAspLeuMetLeuIleLysMetAsnArgLysIleArgAspSerHisSerIleValLysPro 173
QY 595 CACCCTGCTCTACAGCTGTGTACAGTGTGACAGCAGAGCTGCTATTTCCGGCTGGGAG 654
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 173 lGluIleAlaCysAspArgAlaThrGlnGlyThrArgCysMetValSerGlyTrpGly1 193
QY 655 CAGCTGAGCCCGCAGATTACGCTGCTCAACCTTGGAGTGGGCGCAATGCAATGAT 714
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 193 rTrpSerSerHisAsnAspPheProLysValLeuGlnCysLeuAsnIleThrValle 213

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[illegible]

RESULT	10		
08CGR5			
ID	08CGR5	PRELIMINARY:	PRT: 250 AA.
AC	08CGR5		
DT	01-MAR-2003	(TREMBLrel. 23, Created)	
DT	01-MAR-2003	(TREMBLrel. 23, Last sequence update)	
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)	
DE	Glandular kallikrein KlK14.		
GN	KlK14.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22325484; PubMed=12437987;		
RA	Olsson A.Y., Lundwall A.;		
RT	"Organization and evolution of the glandular kallikrein locus in Mus		
RT	musculus.";		
RL	Biochem. Res. Commun. 299:305-311(2002).		
RL	[2]		
RP	SEQUENCE FROM N.A.		
RA	Adams M., Mural R.;		
RL	Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.		
DR	EMBL, AY152433, AAN78421.1, ..		
SO	SEQUENCE 250 AA; 27016 MW; EC2FE8F2290FE8B8 CRC64;		

Alignment Scores:	
Pred. No.:	3,28e+42
Score:	636.00
Percent Similarity:	62.99%
Best Local Similarity:	46.06%
Query Match:	26,418
DB:	11
US-09-856-320A-1 (1-1301) x Q8CGH5 (1-250)	
	Length: 250
	Matches: 117
	Conservative: 43
	Mismatches: 86
	Indels: 8
	Gaps: 3

[illegible]

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Oy      CTCGAAAGGAGGAGGGCTGTGTAGACAGCCCGGAGAGGCACTGAGCTCTTCTCCAGCCAGC
437      :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
Db      TLeagrgtgrbriunlathrgingnlnvalvalagvalaladaglnvalpronihspro
81      :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
Oy      GGGTTCAACAGAGCCTCCCAACAAAGACAGCCAGATGACATTCATCTGTGTGAAGATG
497      :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
Db      GlnlytGln-----PrognlnlnlsasprasnlsrmetleuLyuLyu 116
Oy      GCATGGCAGCTGTCCATACACCTGGGCTGGGAGCCGCGCCAGCTCTCTTACAGCTGTGC
557      :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
Db      GlnlytGlnValArgLeuValArgValValValValValValValValValValValValVal
117      :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
Oy      ACTGGTGGCAGCAGCTGCATTTCCGGCTGGGAGACAGCTGAGCCGCGCCAGTTAGC
617      :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
Db      SereroglythrProCysArgValSerGlytGlytGlytGlytGlytGlytGlytGlytGlyt
137      :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
Oy      CTGGCTCAACACCTGGGAGGCGGACACACCATCATGAGTACAGACAGCAGAGTGGAAAC
677      :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
Db      TytrProthralaleuincysvalasnvalasnlllemerSerGluGlnlnalCyslnizarg
157      :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
Oy      GCGTACCCCGGCAACATCAGACAGACACATGATGTGTGCAGCTGTCCAGAGAGGGGAG
737      :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
Db      AlatytrProGlylleIleIlethrSerGlymetValCysalaglyValProGlnlglyLys
177      :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
Oy      GACTCCCGCCAGGGGTACTCCGGGGGCGCTCTGGTCTGTAAACAGTCTCTTCAAGGCATT
797      :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
Db      AspSerGysglInGlyAspSerGlytGlytProLeuValCysGlyGlyGlnleuGlnGlyLyu
197      :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
Oy      ATCCCTGGGGGCGAGGATCCGATGTGGATGCCCAAGAGCCAGCTGTGTCTACAGAAAGTC
857      :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
Db      ValSerTerpLyuMetGlnArgCysalameTrProGlytGlytProGlytGlytGlytGlyt
217      :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
Oy      TGGAAATATGTGAGCTGATCCAGAGACAGAGAGCATTCAT
917      :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::
Db      CysAsnTyrlHisSerTrpIleGlnArgIleMetGlnSerAsn
237      :::::::::: :::::::::: :::::::::: :::::::::: :::::::::: ::::::::::

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RESULT	11		
09JMT0			
ID	09JMT0	PRELIMINARY:	PR: 261 AA.
AC	09JMT0;		
DT	01-OCT-2000 (TREMblrel. 15, Created)		
DT	01-OCT-2000 (TREMblrel. 15, Last sequence update)		
DT	01-MAR-2003 (TREMblrel. 23, Last annotation update)		
DE	Glandular kallikrein 21 (Similar to kallikrein 21).		
GN	KIK21 OR GK21.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=40534760; PubMed=11082197;		
RA	Matsui H., Moriyama A., Takahashi T.;		
RT	"Cloning and characterization of mouse Kik27, a novel tissue		
RT	kallikrein expressed in testicular Leydig cells and exhibiting		
RT	chymotrypsin-like specificity.";		
RL	Eur. J. Biochem. 267:6858-6865(2000).		

RP SEQUENCE FROM N.A.
RC TISSUE-Salivary gland;
RA Strausberg R.;
RL Submitted (Aug-2001) to the EMBL/Genbank/DBJ databases
DR EMBL; AB039276; BA98219.1; -
DR EMBL; BC012243; AAH12243.1; -
DR HSSP; P00757; 1SGF.
DR MEROPS; S01_038; -
DR MGD; MGI:892022; Kik21.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00089; trypsi1.1.
DR SMART; SM00020; Tryp_SPC.1.
DR PROSITE; PSS0240; TRYPSIN_DOM.1.
DR PROSITE; PS00134; TRYPSIN_HTS.1.
DR PROSITE; PS00135; TRYPSIN_SER.1.


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Db      99 PheasnarylstrleuAen-----AsnspilleMetleulleysleuSer 114
QY      560 TCGCCAGCTCCATCACCTGGGCTGTGCAGCCCTTCACCTCTCTGCTGCTACT 619
      115 SerProvalThrleuAenAlaArgValAlaThrValAlaLeuProSerSerCysAlaPro 134
QY      620 GCTGGCCAGCAGCTGCCCATTTCCGGCTGGGCGAGCAGCTCCACCCCACTTACGCTG 679
      135 AlaglyThrlnCysleuIleSerGlyTyrPglYasnThrleuSerPheGlyValSerGlu 154
QY      680 CCTCACACATGGCGATCGCCAGCCATCATCATCATTCATGACACAGCAAGTGGAGACGCC 739
      155 ProAspleuLeuGlnCysleuAspAlaProleuLeuProGlnAlaAspCysgluAlaSer 174
QY      740 TACCCCGGCAACATCACAGACACCATGTGTGTGCCAGCTGCGAGGAGGGGCGAGCAG 799
      175 TyrProGlyLysIleThrGlnGlyAsnMetCysAlaGlyPheLeuGlnGlyGlyLysasp 194
QY      800 TCGTGGCAGGGGTGACTCGGGGGGCCCTGTGTGTATACAGACTCTCTCAAGCATATATC 859
      195 SerCysGlnGlyAspSerGlyGlyProValCysAsnGlyLysGlnGlyLeuVal 214
QY      860 TCGTGGGCGCAGATCCGTGTGCATCACCCGAAAGCTGTGTGTCTACAGAAAGTCTGC 919
      215 SerTyrPglYtyrGly---CysAlaLeuProAspAsnProGlyValTyrThrLysValCys 233
QY      920 AATATGTGACGTGATTCACAGAGACGATGAACAAT 958
      234 AsnTyrValAspTrpIleGlnAspThrIleAlaAlaAsn 246

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RESULT 13

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ID      09CV76 PRELIMINARY; PRT; 234 AA.
AC      09CV76;
DT      01-JUN-2001 (TREMBLER, 17, Created)
DT      01-JUN-2001 (TREMBLER, 17, Last sequence update)
DE      01-MAR-2003 (TREMBLER, 23, Last annotation update)
DE      2310008B01RLK protein (Fragment).
GN      2310008B01RLK.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
OX      NCBI_Taxid=10090;
RN      [1]
SEQUENCE FROM N.A.
RC      STRAIN-G57B6/6J; TISSUE= Tongue;
RX      MEDLINE=21085660; Pubmed=11217851;
RA      Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA      Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA      Atzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA      Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito K.,
RA      Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA      Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA      Kiehl P., Lewis S., Matsuo Y., Nikaido I., Pezole G., Quackenbush J.,
RA      Schriml L.M., Stambli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA      Sakai K., Okido T., Furuno M., Momo H., Baldarelli R., Barsh G.,
RA      Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA      Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA      Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA      Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA      Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA      Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA      Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA      Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA      Hayashizaki Y.;
RT      "Functional annotation of a full-length mouse cDNA collection.";
CC      1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR      EMBL; AK009217; BAB26143.1; -.
DR      HSSP; P00763; IDPO.
DR      MEROPS; S01.020; -.
DR      MGD; MGI:1916761; 2310008B01RLK.
DR      InterPro; IPR001314; Chymotrypsin.

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DR      InterPro; IPR001254; Ser_protease_Try.
DR      Pfam; PF00089; Trypsin; 1.
DR      PRINTS; PR00722; CHYMOTRYPSIN.
DR      SMART; SM00020; TRYPSIN_DOM; 1.
DR      PROSITE; PS50240; TRYPSIN_DOM; 1.
DR      PROSITE; PS00134; TRYPSIN_HIS; 1.
DR      PROSITE; PS00135; TRYPSIN_SER; 1.
KW      Hydrolase; Protease; Serine protease.
FT      NON_TER 1
SQ      SEQUENCE 234 AA; 25888 MW; 6D81E609EDD39110 CRC64;

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Alignment Scores:

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Pred. No.: 4.52e-40 Length: 234
Score: 599.50 Matches: 108
Percent Similarity: 64.07% Conservative: 40
Best Local Similarity: 46.75% Mismatches: 78
Query Match: 25.30% Indels: 5
DB: 11 Gaps: 4

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US-09-856-320A-1 (1-1301) x 09CV76 (1-234)

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QY      269 AGCATCATCAAGGGGTGAGTGCAGACCTCATCTCCAGCCCTGGCAGGAGCCCTGTTC 328
      8 LysIleTyrAsnGlyValGlyValAlaLysAsnSerInProTyrGlnValGlyLeuPhe 27
QY      329 GAGAGACGGGCTACTCTGTGTGGGCGACGCTCATGCGCCCGAGATGCTCTGACAGCA 388
      28 HisGlyLysTyrLeuAlaGlyGlyGlyValLeuValAspArgLysTyrValLeuThrAla 47
QY      389 GCCACAGCTCCAGACCCCGCTCATATGATCTACCTGGGCGAGCAGCAACCTCCAGAGAG 448
      48 AlaHisCys--ArgAspLysTyrValValArgLeuGlnGlyHisSerLeuThrLysLeu 66
      449 GAGGCTGTGAGCAGACCCGCGACGACCATGATGCTTCCCGCCAGCCGCGCTTCACACAC 508
      67 AspTyrPheThrGlnGlnLeuAlaGlnHisThrPheSerIleThrHisProSerTyrGlnGly 86
QY      509 AGCCTCCCAACAAGACCCAGCATGATCATGCTGTGTAAGATGATGATGATGATGATGATG 568
      87 AlaTyrGlnAsn-----HisGlnHisAspLeuAlaGlyLeuAlaGlyLeuAlaGlyProIle 104
      569 TCCATCTCGGGGCTGGGCGACCCCTCCAGCTCCCGCGAGCTGTGCTGCTGCTGCTGCTG 628
      105 HisLeuThrArgAlaValAlaGlyProValAlaLeuProSerSerCysValThrThrGlyAla 124
QY      629 AGCTGCTCATTTCCGGCTGGGCGACGACGCTCCAGCCCGCCAGTTACGCTGCTCCACACC 688
      125 MetCysHisValSerGlyTyrPglYThrThrAsnLysProTyrAspProPheProAspArg 144
QY      689 TTGGGATGGCCCAACATCACCATCATTTGACACACAGTGTGAGAACGCTTACCCGGCC 748
      145 LeuGlnCysLeuAsnLeuSerThrValSerAsnGlnThrCysArgAlaValAlaPheProGly 164
QY      749 AACATCGACAGACACCATGATGGTGGCCAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 808
      165 ArgValThrThrLysAsnMetLeuCysAlaGly--GlyGlnAlaGlyLysAspAlaCysGln 183
QY      809 GGTGACTCCGGGGGCTGTGTGTGTAACAGTCTTTCAGAGCATATATCTCTGGGGC 868
      184 GlyAspSerIleGlyProLeuValGlyGlyValLeuGlnGlyLeuValSerTyrPglY 203
QY      869 CAG--GATCGGTGTGCGATCACCCGAAAGCTGGTGTATACAGAAAGTCTCAATAT 925
      204 SerValGlyProCysGlyGlnGlyGlyLeuProGlyValTyrThrLysValCysLysTyr 223
QY      926 GTGATCGATTCACAGAGACGATGAACAAT 938
      224 ThrAspTrpIleArgIleValIleArgAsnAsn 234

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RESULT 14

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ID      09ROT7 PRELIMINARY; PRT; 246 AA.
AC      09ROT7;

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DT	01-MAY-2000 (TrEMBLrel_13, Created)
DT	01-MAY-2000 (TrEMBLrel_13, Last sequence update)
DT	01-MAR-2003 (TrEMBLrel_23, Last annotation update)
DE	Pancreatic trypsin (O91000 B19RIK protein) (Trypsinogen 8).
GN	DT OR O91000 B19RIK OR TRYPSINOGEN.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J;
RC	STRAIN=129SVJ;
RX	MEDLINE=21085660; PubMed=11217851;
RA	Kawai J., Shinnaga A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA	Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA	Altava K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA	Fleischmann W., Gaasterland T., Glisai C., King B., Kochia H.,
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush
RA	Schirrl L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio
RA	Sakai K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G.,
RA	Blake J., Botfield D., Bojunga N., Carrinci P., de Bonaldo M.F.,
RA	Gustincich M.J., Balt C., Fletcher C., Fujita M., Gariboldi M.,
RA	Brownstein S., Hill D., Hofman C., Fujita M., Kamiya M., Lee N.H.,
RA	Lions P., Marchionni L., Mashima J., Mazzarelli J., Momhaerts P.,
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storck K.-
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming
RA	Yushaw-Boris A.Y., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA	Hayashizaki Y.;
RT	"Functional annotation of a full-length mouse cDNA collection.";
RL	Nature 409:685-690(2001).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	STRAIN=129;
RC	MEDLINE=21103195; PubMed=11160223;
RA	Chen F., Rowen L., Hood L., Rothenberg E.V.;
RT	"Differential transcriptional regulation of individual TCR beta
RT	segments before gene rearrangement.";
RL	J. Immunol. 166:1771-1780(2001).
CC	-1 - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR	EMBL: AB017032; BAA74761.1; -
DR	EMBL: AK008667; BAB25821.1; -
DR	EMBL: AK003064; BAB25242.1; -
DR	EMBL: AE000664; AAB69056.1; -
DR	HSSP: P00763; ISLU.
DR	MEROPS: S01.057; -
DR	MCD: MGI:1913350; O91000 B19RIK.
DR	InterPro: IPR001314; Chymotrypsin.
DR	InterPro: IPR001254; Ser_Protease_Try.
DR	Pfam: PF00089; trypsin. 1.
DR	PRINTS: PR00722; CHYMOTRYP SIN.
DR	SMART: SM00020; TRYP_SPC: 1.
DR	PROSITE: PSS0240; TRYPSIN_DOM: 1.
DR	PROSITE: PS00134; TRYPSIN_HIS: 1.
DR	PROSITE: PS00135; TRYPSIN_SER: 1.
DR	Hydrolase; Protease; Serine protease.
SQ	SEQUENCE 246 AA; 26274 MW; B6A9F4C9079633F CRC64;

Best Local Similarity:	46.64%	Mismatches:	87
Query Match:	25.25%	Indels:	7
DB:	11	Gaps:	4
US-09-856-320A-1 (1-1301) x Q9ROT7 (1-246)			
QY	200	CTCCAGGCCATGAGGATTTGCGAGTTAAATCTTCCTGCTCTGCGCAACAGGGCTTTGAGG	259
DB	1	MetaAgalialeuleuPheuleuAlauleuValIglYAlaAlaValAlaPhePro--ValAsp	19
QY	260	GGAGGAGCAGGATATCATAGGAGGGTTCGAGTGGACCCATCACCCAGCCCGGACAGGCA	319
DB	20	AspAspAspIleValIleValIleYlyThrCysAlaGluInsSerVal)ProYrgIlnVal	39
QY	320	GCCCTGTTGAGAGAGACGGGGCTACTCTGTGGGGCAGCGCTCATCCGCCCAATGGCTC	379
DB	40	SeuIeu---AsnSerGlyThrHisPheCysGlyGlySerIeuIleAsnAspGlnTrpVal	58
QY	380	CTGACAGACAGCCCACTGCTCATAGCCCGCTCATATGTTCCACTGGGGACAGCAACCTC	439
DB	59	ValSerAlaAlaHisCysArgIlySerArgIleGlnValAlaArgIleuGlyIlnHisAsnIle	78
QY	440	CAGAGGAGGAGGGGTGTGAGCAGACCCGGACAGCCACAGAGCTCTCCGCCACCCGGC	499
DB	79	AsnValIleuGlyIlnGlyAsnIleuIlnPheValAlaAsnSerAlaIleIleYlyHisProAsn	98
QY	500	TTTCAACAACAGCGCTCCCAACAAGAACACCCGATGATCATGCTGTGGAGATGGCA	559
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QY	560	TCCGAGTCTCTCATGACCTGGGCTGTGCGACCCCTCACCCCTCTCCACAGCTGTGCAT	619
DB	115	SerProValThrLeuAsnAlaArgValAlaThrValAlaLeuProSerSerCysAlaPro	134
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DB	135	AlaGlyThrIlnGlyCysLeuIleSerIlyTrpGlyAsnThrLeuSerPheGlyIlnAsnAsn	154
QY	680	CCTCACACCTTGCGAGTGGCGCCAAACATCACATGATGACACACAGAGAGTGTGAGACGGC	739
DB	155	ProAspIleuGlnIlnCysLeuAspAlaProLeuIlnProGlnAlaIlnAspCysGlnAlaSer	174
QY	740	TACCCGGCCATCATCAGACACACCATGTGTGTGCCAGCGTCAGAGAGGGGCGCAAGAC	799
DB	175	TyrProGlyIlyIleThrAsnAsnMetIleCysValIglYPhelGlnIlnGlyIlyAsp	194
QY	800	TCTCTGCCAGGAGATCCGGGGGCCCTCTGGTCTGTAAACCACTTCTTAAAGCAATTAC	859
DB	195	SerCysGlnIlnGlyAspSerIlyIlyProValIlnCysAsnGlyIlnIlnIlnGlyIlnIleVal	214
QY	860	TCTCTGGGCGCAGAGTCCGTGTCAGATCACCCGAAAGCCGTGTGTACAGAAAGTCTGC	919
DB	215	SerTrpGlyIlyTrgIly---CysAlaIlnIlnGlyAspAsnProGlyIlyAllyThrIlyAsCys	233
QY	920	AAATATGTGACTGATCCAGAGAGAGCAAGAAACAT	958
DB	234	AsnTrpValAspTrpIleGlnAsnThrIleAlaIlnAsn	246
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ID	Q63275	PRELIMINARY;	PRT; 239 AA.
AC	Q63275;		
DT	01-NOV-1996 (TREMBLrel. 01, Created)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DE	Kallikrein (Fragment).		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Sprague-Dawley; TISSUE=Submandibular gland;		

Search completed: October 15, 2003, 20:25:39
Job time : 96.3292 secs

RA Zintz C.B., Ma J.-X., Chao J., Chao L.:
RT "Isolation and characterization of a new rat kallikrein cDNA with
predominant expression in the kidney."
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: L33840; AAA58782.1; -
DR HSSP: P00759; 1TON.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; Trypsin; 1.
DR SMART: SM00020; TRYP_SPC; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
FT NON_TER 1
SQ SEQUENCE 239 AA; 26382 MW; 3CBD761AF06AB53 CRC64;

Alignment Scores:

Pred. No.:	6,58e-40	Length:	239
Score:	597.50	Matches:	107
Percent Similarity:	64.85%	Conservative:	48
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US-09-856-320a-1 (1-1301) x Q63275 (1-239)

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OY 320 GCCCTGTTCGAGAGCGGGCTACTCTGTGGGGCGGCGTCATCGCCCGCAGATGGCTC 379
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Db 25 AlaValIleasnGluasp-----LeucyG1yG1yValIleuIleaspProSerTrpVal 42
OY 380 CTGACAGACGACCCGACCTGCTCAAGCCCGCTACATAGTCACCTGGGGCAGACAACTC 439
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OY 500 TTC-----AACACAGCCTCCCAACAAAGCCACCGCATGACATC 541
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OY 542 ATGCTGTGTAAGATGCGATCGCATCTCCATCACTGAGGCTGCGACCCCTCACCCCTC 601
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OY 602 TCCTCAGCGTGTGTCACTGTGTCGACACGAGCTGCCTCAATTCGGCTGGGGCAGACGTC 661
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Db 120 ProThrLysGlnProLysValG1ySerThrCysLeuValSerGlyTrpGlySerThrAsn 139
OY 662 AGCCCCAGTTAGCCCTTCACACCTTCGATCGCCCAACATCACCATCATTTGACAC 721
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Db 140 ProSerGlnTrpGlnPheProAspAspLeuGlnCysValAsnIleHisIeuLeuSerAsn 159
OY 722 CAGAGTGTGAGAGCGCTACCCCGGACGATCAGACACACCATGCTGTGCGCAGCGCTG 781
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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OY 782 CAGGAAGGGGCGAAGCACTCTCCAGAGGTGACTCCGGGGGCCCTGTGTCTGAACCA 841
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OY 842 TCTCTCAAGGCATTTACTCTGGGGCGAGATCCGTGTGCGATCACCCGAAGCGTGT 901
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Db 220 IleTyLrThrLysIleuIleLysPheThrSerTrpIleLysGlnValMetLysLysAsn 238
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 15, 2003, 11:49:23 ; Search time 3549.61 Seconds

(without alignments)
8908.057 Million cell updates/sec

Title: US-09-856-320A-1

Perfect score: 1301
Sequence: 1 cgccttgcctccacaccttgg.....aaaaaaaaaaaaaaaaaaaa 1301

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Database :

EST:*
1: em_estdb:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_huv:*
19: em_gss_pin:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_pig:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1263.8	97.1	1294	11	BC015551 Homo sapi
2	855.6	65.8	1072	12	BM559782 AGENCOURT
3	825.2	63.4	1074	12	BM559617 AGENCOURT
4	757.4	58.2	761	12	BM982377 UI-CF-EN1

5	725.6	55.8	853	10	BG720793	BG720793 602692015
6	719.4	55.3	841	12	B1818697	B1818697 603037514
7	701.4	53.9	747	13	BX109836	BX109836 Bx109836
8	668.2	51.4	673	13	B0684799	B0684799 UI-CF-EN1
9	659.6	50.7	678	12	B1763040	B1763040 603047836
10	657.4	50.5	973	10	BE867930	BE867930 601443517
11	638.2	49.1	1295	11	AK009360	AK009360 Mus muscu
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14	626.2	48.1	1269	11	AK009659	AK009659 Mus muscu
15	616	47.3	654	13	B0676834	B0676834 UI-CF-D01
16	559.8	43.0	639	10	BG747134	BG747134 602704354
17	548	42.1	644	10	BE219655	BE219655 hv60910.x
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19	525.4	40.4	560	10	BF476474	BF476474 naa25d06..
20	493.6	37.9	517	9	A1217150	A1217150 qf47e06.x
21	491.4	37.8	501	9	A1521607	A1521607 t65e07.x
22	480.4	36.9	483	9	A1183346	A1183346 qd41b10.x
23	469	36.0	469	14	CA437458	CA437458 UI-H-D10-
24	468.4	36.0	539	12	BM837078	BM837078 K-EST0113
25	456.2	35.1	502	9	A1283289	A1283289 qul3f05.x
26	445	34.2	579	12	B1046611	B1046611 MR3-FN020
27	444.6	34.2	479	9	AW000834	AW000834 w46b01.x
28	435	33.4	449	9	AA436049	AA436049 zu01c07.t
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31	421.4	32.4	425	14	CD107547	CD107547 AGENCOURT
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33	406.2	31.2	422	9	A1624187	A1624187 ts42a04.x
34	404.2	31.1	417	9	AA403004	AA403004 zu54e10.s
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37	387.6	29.8	528	4	BX528424	BX528424 R2PD Mus
38	370.6	28.5	484	14	CB270157	CB270157 1009064.H
39	370.2	28.5	696	12	BM020073	BM020073 603648624
40	369.4	28.4	419	9	A1913780	A1913780 w401g10.x
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ALIGNMENTS

RESULT 1
LOCUS BC015551 1294 bp mRNA HTC 29-OCT-2001
DEFINITION Homo sapiens, kallikrein 11, clone IMAGE:3847565, mRNA.
ACCESSION BC015551
VERSION BC015551.1 GI:15930236
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1294)
REFERENCE
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LML)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>


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Site.2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb. Insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC library."
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801 ACTCTGCCAGGCTACTCCGGGGCCCTGTGCTGTGAACAGCTCTTCAAGCATTA 860
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858 TCTCTGTGGG-CCAGGATCCGTGTGCGATCACCCGAAAGCCTGTGTCTACAC---GAAA 913
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RESULT 3
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LOCUS AGENCOURT_6565456 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5744314
DEFINITION 5', mRNA sequence.
ACCESSION BM559617
VERSION BM559617.1 GI:18803348
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1074)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-riemail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNT)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNT at:
http://image.llnl.gov
Plate: L14M12765 row: h column: 11
High quality sequence stop: 689.
Location/Qualifiers
1. 1074

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Site.2: EcoRV (destroyed); RNA source normal medulla from
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directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb. Insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC library."
this is a NIH_MGC library."
BASE COUNT      238 a      339 c      311 g      184 t      2 others
ORIGIN

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Best Local Similarity 98.3%; Pred. No. 8.5e-78;
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Best Local Similarity 98.3%; Pred. No. 8.5e-78;
Matches 885; Conservative 0; Mismatches 10; Indels 5; Gaps 5;

18 TGGTCAGGGGAGAGGGGAGGAAAGCCAGGAGGAGGACCTTAAGTGAAGAAACAAACAGC 77
|||||
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|||||
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QY      738  CCTACCCCGGAGCATACAGACACCATGCTGTGGAGCGTGCAGAGAGGGGGAGG 797
Db      740  CCTACCCCGGAGCATACAGACACCATGCTGTGGAGCGTGCAGAGAGGGGGAGG 799
QY      798  ACTCTCCGAGAGGCTGACTCC-GGGGGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 856
Db      800  ACTCTCCGAGAGGCTGACTCCGGGGGGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 859
QY      857  ATCTCTCT-GGGGCCAGATCCGT-GTGGCATCACCCGAAA-GCCTGTGTCTACAGAAA 913
Db      860  ATCTCTCTGGGGGGGAGNATCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 919

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RESULT 4

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BM982377/c 761 bp mRNA linear EST 21-FEB-2003
LOCUS      BM982377
DEFINITION UI-CF-EN1-acs-o-17-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
ACCESSION  BM982377
VERSION    BM982377.1 GI:19605813
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 761)
            Bonaldi,M.F., Lennon,G. and Soares,M.B.
            Normalization and subtraction: two approaches to facilitate gene
            discovery
            Genome Res. 6 (9), 791-806 (1996)
JOURNAL    MEDLINE 97044477

```

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PUBMED 8889548
COMMENT Contact: McCray, PB
        McCray Lab
        University of Iowa
        2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
        Tel: 319 356 4866
        Fax: 319 356 7171
        Email: paul-mccray@uiowa.edu
        Tissue Procurement: Dr. M. J. Welsh, University of Iowa
        CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
        CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
        DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
        Clone Distribution: Researchers may obtain clones from Research
        Genetics (www.resgen.com) or from Open Biosystems
        (www.openbiosystems.com).
        The following repetitive elements were found in this CDNA
        sequence: 17-100, >LINE2 (matched compliment)
        Seq primer: M13 FORWARD
        POLYA-Tes.

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FEATURES

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source Location/Qualifiers
1..761
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-EN1-acs-o-17-0-UI"
/lissue_type="Primary Lung Cystic Fibrosis Epithelial
Cells"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EN1"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-EN1 is a normalized cDNA library containing the
following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT73-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dr)18 tail. The
sequence tag for this library is CTGCTCAGT.
TAG_LIB-UI-CF-EN1
TAG_TISSUE=Human Lung Epithelial Cell lines untreated LPS
6hr to LPS 24h
TAG_SFO=CTGCTCAGT"
BASE COUNT 172 a 170 c 222 g 195 t 2 others
ORIGIN
Query Match 58.2%; Score 757.4; DB 12; Length 761;
Best Local Similarity 99.6%; Pred. No. 1.3e-70;
Matches 758; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY      527  CACCGCAATGATCATGCTGTGAGAGAGGATCGGCACTGTCATCAGCTGGGCTGTG 586
Db      761  CACCGCAATGATCATGCTGTGAGAGAGGATCGGCACTGTCATCAGCTGGGCTGTG 702
QY      587  CGACCCCTACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 646
Db      701  CGACCCCTACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 642
QY      647  TGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 706
Db      641  TGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 582
QY      707  ACCATATTGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 766
Db      581  ACCATATTGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 522
QY      767  GTGTGTGACAGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 826

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Db      521 GGTGTGCCAGGCTGACGAGAGGGGCAAGAGACTCTCTGCCAGGCTGACTCCGGGGCCCT 462
QY      821 CTGTCTGTACACAGTCTCTTAAGGCAATTATCTCTGGGGCCAGAGATCGTGTGGATC 886
Db      461 CTGTCTGTACACAGTCTCTTAAGGCAATTATCTCTGGGGCCAGAGATCGTGTGGATC 402
QY      887 ACCCGAAGCCGCTGTACACAGAGAGCTGCAAAATATGTGAGCTGGATCCAGAGAGAC 946
Db      401 ACCCGAAGCCGCTGTACACAGAGAGCTGCAAAATATGTGAGCTGGATCCAGAGAGAC 342
QY      947 ATGAAGAACATTAAGACTGAGACCCACCCACAGCCCATCCATTCACCTTGG 1006
Db      341 ATGAAGAACATTAAGACTGAGACCCACCCACAGCCCATCCATTCACCTTGG 282
QY      1007 TGTGTGTTCTGTCTGCTCTGTATATAAGAAACCCCTAAGCAGCCCTTACGAAAT 1066
Db      281 TGTGTGTTCTGTCTGCTCTGTATATAAGAAACCCCTAAGCAGCCCTTACGAAAT 222
QY      1067 TGTGTGTTCTGTCTGCTCTGTATATAAGAAACCCCTAAGCAGCCCTTACGAAAT 1126
Db      221 TGTGTGTTCTGTCTGCTCTGTATATAAGAAACCCCTAAGCAGCCCTTACGAAAT 162
QY      1127 ATCAGTGAAGACCTGATTCATTAATTCGCTTGAATATGTGACTCTGGGAATGACAA 1186
Db      161 ATCAGTGAAGACCTGATTCATTAATTCGCTTGAATATGTGACTCTGGGAATGACAA 102
QY      1187 CCTGTGTTGTTCTGTCTGTTATCCCGAGCCCAAGACAGCTCTGGCCATATATCAAG 1246
Db      101 CCTGTGTTGTTCTGTCTGTTATCCCGAGCCCAAGACAGCTCTGGCCATATATCAAG 42
QY      1247 TTTCATATAATTTTTCCTAATGAAAAAATTTTAAAAA 1287
Db      41 TTTCATATAATTTTTCCTAATGAAAAAATTTTAAAAA 1

RESULT 5
Bg720793      853 bp      mRNA      linear      EST 08-MAY-2001
LOCUS      602692015F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4824387 5',
DEFINITION      mRNA sequence.
ACCESSION      Bg720793
VERSION      Bg720793.1 GI:13999980
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 853)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki
Toshiyuki and Piero Carninci (RIKEN)
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM10735 row: n column: 04
High quality sequence stop: 826.
Location/Qualifiers
1..853
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4824387"
/lab_host="DHI0B"
/clone_11b="NIH_MGC_97"
/note="Organ: testis; Vector: pBluescriptR (modified
pbluescript Ks+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag

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); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.2 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH-MGC library."
BASE COUNT      180 a      285 c      227 g      161 t
ORIGIN
Query Match      55 8%; Score 725.6; DB 10; Length 853;
Best Local Similarity 99.2%; Pred. No. 2.5e-67;
Matches 750; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
174 AGGAACCTGGGGCCCGCTCTCCCTCCCTCAGAGCCATGAGATTCTGCAATATCTCC 233
98 AGGAACCTGGGGCCCGCTCTCTCCCTCCAGGCAATGAGATTCTGCAATATCTCTC 157
234 TTGCTGTGGCAACAGGGCTTTAGGGGAGAGACAGATCATCAAGGGGTTGAGTGCA 293
158 TTGCTGTGGCAACAGGGCTTTAGGGGAGAGACAGATCATCAAGGGGTTGAGTGCA 217
294 AGCCTCAGTCCAGAGCCCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 353
218 AGCCTCAGTCCAGAGCCCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 277
354 GCAGCTCATGCGCCCGCAGATGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 413
278 GCAGCTCATGCGCCCGCAGATGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 337
414 TAGTTTACCTGGGGAGAGCAACCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 473
338 TAGTTTACCTGGGGAGAGCAACCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 397
474 CCAGTGAAGTCTTCCCGCCAGCCCGGCTTCAAAAGAGTCTCCCAAGAGAGAGAG 533
398 CCAGTGAAGTCTTCCCGCCAGCCCGGCTTCAAAAGAGTCTCCCAAGAGAGAGAG 457
534 ATGACATCATGCTGTGTAAGATGATGATGATGATGATGATGATGATGATGATGAT 593
458 ATGACATCATGCTGTGTAAGATGATGATGATGATGATGATGATGATGATGATGAT 517
594 TCACCTCTCTCTACAGCTGTGCTACTGCTGGACACAGCTGCTCATTTCCGGCTGG 653
518 TCACCTCTCTCTACAGCTGTGCTACTGCTGGACACAGCTGCTCATTTCCGGCTGG 577
654 GCAGCTCAGAGCCCGCAGTATGAGCCCTGCTCAGACCTTGGAGTGGCCAAATC 713
578 GCAGCTCAGAGCCCGCAGTATGAGCCCTGCTCAGACCTTGGAGTGGCCAAATC 637
714 TTGAGCAGCAGAGTGTGAGAGAGCTACCCCGGCAATCATCAGACACATGATGTG 773
638 TTGAGCAGCAGAGTGTGAGAGAGCTACCCCGGCAATCATCAGACACATGATGTG 697
774 CCAGGCTGAGAGAGGGGGCAAGAGCTCTGCGAGAGTACTCCGGGGCCCTCTGTC- 832
698 CCAGGCTGAGAGAGGGGGCAAGAGCTCTGCGAGAGTACTCCGGGGCCCTCTGTC- 756
833 TGTACACAGTCTCTTCAAGAGCTTATCTCTCTGGGGCCAGAGATCTGTGATCAGCG 892
757 TGTACACAGTCTCTTCAAGAGCTTATCTCTCTGGGGCCAGAGATCTGTGATCAGCG 816
893 AAGCTGTGTCTTACAGAGAGTGTGCAAAATGTG 928
817 AAGCTGTGTCTTACAGAGAGTGTGCAAAATGTG 852

RESULT 6
Bg18697      841 bp      mRNA      linear      EST 04-OCT-2001
LOCUS      603037514F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178746 5',
DEFINITION      mRNA sequence.
ACCESSION      Bg18697

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VERSION B1818697.1 GI:15930247
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Mammalia: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 841)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs.fda.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LNL1445 row: k column: 03
High quality sequence stop: 784.
Location/Qualifiers
1..841
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:518746"
/lab_host="DH10B"
/clone_11b="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector:
PCMV-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

BASE COUNT 180 a 288 c 206 g 167 t
ORIGIN

Query Match 55.3%; Score 719.4; DB 12; Length 841;
Best Local Similarity 97.1%; Pred. No. 1.1e-66;
Matches 817; Conservative 0; Mismatches 16; Indels 8; Gaps 8;

QY 286 CGAGTGCAGGCTCTACTCCAG-CCCTGGAGGAGCCCTGTGGAGAAGACGGGCTAC 344
Db 1 CGAGTGCAGGCTCTACTCCAGTCCCTGGAGGAGCCCTGTGGAGAAGACGGGCTAC 60

QY 345 TCTGTGGGGGAGCCTATGCCCCGAGATGCTCTGACAGCAGCCCACTGCTCAAGC 404
Db 61 TCTGTGGGGGAGCCTATGCCCCGAGATGCTCTGACAGCAGCCCACTGCTCAAGC 120

QY 405 CCGGCTACATAGTTCACCTGGGGAGCAACAACCTCCAGAAAGAGAGGGGCTGTAGAGA 464
Db 121 CCGGCTACATAGTTCACCTGGGGAGCAACAACCTCCAGAAAGAGAGGGGCTGTAGAGA 180

QY 465 CCC-GGACAGGACATGAGTCTTCCACCCAGCCGGCTTCAACAACAGCCTCCCAACAA 523
Db 181 CCGGAGAGGACATGAGTCTTCCACCCAGCCGGCTTCAACAACAGCCTCCCAACAA 240

QY 524 GACACCGCAATGACATGCTGTGTAGATGAGGATGCGCATGCTCC-ATCAGCTGGGC 582
Db 241 GACACCGCAATGACATGCTGTGTAGATGAGGATGCGCATGCTCC-ATCAGCTGGGC 300

QY 583 TGTGCGAGCCCTCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 642
Db 301 TGTGCGAGCCCTCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360

QY 643 CGGCTGGGGAGAGCAGTTCAGAGCCCGAGTTACGCTGCTTCACACCTTGGAGTGGCAA 702
Db 361 CGGCTGGGGAGAGCAGTTCAGAGCCCGAGTTACGCTGCTTCACACCTTGGAGTGGCAA 420

QY 703 CATCACCATCATTTAGACACGAGAGTGTGAGAACGCCCTACCCCGCAATCATCAGACAC 762
Db 421 CATCACCATCATTTAGACACGAGAGTGTGAGAACGCCCTACCCCGCAATCATCAGACAC 480

QY 763 CATGCTGTGTGCCAGCTGTCAGAGA-AGGGGCAAGAGACTCTGCGAGGAGTCTCCGGG 821
Db 481 CATGCTGTGTGCCAGCTGTCAGAGAAGGGGCAAGAGACTCTGCGAGGAGTCTCCGGG 540

QY 822 GCCCTGTGTGTGTAACAGATCTCTTCA-AGCATTTATCTCTGGGGCCAGAGATCCGTGT 880
Db 541 GCCCTGTGTGTGTAACAGATCTCTTCAAGCATTTATCTCTGGGGCCAGAGATCCGTGT 600

QY 881 GCGATTCACCCGAAAGCCTGTGTGTACACGAAAGTGTCAAAATGTGTGAGATGATCAG 940
Db 601 GCGATTCACCCGAAAGCCTGTGTGTACACGAAAGTGTCAAAATGTGTGAGATGATCAG 660

QY 941 GAGACGATGAAAGCAATTTAGACTGAGACCCACCA-CCACAGCCCATCACCCTTCATTC 999
Db 661 GAGACGATGAAAGCAATTTAGACTGAGACCCACCAAGCATTCATGCAATCACCCTTCATTC 720

QY 1000 CACTTGTGT-TTGTCTCTGTCTACTCTGTATA-AGAAACCTTAAGCAAGACCTC 1057
Db 721 CACTTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 780

QY 1058 TACGACATCTTTGGGCTCTCTGACTACAGAGATGCTGTCTTAATATCAACCTG 1117
Db 781 TGCAGACCTCTTTGGGCTCTCTGACTACAGAGATGCTGTCTTAATATCAACCTG 840

QY 1118 G 1118
Db 841 G 841

RESULT 7
BX109836 747 bp mRNA linear EST 07-FEB-2003
BX109836 Soares, fetal, heart, NBH19W Homo sapiens cDNA clone
IMAGE:98A02781; IMAGE:342025, mRNA sequence.
BX109836
BX109836 B1:2877879
EST.
Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Mammalia: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 747)
AUTHORS Ebert, L., Hell, O., Hennig, S., Neubert, P., Parsch, E., Peters, M.,
Radeflo, U., Schneider, D., and Korn, B.
TITLE Human UniGeneSet - RZPD3
JOURNAL Unpublished
COMMENT Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD: IMAGP98A02781.
RZPDLIB: I.M.A.G.E. cDNA Clone Collection;
Human UniGeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/cloneCards/cg1-
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 101
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTTCACACAGGAAACGCTATGAC.
Location/Qualifiers
1..747
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:98A02781; IMAGE:342025"

Best Local Similarity 99.6%; Pred. No. 2.9e-61;
Matches 670; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 619 TGCTGGACACAGCTGCTCATTTTCGGGCTGGGAGACGTCAGCCCGCATTTACGCT 678
Db 673 TGCTGGACACAGCTGCTCATTTTCGGGCTGGGAGACGTCAGCCCGCATTTACGCT 614
QY 679 GCTTCACACCTTGGATGCGGCAACATCACCATTCATTGAGCAGCAAGTGTGAAGCG 738
Db 613 GCTTCACACCTTGGATGCGGCAACATCACCATTCATTGAGCAGCAAGTGTGAAGCG 554
QY 739 CTACCCGGGCAACATCAGACACCATGCTGTGCGAGCGTGCAGGAAGGGGCAAGA 798
Db 553 CTACCCGGGCAACATCAGACACCATGCTGTGCGAGCGTGCAGGAAGGGGCAAGA 494
QY 799 CTCTGGCAGGGTACTCCGGGGCCCTGCTGTGTAAACCACTCTCTTCAAGCATAT 858
Db 493 CTCTGGCAGGGTACTCCGGGGCCCTGCTGTGTAAACCACTCTCTTCAAGCATAT 434
QY 859 CTCTGGGGCCAGATCCGTGTGCGATCACCAGAAAGCTGTGTACAGAAAGTCTG 918
Db 433 CTCTGGGGCCAGATCCGTGTGCGATCACCAGAAAGCTGTGTACAGAAAGTCTG 374
QY 919 CAATATGTGAGTGCATGATCCAGAGATGAAGAATAGATGACCCAGCCACCA 978
Db 373 CAATATGTGAGTGCATGATCCAGAGATGAAGAATAGATGACCCAGCCACCA 314
QY 979 CAGCCATCAACCTTCATCTTCTCACTTGTGTCTGCTGCTGTATTAAGA 1038
Db 313 CAGCCATCAACCTTCATCTTCTCACTTGTGTCTGCTGCTGTATTAAGA 254
QY 1039 ACCCTAAGCCAAAGCCTCTACAGCAATCTTTGGCCCTCTGATACAGAGATGCTG 1098
Db 253 ACCCTAAGCCAAAGCCTCTACAGCAATCTTTGGCCCTCTGATACAGAGATGCTG 194
QY 1099 TCACTTAATATCAACCTGGGGTCTGAAATCAGTGAACCTGATTAATTCGCTTG 1158
Db 193 TCACTTAATATCAACCTGGGGTCTGAAATCAGTGAACCTGATTAATTCGCTTG 134
QY 1159 AAATATTTGTGACTGTGGGAATGACAAACCTGTTTCTCTGTTATCCAGCCG 1218
Db 133 AAATATTTGTGACTGTGGGAATGACAAACCTGTTTCTCTGTTATCCAGCCG 74
QY 1219 AAAGACAGCTCTGTGCAATATATCAAGTTTCAATTAATTTCTTAATGAAAAA 1278
Db 73 AAAGACAGCTCTGTGCAATATATCAAGTTTCAATTAATTTCTTAATGAAAAA 14
QY 1279 AAAAAAAAAA 1291
Db 13 AAAAAAAAAA 1

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RESULT 9
B1763040 678 bp mRNA linear EST 25-SEP-2001
LOCUS 603047836F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:518796 5',
DEFINITION mRNA sequence.
ACCESSION B1763040
VERSION B1763040.1 GI:15754618
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 678)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgs@bldc.ncl.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://lml1469.ncl.nih.gov
plate: lml1469 row: h column: 09
High quality sequence stop: 647.

FEATURES
source
Location/Qualifiers
1..678

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5187896"
/lab_host="DH10B"
/clone_id="NIH_MGC_116"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMW-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 3 clones; age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

BASE COUNT 152 a 234 c 172 g 120 t
ORIGIN

Query Match 50.7%; Score 659.6; DB 12; Length 678;
Best Local Similarity 98.7%; Pred. No. 2.3e-60;

Matches 665; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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QY 321 CCTGTTTCGAGAAAGCAGCGCTACTCTGTGGGGGAGAGCTCAGTCCGCGAGATGCTCC 380
Db 5 CCTGTTTCGAGAAAGCAGCGGTACTCTGTGGGGGAGAGCTCAGTCCGCGAGATGCTCC 64
QY 381 TGACAGCAGCCACTGCTCTCAAGCCCGCTACATATGTTCACTGGGGCAGACACCTCC 440
Db 65 TGACAGCAGCCACTGCTCTCAAGCCCGCTACATATGTTCACTGGGGCAGACACCTCC 124
QY 441 AGAAGGAGGAGGGGTGTGAGAGAGACCGGAGCAGTGAAGTCTTCCGACCCGCGCT 500
Db 125 AGAAGGAGGAGGGGTGTGAGAGAGACCGGAGCAGTGAAGTCTTCCGACCCGCGCT 184
QY 501 TCAACAACAGCTTCCCAACAAGAACCCGCAATGATCATATGCTGTGAAGTGCAT 560
Db 185 TCAACAACAGCTTCCCAACAAGAACCCGCAATGATCATATGCTGTGAAGTGCAT 244
QY 561 CGCCAGTCTCATACCTGGGCTGTGAGACCCCTCAACCTCTCTCAAGCTGTCTCACTG 620
Db 245 CGCCAGTCTCATACCTGGGCTGTGAGACCCCTCAACCTCTCTCAAGCTGTCTCACTG 304
QY 621 CTGGCAGCAGGTGCTCATTTCCGGCTGGGGGAGCAGTCCAGGCCGCTTACGCTGC 680
Db 305 CTGGCAGCAGGTGCTCATTTCCGGCTGGGGGAGCAGTCCAGGCCGCTTACGCTGC 364
QY 681 CTGACACCTTGCATGCGGCAACATCAATCAATTTGAGCAACGAAGTGTGAGAACGCT 740
Db 365 CTGACACCTTGCATGCGGCAACATCAATCAATTTGAGCAACGAAGTGTGAGAACGCT 424
QY 741 ACCCGGCAACATCAACAGACATCATGTTGTGCGACGCTGACAGAAAGGGGCAAGACT 800
Db 425 ACCCGGCAACATCAACAGACATCATGTTGTGCGACGCTGACAGAAAGGGGCAAGACT 484
QY 801 CTGCGCAGGGTGAATCCGGGGGCGCTGTGTGTATCAACAGTCTCTTCAAGGATATATCT 860
Db 485 CTGCGCAGGGTGAATCCGGGGGCGCTGTGTGTATCAACAGTCTCTTCAAGGATATATCT 544
QY 861 CTTGGGGCCAGGATCCGCTGTGCGATCACCGGAAGCGTGTGTCTACAGAAAGTGTGCA 920
Db 545 CTTGGGGCCAGGATCCGCTGTGCGATCACCGGAAGCGTGTGTCTACAGAAAGTGTGCA 604
QY 921 AATATGTGAGTGCATGATCCAGAGACGATGAAGAAATTAATGACTGACCCACCCACCA 980

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Db      605 AATATGTGGACTGATCCAGAGAGCATGAAGAAACATTAGACTGGACCCAGCCACCAAG 664
Oy      981 GCCCATCACCCTCC 994
        |||||
Db      665 GCCCATCACCCTTC 678

RESULT 10
LOCUS   BB867930
DEFINITION 60143517F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847565 5',
          mRNA sequence.
ACCESSION BE867930
VERSION   BE867930.1 GI:10316706
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 973)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT    Contact: Robert Strausberg, Ph.D.
          Email: cgabbs-remail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Life Technologies, Inc.
          DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          plate: LLAM9562 row: a column: 06
          High quality sequence stop: 714.
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  /clone="IMAGE:3847565"
  /tissue_type="adenocarcinoma"
  /lab_host="DH10B (phage-resistant)"
  /clone_11b="NIH_MGC_65"
  /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
  Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
  Average insert size 1.8 kb. Library constructed by Life
  Technologies."
BASE COUNT  241 a 302 c 288 g 142 t
ORIGIN
Query Match 50.5%; Score 657.4; DB 10; Length 973;
Best Local Similarity 90.7%; Pred. No. 3.1e-60;
Matches 759; Conservative 0; Mismatches 66; Indels 12; Gaps 5;

Oy      16 CCTGTCAGGGAGAGAGGGGAGAAAGCCAAAGGAGACCTTAAGTGAACAAACA 75
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        |||||
Db      61 GCTGGAGAGAGAGAGATCTCGCTCGGGTCCGAGATGCGAGATTGAGGTGCTCGC 120
Oy      136 GGACTGGAAGTCATCGGGCAGAGAGTCTCACAGCAGCAAGAACCTGGGCCCTCTCTC 195
        |||||
Db      121 GGACTGGAAGTCATCGGGCAGAGAGTCTCACAGCAGCAAGAACCTGGGCCCTCTC 180
Oy      136 CCCCTCCAGAGCCATGAGAGATTCTCAATTAACTCTGCTGTGGCAACAGGGCTTGT 255
        |||||
Db      181 CCCCTCCAGAGCCATGAGAGATTCTCAATTAACTCTGCTGTGGCAACAGGGCTTGG 240
Oy      256 AGGGGAGAGAGACAGATCATC---AAGGGGTGAGTGAAGCCTCACTCCAGCCCT 311
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Db      241 TAGGGGGAAGAGACAGAGATCATCAAGGGGGTTCGAGTGCAGACCTCACTCCAGCCCT 300
Oy      312 GCAGAGCAGCCCTGTTTCGAGAGACGGCGCTACTCTGTGGGGAGAGCGTCATCGGCCCA 371
        |||||
Db      301 GGCAGGCAACCCCTGTTCAAGAGACGGCGCTACTCTGTGGGGAGAGCGTCATCGGCCCA 360
Oy      372 GATGGCTCTGACAGAGCCCACTGCTCAAGCC---CCGTTACATTAATTCACTTCCAGG 427
        |||||
Db      361 GATGGCTCTGACAGAGCCCACTGCTCAAGCCCGTGGCGCTACATTAATTCACTTCCAGG 420
Oy      428 CAGCAACAACCTCCAGAGAGAGAGGGCTGTGAGCAGACCCGAGACCCCACTGAGTCTTC 487
        |||||
Db      421 CAGCAACAACCTCCAGAGAGAGAGGGCTGTGAGCAGACCCGAGACCCCACTGAGTCTTC 480
Oy      488 CCCCAACCCCGGCTTCAACAACAGACCTCCCAACAAAGACACCGCAATGACATCATGCTG 547
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Oy      548 GTGAAGATGGCATTCGCCAGTCTTCATCACTGAGGCTGTGGCAACCCCTCACTTCTCA 607
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Db      541 GTGAAGATGGCATTCGCCAGTCTTCATCACTGAGGCTGTGGCAACCCCTCACTTCTCA 599
Oy      608 CGCTGTGTCACGTGTGGACACAGCTGCGCTCATTTCCGGGTGGGG--CAGCAGTCCAGGC 665
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Db      660 CCCAGTTACGCTGCTGCCTCACACCTTGCATGCGGCCCAACATCAATCATTTAGACACAGA 719
Oy      726 ACTGTGAGAGAGCCTTACCCCGGCAATCAACAGACACCATGTGTG--TGCCAGCGTGCAG 784
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LOCUS   AK009360
DEFINITION 1295 bp mRNA linear HTC 05-DEC-2002
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          library, clone:2310015108 product:protease, serine, 20, full insert
          sequence.
ACCESSION AK009360
VERSION   AK009360.1 GI:12844110
KEYWORDS  HTC; CAP trapper.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS   Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
          Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
          High-efficiency full-length cDNA cloning
          Meth. Enzymol. 303, 19-44 (1999)
JOURNAL   99279253
MEDLINE   10349636
PUBMED    11042159
TITLE     Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
          Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
          Normalization and subtraction of cap-trapper-selected cDNAs to
          prepare full-length cDNA libraries for rapid discovery of new genes
          Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL   20499374
MEDLINE   11042159
PUBMED    11042159
AUTHORS   Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
          Konno, H., Akiyama, T., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,
          Sumi, N., Ishii, Y., Nakamura, S., Hazama, T., Nishino, T., Harada, A.,
          Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
          Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Katsuhiki, M.,
          Takeda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,

```


REFERENCE 1 (bases 1 to 708)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaphs@email.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL), DNA
 Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L14M10699 row: a column: 21
 High quality sequence stop: 704.
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone IMAGE:4803356"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_11b="NCI CGAP_Skn3"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.5kb. Library constructed by Life
 Technologies. Note: this is a NCI CGAP Library."
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 ORIGIN
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 Best Local Similarity 99.7%; Pred. No. 2.3e-57;
 Matches 632; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 195 GTGCAAGCTCTACCTCCAGCCCTGGGACAGCCCTGTTGAGAAAGCGGCTACTCTG 254
 349 TGGGGCGAGCTCATCGCCCGAGATGGCTCCCTGACAGAGCCCACTGCTCAACCCCG 408
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 435 CCGCAATGACATCATGTGTGAAGATGGATCGGCAGTTCATCACTGGGGCTGTGCG 494
 589 ACCCTCAACCTCTCTCAGCTGTGTGACAGCTGGGACAGAGTCCCTCATTTCCGGGTG 648
 495 ACCCTCAACCTCTCTCAGCTGTGTGACAGCTGGGACAGAGTCCCTCATTTCCGGGTG 554
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RESULT 14
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 LOCUS
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 ACCESSION AK009659
 VERSION AK009659.1 GI:12844589
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636

REFERENCE
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159

REFERENCE
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabe, K., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
 TITLE RIKEN Integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861

REFERENCE
 AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, K., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiya, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaudo, I., Pesole, G., Quackenbush, J., Schriml, L. M., Stabli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Botjuna, N., Carinci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarilli, J., Momberts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyokawa, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohitsuki, S., and Hayashizaki, Y.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409 (6821), 685-690 (2001)
 MEDLINE 21085660
 PUBMED 11217851

REFERENCE
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.


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DB      1188 TTTTGTGTTTGTGTTTGTCCAGCTTGGAAGACAGTCCCTGG-CATATCCACAGG 1246
OY      1247 TTTCATATAATATTTGCTTAATG 1269
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RESULT 15
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DEFINITION
UT-CE-DUI-aam-j-17-0-UI.s1 UT-CE-DUI Homo sapiens cDNA clone
BU676834
ACCESSION BU676834.1 GI:23522189
VERSION   EST.
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 654)
AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE     Normalization and subtraction: two approaches to facilitate gene
          discovery
JOURNAL   Genome Res. 6 (9), 791-806 (1996)
MEDLINE   97044477
PUBMED    8889548
COMMENT   Contact: McCray, PB
          University of Iowa
          2024 University of Iowa Med Labs, Iowa City, IA 52242, USA.
          Tel: 319 356 4866
          Fax: 319 356 7171
          Email: paul-mccray@uiowa.edu
          Tissue Procurement: Dr. M. J. Welsh, University of Iowa
          cDNA library preparation: Dr. M. Bento Soares, University of Iowa
          DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
          Clone Distribution: Researchers may obtain clones from Research
          Genetics (www.resgen.com) or from Open Biosystems
          (www.openbiosystems.com).
          The following repetitive elements were found in this cDNA
          sequence: 17-100, >LINE2 (matched complement)
          Seq primer: M13 FORWARD
          POLYA-Yes.

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/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: Lung; Vector: pTT73-Pac (Pharmacia) with a
modified polylinker; Site.1: EcoR I; Site.2: Not I;
UI-CE-DUI is a normalized cDNA library containing the
following tissue(s): Primary Lung Epithelial Cells The
library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pTT73-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is GCGTGTAGGC.
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TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368
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Query Match
Best Local Similarity 47.3%; Score 616; DB 13; Length 654;
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      732 AGAAGCGCTTACCCCGGCAACATCAGACAGACCAATGTTGTGCGACGTCAGAGAGGG 791
DB      556 AGAAGCGCTTACCCCGGCAACATCAGACAGACCAATGTTGTGCGACGTCAGAGAGGG 497
OY      792 GCAAGGACTCTGCCAGGGTGAAGTCCGGGGGCGCTGTGTCGTATACCAAGTCTCTCAAG 851
DB      496 GCAAGGACTCTGCCAGGGTGAAGTCCGGGGGCGCTGTGTCGTATACCAAGTCTCTCAAG 437
OY      852 GCATTATCTCTGCGGCGCAGATCCGTGTGCGATCACCCGAAAGCCTGGTGTACAGCA 911
DB      436 GCATTATCTCTGCGGCGCAGATCCGTGTGCGATCACCCGAAAGCCTGGTGTGTACAGCA 377
OY      912 AAGTCTGCAATATATGTGACTGTGATCCAGAGACGATGAAGAACAAATAGACTGACCCCA 971
DB      376 AAGTCTGCAATATATGTGACTGTGATCCAGAGACGATGAAGAACAAATAGACTGACCCCA 317
OY      972 CCCACACAGCCCATTCACCTTCATTTCCACTTGTGTGTTGTTCTCTGTCTACCTGTTA 1031
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DB      256 ATTAGAAGACCTTAGCCAGACACCTCTAGAACATTTGGGCGCTCGAGCTACAGCA 197
OY      1092 GATGCTGTACTTATATATCAACCTTGGGTTGAAATCAGTGAAGCTGATTCAAATTC 1151
DB      196 GATGCTGTACTTATATATCAACCTTGGGTTGAAATCAGTGAAGCTGATTCAAATTC 137
OY      1152 TGCCTGAAATATTTGGAAGTCTGGGAATGACAACACCTGGTTGTTCTGTGTTGTATCC 1211
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Ygapop 10.0 , Ygapext 0.5
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Delop 6.0 , Delext 7.0

Searched: 127863 seqs, 47026705 residues

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOC
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	692.5	29.2	260	1	KIKR_HUMAN
6	690	29.1	260	1	KIKR_HUMAN
7	687.5	29.0	277	1	KIKR_HUMAN
8	650.5	27.4	293	1	KIKR_HUMAN
9	632.5	26.7	251	1	KIKR_HUMAN
10	618.5	26.1	248	1	KIKR_HUMAN
11	618.5	26.1	261	1	KIKR_HUMAN
12	617.5	26.1	261	1	KIKR_HUMAN
13	612	25.8	248	1	KIKR_HUMAN
14	611.5	25.8	259	1	KIKR_HUMAN
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22	595	25.1	261	1	KIKR_HUMAN
23	594	25.1	238	1	TRY3_SALSA
24	594	25.1	244	1	KIKR_HUMAN
25	586	24.7	261	1	KIKR_HUMAN
26	585.5	24.7	246	1	TRY2_MOUSE
27	580.5	24.5	261	1	KIKR_HUMAN
28	580	24.5	231	1	TRY2_PIG
29	580	24.5	262	1	KIKR_HUMAN
30	578.5	24.4	244	1	KIKR_HUMAN
31	578.5	24.4	246	1	KIKR_HUMAN
32	576	24.3	247	1	TRY2_CANFA
33	572.5	24.2	243	1	TRY1_BOVIN
34	572.5	24.2	257	1	KIKR_HUMAN
35	572.5	24.2	261	1	KIKR_HUMAN
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38	567	23.9	247	1	TRY3_RAT
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40	565	23.8	243	1	TRY1_XENLA
41	565	23.8	256	1	KIKR_HUMAN
42	564.5	23.8	261	1	KIKR_HUMAN
43	564	23.8	248	1	TRY1_CHICK
44	564	23.8	259	1	KIKR_HUMAN
45	563	23.8	247	1	TRY2_BOVIN

ALIGNMENTS

RESULT 1	ID	KLKB_HUMAN	STANDARD;	PRT;	250 AA.
AC	09UBX7: 075837; Q9NS65;				
DT	16-OCT-2001 (Rel. 40; Created)				
DT	16-OCT-2001 (Rel. 40; Last sequence update)				
DT	15-SEP-2003 (Rel. 42; Last annotation update)				
DE	Kallikrein 11 precursor (EC 3.4.21.-) (Hippoboscidae) (trypsin-like protease).				
GN	Klik11 OR PRSS20 OR TLSP.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RC	TISSUE=Hippocampus;				
RX	MEDLINE=98438738; PubMed=9765601;				
RA	Yoshida S., Taniguchi M., Suemoto T., Oka T., He X.P., Shiosaka S.;				
RT	"CDNA cloning and expression of a novel serine protease, TLSP.;"				
RL	Biochim. Biophys. Acta 1399:225-228(1998).				
RN	[2]				
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).				
RC	TISSUE=Hippocampus, and Prostate;				
RX	MEDLINE=20329229; PubMed=10872828;				
RA	Mitsui S., Yamada T., Okui A., Komiyama K., Uemura H., Yamaguchi N.;				
RT	"A novel isoform of a kallikrein-like protease, TLSP/hippoboscasin,				
RL	(PRSS20), is expressed in the human brain and prostate.;"				
RN	Biochem. Biophys. Res. Commun. 272:205-211(2000).				
RP	[3]				
RC	SEQUENCE FROM N.A. (ISOFORM 1).				
RX	MEDLINE=20330117; PubMed=10662248;				
RA	Yousef G.M., Scorilas A., Diamandis E.P.;				
RT	"Genomic organization, mapping, tissue expression, and hormonal				
RL	regulation of trypsin-like serine protease (TLSP PRSS20), a new				
RN	member of the human kallikrein gene family.;"				
RL	Genomics 63:88-96(2000).				
RP	[4]				
RC	SEQUENCE FROM N.A. (ISOFORM 1).				
RX	MEDLINE=20510030; PubMed=11054574;				
RA	Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.;				
RT	Mass P., Paepke B., Wang K.;				

"Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region." [5]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RA Iamertin J.E., McCreedy P.M., Skowronski E., Wiswanathan V.,
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,
 RA Dangnan L., Eiler A., Christensen M., Georgescu A., Avila J., Liu S.,
 RA Andreise T., Trankheim M., Attix C., Amico-Keller G., Coffield J.,
 RA Duarte S., Lucas S., Bruce R., Thomas R., Nolan M., Krommiller B.,
 RA Ariellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 RA Olsen A.S., Carrano A.V.,
 RA "Sequence analysis of chromosome 19q13.4." [6]
 RA Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE-Testis;

RA MEDLINE-22388257; PubMed-12477932;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshlyuk S., Carchini P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Moxley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.J., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences." [7]
 RA Proc. Natl. Acad. Sci. U.S.A. 99:11689-16903(2002).

CC -1- FUNCTION: POSSIBLE MULTIFUNCTIONAL PROTEASE. EFFICIENTLY CLEAVES
 CC BE-PHE-ARG-4-METHYLCOMARIL-7-AMIDE. A KALLIKREIN SUBSTRATE, AND
 CC WEAKLY CLEAVES OTHER SUBSTRATES FOR KALLIKREIN AND TRYPSIN.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- ALTERNATIVE PRODUCTS:

CC Event-Alternative splicing; Named Isoforms-2;

CC Name=1;

CC IsoId=09UBX7-1; Sequence-Displayed;

CC Name=2;

CC IsoId=09UBX7-2; Sequence-VSP_005402;

CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SKIN AND PROSTATE. ISOFORM
 CC 1 IS EXPRESSED PREFERENTIALLY IN BRAIN; ISOFORM 2 IN PROSTATE.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.

CC -----

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CC -----

DR EMBL; AB012917; BAA33404.1; ALT_INIT.
 DR EMBL; AB013730; BAA8713.1; -
 DR EMBL; AB041036; BAA96797.1; -
 DR EMBL; AF164623; AAD47815.1; -
 DR EMBL; AF243527; AAG33364.1; -
 DR EMBL; AC011473; AAG23257.1; -
 DR EMBL; BC022068; AAH22068.1; -
 DR HSSP; P00763; IDPO.
 DR MEROPS; S01.257; -
 DR Genew; HGNC:6359; KLK11.
 DR MIM; 604434; -
 DR InterPro; IPR001314; Chymotrypsin.

DR InterPro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00089; trypsin.1.
 DR PRINTS; PRO0722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolyse; Serine protease; Glycoprotein; Signal; zymogen;
 KW Alternative splicing.
 FT SIGNAL 1
 FT PROPEP 19 21
 FT CHAIN 22 250
 FT ACT_SITE 62 62
 FT ACT_SITE 110 110
 FT ACT_SITE 203 203
 FT DISULFID 28 163
 FT DISULFID 47 63
 FT DISULFID 135 237
 FT DISULFID 142 209
 FT DISULFID 174 188
 FT DISULFID 199 224
 FT CARBOHYD 99 99
 FT CARBOHYD 165 165
 FT CARBOHYD 181 181
 FT CARBOHYD 210 210
 FT VARSPLIC 1
 FT FT
 FT FT

SO SEQUENCE 250 AA; 27466 MW; 192D910B8C9C7A56 CRC64;

Alignment Scores:
 Pred. No.: 2,4e-81 Length: 250
 Score: 1355.00 Matches: 250
 Percent Similarity: 100.00% Conservative: 0
 Best local Similarity: 100.00% Mismatches: 0
 Query Match: 57.17% Indels: 0
 Dbs: 1 Gaps: 0

US-09-856-320a-1 (1-1301) x KLRB_HUMAN (1-250)

QY 209 ATGAGGATTCGACGATTAACCGCTGCTGGCGCAACAGGCGTTGAGGAGAGAGACC 268
 |||||||
 Db 1 MetcArgLeuLeuGlnLeuIleLeuLeuAlaLeuAlaThrGlyGlyGluThr 20
 |||||||

QY 269 AGGATCATCAAGGGGTTCGAGTCCAGGCTCACTCCAGCGCTGGAGCAGCGCTGTC 328
 |||||||
 Db 21 ArgIleIleLeuGlyPheGlnCysIleProHisSerGlnProIleAlaLeuPhe 40
 |||||||

QY 329 GAGAGACGCGGCTACTCTGTGGGGCAGCCTATGCGCCCGCAGATGGCTCTGACAGCA 388
 |||||||
 Db 41 GlnIleThrArgLeuLeuGlyAlaThrLeuIleAlaProArgTrpLeuThrAla 60
 |||||||

QY 389 GCCCAGCTCCCAAGCCCGCTACATGATGTCACCTGGGGAGAGCAACCCGCAAGGAG 448
 |||||||
 Db 61 AlaHisCysLeuLeuSproAlaGlyTyrIleValHisLeuGlyGlnHisLeuGlnIle 80
 |||||||

QY 449 GAGGCGTGTGAGCAGACCCGAGCAGCAGCTAGTCTCTCCCGCAGCCCGGCTCAACAC 508
 |||||||
 Db 81 GlnGlyCysLeuGlnIleThrAlaGlyThrAlaThrGlnSerPheProHisProGlyPheAsnAsn 100
 |||||||

QY 509 AGCCTCCCAACAAAGACACCGCAATGACATGATCTGTGTAAGTGGATGGCCAGTCC 568
 |||||||
 Db 101 SerLeuProAsnIleLysAspHisAlaGlnAsnAspIleMetLeuValLysMetAlaSerProVal 120
 |||||||

QY 569 TCCATACCTGGGCTGTGGCAGCCCTCAGCTCTCTCAGCGCTGTGTCTGCTGACACC 628
 |||||||
 Db 121 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 140
 |||||||

QY 629 AGCTGCCTCATTCCTCGGCTGGGAGCAGCTCCAGCCCGCAGTATGAGCTGCTCAGCC 688
 |||||||
 Db 141 SerCysLeuIleSerIleTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 160
 |||||||

QY 689 TTGCGATGGCGCAACATCAACATCATTTGAGACACAGAGTGTGAGAACGCTTACCCGGCG 748
 |||||||

```

DB 161 LeuAlaGcysAlaAsnIleThrIleIleGluHisGlnLysCysGlnAsnLarYrProGly 180
OY 749 AACATCACAGACACCATGGTGTGTGTCACAGTCGACAGAGGGGCAAGAGCTCTGCCAG 808
DB 181 AsnIleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAspSerCysGln 200
OY 809 GGTGACTCCGGGGGCGCTGTGTCTGTATACAGCTCTTCACAGCATATATCTCGGGC 868
DB 201 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 220
OY 869 CAGATCCGTCGTGCGTACCCGGAAGCCTGGTGTCTACAGAAAGTGTGCAAAATATG 928
DB 221 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 240
OY 929 GACTGATCCAGACAGATGAAACAT 958
DB 241 AspTrpIleGlnGlnThrMetLysAsnAsn 250

RESULT 2
KLK9_HUMAN STANDARD; PRT; 250 AA.
AC Q9UKO9;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 41, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Kallikrein 9 precursor (EC 3.4.21.-) (Kallikrein-like protein 3) (KLK-
DE L3).
GN KLK9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP MEDLINE FROM N.A. MEDLINE=20118156; PubMed=10652563;
RX Yousef G.M., Luo L.-Y., Diamandis E.P.;
RT "Identification of novel human kallikrein-like genes on chromosome
RT 19q13.3-q13.4."
RL Anticancer Res. 19:2843-2852(1999).
RN [2]
RP MEDLINE FROM N.A. MEDLINE=20247258; PubMed=10783266;
RX Yousef G.M., Diamandis E.P.;
RT "The expanded human kallikrein gene family: locus characterization and
RT molecular cloning of a new member, KLK-13."
RL Genomics 65:184-194(2000).
RN [3]
RP MEDLINE FROM N.A. MEDLINE=20510030; PubMed=11054574;
RX Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
RA Moss P., Paepker B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region."
RL Gene 257:119-130(2000).
RN [4]
RP MEDLINE FROM N.A.
RX Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
RA Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., garnes J.,
RA Darganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Andeise T., Trankheim M., Atlix C., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carraro A.V.;
RT "Sequence analysis of chromosome 19q13.4."
RL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- TISSUE SPECIFICITY: SKIN, THYMUS, TRACHEA, CEREBELLUM AND SPINAL
CC CORD.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, KALLIKREIN SUBFAMILY,
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CC -----
DB EMBL: AF135026; AAD26427.2; -.
DR EMBL: AF243527; AAG33362.1; -.
DR EMBL: AC011473; AAG23255.1; -.
DR HSSP: P00763; IDPO.
DR MEROPS: S01.307; -.
DR Genew: HGNC:6370; KLK9.
DR MIM: 605504; -.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0006508; P:proteolysis and peptidolysis; NAS.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYP_SPE; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Serine protease; Glycoprotein; Signal.
FT SIGNAL 1 15
FT CHAIN 16 250
FT ACT_SITE 63 63 KALLIKREIN 9.
FT ACT_SITE 111 111 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 204 204 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 29 164 BY SIMILARITY.
FT DISULFID 48 64 BY SIMILARITY.
FT DISULFID 136 238 BY SIMILARITY.
FT DISULFID 143 175 BY SIMILARITY.
FT DISULFID 175 189 BY SIMILARITY.
FT DISULFID 200 225 BY SIMILARITY.
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 250 AA; 27512 MW; F2785245B063E98B CRC64;

Alignment Scores:
Pred. No.: 3.23e-42 Length: 250
Score: 756.00 Matches: 138
Percent Similarity: 72.31% Conservative: 37
Best Local Similarity: 57.02% Mismatches: 67
Query Match: 31.90% Indels: 0
DB: 1 Gaps: 0

US-09-856-320A-1 (1-1301) x KLK9_HUMAN (1-250)
OY 230 CTGCTTGCCTTCGGCAACAGGCGCTTGAAGGGGAGACGAGATCATCAAGGCTTCGAG 289
DB 9 LeuIleuSerLeuIleuAlaGlyHisGlyTyrPalaAspThrArgAlaIleIleGluGln 28
OY 290 TCGAAGCCTCACTCCAGCCTTCGAGAGGCGAGGCTTGTGAAAGAGAGGGGCTACTCTGT 349
DB 29 CysArgProAsnSerGlnProIleTrpGlnAlaGlyLeuPheHisLeuThrArgLeuPheCys 48
OY 350 GGGGAGAGCCTATGCGCCCGCCAGATGCTCTGACAGAGCCCATGCTCAAGCCCGC 409
DB 49 GlnAlaThrLeuIleSerAspArgTyrPleuLeuThrAlaIleHisCysArgLysProTyr 68
OY 410 TACATAGTTCACCTCGGGGAGCAACACCTCCAGAGGAGAGAGGCGCTGACAGACCCGG 469
DB 69 LeuTrpValArgLeuGlyGlnHisIleThrLysTyrTrpGlnGlyProGlnIleuPhe 88
OY 470 ACAGCCATGATCTCTCCCGCCAGCCCGGCTTCAACAAGAGCTCCCAACAAGACAC 529
DB 89 ArgValThrAspPhePheProHisProGlyPheAsnLysAspLeuSerAlaAsnSphis 108
OY 530 CGCAATGACATATGCTGTGTAAGATGGCATCGCAGCATGTCATCACTGAGGCTTGCGA 589

```

Db 109 AsnAspSerPleMetLeuIleArgLeuProArgGlnAlaArgLeuSerProAlaValGln 128
 QY 590 CCCCTCAACCTCTCTCAAGCTGTGTCTGACCTGGACACCACTGCTCATTTCCGGCTGG 649
 Db 129 ProLeuAsnLeuSerGlnThrCysValSerProGlyMetGlnCysLeuIleSerGlyTyr 148
 QY 650 GGCAGCAGCCGACCCCAAGTTACGGCTGCTCAACCTTGGCATGGCCCAATATCAC 709
 Db 149 GLYAlaValSerSerProLysAlaLeuPheProAlaThrLeuGlnCysAlaAsnIleSer 168
 QY 710 ATCATTCAGCAGCAGAGAGTGTGAGAGCCCTTACCCCGGCAACACAGACCATGGT 769
 Db 169 IleLeuGlnAsnLysLeuGlnCysHisThrAlaTyrProGlnHisIleSerAspSerMetLeu 188
 QY 770 TGTGCCAGCTGTGACGAGAGGGGCGACACTCTGCCAGGGGTGACTCCGGGGCTCTGT 829
 Db 189 CysAlaGlyLeuTyrPGLysGlyArgGlySerCysGlnGlyAspSerGlyGlyProLeu 208
 QY 830 GTCTGTACACAGTCTCTTCAAGGCATATCTCCCTGGGGCGAGATCCGTGTGCATCAC 889
 Db 209 ValCysAsnGlyThrLeuAlaGlyValValSerGlyGlyAlaGluProCysSerArgPro 228
 QY 890 CGAAGCCTGCTGTCTACACGAAAGTGTGCAATATGTGACGTGATCCAGACAGCATG 949
 Db 229 ArgArgProAlaValTyrThrSerValCysHisThrLeuAspTrpIleGlnGluIleMet 248
 QY 950 AAGAAC 955
 Db 249 GluAsn 250

RESULT 3
 NRPN_RAT
 ID NRPN_RAT STANDARD: PRT: 260 AA.
 AC 088780;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuropilin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Brain serine
 protease 1)
 GN KIK8 OR PRS19 OR NRPN OR BSPI.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Fischer; TISSUE=Brain;
 RX MEDLINE=98389725; PubMed=9722524;
 RA Davies B.J., Pickard B.S., Steel M., Morris R.G.M., Lathe R.;
 RT "Serine proteases in rodent hippocampus";
 RL J. Biol. Chem. 273:23004-23011(1998).
 CC -1- FUNCTION: SUGGESTED TO BE INVOLVED IN KINDLING EPILEPTOGENESIS AND
 CC HIPPOCAMPAL PLASTICITY. HAS A STRONG PROTEOLYTIC ACTIVITY AGAINST
 CC FIBRONECTIN (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- TISSUE SPECIFICITY: RESTRICTED TO HIPPOCAMPUS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AI005641; CA006643.1; -
 DR HSP: Q61955; INPM.
 DR MEROPS: S01.244; -
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser.protease_Try.
 DR Pfam: PF00089; trypsin_1.

DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRYP-SPEC. 1.
 DR PROSITE: PS00240; TRYP-SIN_DOM. 1.
 DR PROSITE: PS00134; TRYP-SIN_HIS. 1.
 DR PROSITE: PS00135; TRYP-SIN_SER. 1.
 KW Hydrolyase; Serine protease; Glycoprotein; zymogen; signal.
 FT SIGNAL 1 28
 FT PROPEP 29 32
 FT CHAIN 33 260
 FT ACT_SITE 73 73
 FT ACT_SITE 120 120
 FT ACT_SITE 212 212
 FT DISULFID 39 173
 FT DISULFID 58 74
 FT DISULFID 145 246
 FT DISULFID 152 218
 FT DISULFID 184 198
 FT DISULFID 208 233
 FT CARBOHD 110 110
 SQ SEQUENCE 260 AA; 28510 MW; 58DFAF0602A0B7F5 CRC64; (POTENTIAL).
 N-LINKED (GLCNAC...) (POTENTIAL).
 Alignment Scores:
 Pred. No.: 1,18e-38 Length: 260
 Score: 701.50 Matches: 129
 Percent Similarity: 66.67% Conservative: 35
 Best Local Similarity: 52.44% Mismatches: 75
 Query Match: 29.60% Indels: 7
 DB: 1 Caps: 3

US-09-856-320A-1 (1-1301) x NRPN_RAT (1-260)

QY 227 ATCTGCTGCTCTGCGACACAGGCTGTAGGGGAGACAGCAG----- 271
 Db 13 IleLeuLeuPheLeuLeuMetGlyAlaThrAlaGlyLeuThrAlaGlnGlySerLys 32
 QY 272 ATCATCAGAGGGGTGTGAGTGCAGACCTCATCTCCAGCGCTGGACGAGCGCTGTGAG 331
 Db 33 IleLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 52
 QY 332 AAGAGGGGCTACTCTGTGGGGCGAGCTCATGCGCCCGGAGATGCTCTGACAGAGCC 391
 Db 53 GlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 72
 QY 392 CACTGCTCAAGCCCGCTCATATGTTACCTGGGGGAGACACCACTCCGAGAGAGAG 451
 Db 73 HisCysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 92
 QY 452 GGCTGTGAGGAGACCCGAGACGACCATGATGCTCCCGGAGATGCTCCGAGAGAG 511
 Db 93 GluProGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 112
 QY 512 CTCCCAACAAGACCAACCGCAATGATCATGCTGTGGAATGGCATCCGACAGTCTCC 571
 Db 113 AsnPro--GlnAspHisSerHisAspIleMetLeuLeuArgLeuGlnAsnSerAlaAsn 131
 QY 572 ATCAGCTGGGCTGGACCCCTCATCCTCTCTGACGCTGTGTGCTGCTGCTGCTG 631
 Db 132 LeuGlyAspLysValLysLysProIleGlnLeuAlaAsnLeuGlnProLysValGlnLys 151
 QY 632 TGCTCATTTCCGGCTGGGAGAGCGTCCAGGCGCCAGTTCAGCTGCTGACACCTG 691
 Db 152 CysIleIleSerGlyTrpGlyThrValThrSerProGlnGlnAsnPheProAsnThrLeu 171
 QY 692 CGATGCGCAACATCACCATTGATGAGCAGACAGAGTGTGAGAGCGCTTACCGGAC 751
 Db 172 AsnGlyAlaGlnValLysLysIleTyrSerGlnAsnLysCysGlnLysAlaTyrProGlyLys 191
 QY 752 ATCAGACAGACCATGTGTGTGCGAGCGTCCAGAGAGGGGAGAGCTCTCCAGAGT 811
 Db 192 IleThrGlnGlnLysValCysAlaGly---SerSerAsnGlyAlaAspThrCysGlnGly 210
 QY 812 GACTCCGGGGGCGCTGTGCTGTATACCAATCTCTTCAAGCATATATCTCTGGGGCAG 871

Db 211 AspSerGlyGlyProLeuValCysAsnGlyValLeuGlnGlyIleThrThrTrpGlySer 230
 QY 872 GATCCGTGTGCATACCCGAAAGCCTGTGTCTACACGAAAGTGTCAATATGTGAC 931
 Db 231 AspProCysGlyLysProGlnLulysProGlyValTyrThrLysIleCysArgTyrThrAsn 250
 QY 932 TGGATCCAGGAGCAGT 949
 Db 251 TrpIleLysLysThrMet 256
 RESULT 4
 NRPN_MOUSE
 ID NRPN_MOUSE STANDARD: PRT; 260 AA.
 AC 061955;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neutropin precursor (EC 3.4.21.-) (NP) (Kallikrein 8).
 GN KLK8 OR PRSS19 OR NRPN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-Hippocampus;
 RX MEDLINE=95348817; PubMed=7623137;
 RA Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T.,
 Ito J., Nishino H., Aimoto S., Kiyama H., Shiosaka S.;
 RT "Expression and activity-dependent changes of a novel limbic-serine
 protease gene in the hippocampus.";
 RL J. Neurosci. 15:5088-5097(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yoshida S., Hirata A., Inoue N., Shiosaka S.;
 RT "Cloning and assignment of mouse neutropin gene, Prss19 to chromosome
 7B4.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF N-TERMINUS, AND CHARACTERIZATION.
 RC STRAIN-BALB/C; TISSUE-Brain;
 RX MEDLINE=9825202; PubMed=9556608;
 RA Shamlu C., Yoshida S., Shibata M., Kato K., Momota Y., Matsumoto K.,
 Shiosaka T., Midorikawa R., Kamachi T., Kawabe A., Shiosaka S.;
 RT "Characterization of recombinant and brain neutropin, a
 plasticity-related serine protease.";
 RL J. Biol. Chem. 273:11189-11196(1998).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 33-257.
 RC TISSUE-Hippocampus;
 RX MEDLINE=99134351; PubMed=9933620;
 RA Kishi T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S.,
 Shiosaka S., Hakoshima T.;
 RT "Crystal structure of neutropin, a hippocampal protease involved in
 kindling epileptogenesis.";
 RL J. Biol. Chem. 274:4220-4224(1999).
 CC -1- FUNCTION: SUGGESTED TO BE INVOLVED IN KINDLING EPILEPTOGENESIS AND
 HIPPOCAMPAL PLASTICITY. HAS A STRONG PROTEOLYTIC ACTIVITY AGAINST
 FIBRONECTIN.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
 CC -1- ENZYME REGULATION: STRONGLY INHIBITED BY DIISOPROPYL
 FLUOROPHOSPHATE, LEUPEPTIN AND (4-AMIDINOPHENYL)METHANESULFONYL 1-
 FLUORIDE.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN THE LIMBIC SYSTEM OF
 MOUSE BRAIN AND IS LOCALIZED AT HIGHEST CONCENTRATION IN PYRAMIDAL
 NEURONS OF THE HIPPOCAMPAL CA1-3 SUBFIELDS.
 CC -1- MASS SPECTROMETRY: MW=26613; METHOD-MALDI; RANGE=29-260.
 CC -1- MASS SPECTROMETRY: MW=26229; METHOD-MALDI; RANGE=33-260.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
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 CC or send an email to license@isb-sib.ch).
 DR EMBL: D30785; BAA06451.1; -.
 DR EMBL: AB032202; BAA92435.1; -.
 DR PIR: I56559; I56559.
 DR PDB: INPM; 23-MAR-99.
 DR MEROPS: S01.244; -.
 DR MGD: MGI:892018; Klk8.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRYPSIN_SPC; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR HydroLase: Serine protease; Glycoprotein; zymogen; signal;
 KW 3D-structure.
 FT SIGNAL. 1 28
 FT PROPEP 29 32
 FT CHAIN 33 260
 FT ACT_SITE 73 73
 FT ACT_SITE 120 120
 FT ACT_SITE 212 212
 FT DISULFID 39 173
 FT DISULFID 58 74
 FT DISULFID 145 246
 FT DISULFID 152 218
 FT DISULFID 184 233
 FT DISULFID 208 233
 FT CARBOHYD 110 110
 FT STRAND 34 34
 FT STRAND 37 38
 FT TURN 41 42
 FT TURN 45 46
 FT STRAND 47 52
 FT TURN 53 54
 FT STRAND 55 64
 FT TURN 65 66
 FT STRAND 67 70
 FT HELIX 72 74
 FT STRAND 80 83
 FT STRAND 87 87
 FT STRAND 88 89
 FT STRAND 96 98
 FT STRAND 100 105
 FT TURN 107 108
 FT TURN 114 115
 FT TURN 118 119
 FT STRAND 122 126
 FT STRAND 140 141
 FT TURN 148 149
 FT STRAND 151 156
 FT STRAND 170 170
 FT STRAND 172 178
 FT STRAND 181 187
 FT HELIX 189 191
 FT TURN 189 191
 FT TURN 194 195
 FT STRAND 196 200
 FT TURN 202 203
 FT STRAND 206 206
 FT TURN 209 210
 FT TURN 212 213
 FT STRAND 215 218
 FT TURN 219 220
 FT STRAND 221 228
 FT STRAND 235 235
 FT TURN 236 237
 FT STRAND 238 238
 N-LINKED (GLCNAC. .) (POTENTIAL).
 NEUTROPSIN.
 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CHARGE RELAY SYSTEM (BY SIMILARITY).

FT STRAND 240 244
 HT 245 256
 SEQUENCE 260 AA; 28523 MW; B5F6F6BE37CD60E CRC64;
 Alignment Scores:
 Pred. No.: 1,85e-38 Length: 260
 Score: 698.50 Matches: 129
 Percent Similarity: 56.13% Conservative: 35
 Best Local Similarity: 52.02% Mismatches: 77
 Query Match: 29.47% Indels: 7
 Gaps: 3
 DB: 1
 US-09-856-320a-1 (1-1301) x NRPN_MOUSE (1-260)
 QY 227 ATCTGCTGCTGCTGCGAACAAGGCGCTGTAGGGGAGAGACAGC----- 271
 Db 13 lIleuLeuLeuLeuLeuPheMetGlyAlaTrpAlaGlyLeuThrArgAlaGlnGlySerLys 32
 QY 272 ATCATCAAGGGGTTCGAGTGCAGACCTCACCCTCCAGCCCTGGCAGGAGCCCTTTCGAG 331
 Db 33 lIleuLeuGlnGlyArgGlnGlyCysIleProHisSerGlnProTrpGlnAlaAlaLeuPheGln 52
 QY 332 AAGACGGGCTACTCTGTGGGGGAGCGCTCATCGCCCGCCAGATGCGCTGTAGCAGACGCC 391
 Db 53 GlyAlaArgLeuIleCysGlyGlyValLeuValGlyAspArgTrpValLeuThrAlaAla 72
 QY 392 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGAGACCAACTCCAGAGAGAGAG 451
 Db 73 HisCysLysLysGlnLysTyrSerValArgLeuGlnLysHisSerLeuGlnSerArgAsp 92
 QY 452 GCGTGTAGCAGACCGCGGAGCGACGTCGTCCTCCCGCCCGCCGCTTCAACAAGC 511
 Db 93 GlnProGlnGlnGlnIleGlnValAlaGlnSerIleGlnHisProCysTyrAsnAsnSer 112
 QY 512 CTCGCCAACAAGACCGCCGCAATGATCATGCTGTTGAGATGATGATGATGATGATGATGAT 571
 Db 113 AsnPro---GlnAspHisSerHisAspIleMetLeuLeuArgLeuGlnAsnSerAlaAsn 131
 QY 572 ATCAGCTGGGCTGTGCACCCCTCACCCTCTCCCTGACGCTGTGCTGCTGCGACGACG 631
 Db 132 LeuGlnLysLysValLysProValGlnLeuAlaAsnLeuCysProLysValGlnLys 151
 QY 632 TGCTCATTTCCGGCTGGGGAGCGATGCCAGCCCGAGTTAGCCCTGCTGACACCTG 691
 Db 152 CysIleIleSerGlyTrpGlyThrValThrSerProGlnGlnAsnPheProAsnThrLeu 171
 QY 692 CGATGCCCAACATCACCATCATGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 751
 Db 172 AsnCysAlaGlnValLysIleTyrSerGlnAsnLysCysGlnAlaGlnAlaTyrProGlnLys 191
 QY 752 ATCAGACAGACATGTTGTGTGCCAGCGTGCAGAGAGGGGAGGAGGAGGAGGAGGAGGAG 811
 Db 192 lIleThrGlnGlnMetValCysAlaGly---SerSerAsnGlnAlaAspThrCysGlnGly 210
 QY 812 GACTCCGGGGGCTCTGTGTCTGTACACAGTCTTCAAGGATTAATCTCTGGGGCAG 871
 Db 211 AspSerIleGlyProLeuValCysAspGlyMetLeuGlnGlyIleThrSerTrpGlySer 230
 QY 872 GATCCGTTGGGATCACCAGCCGAAAGCTGGTGTCTACAGGAAGCTGCAATATGTCGAC 931
 Db 231 AspProCysGlnLysProGlnLysProGlnLysValTyrThrLysIleCysArgTyrThrThr 250
 QY 932 TGGATCCAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 955
 Db 251 TrpIleLysLysThrMetAspAsn 258
 RESULT 5
 KLF_HUMAN STANDARD; PRT; 256 AA.
 AC Q9H2R5; Q15358; Q9H2R3; Q9H2R4; Q9H2R6; Q9HBG3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE kallikrein 15 precursor (EC 3.4.21.-) (ACO protease).
 GN KLIK15.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
 RX PubMed=11010966;
 RA Yousef G.M., Scorillas A., Jung K., Ashworth L.K., Diamandis E.P.;
 RT "Molecular cloning of the human kallikrein 15 gene (KLK15). Up-
 regulation in prostate cancer."
 RL J. Biol. Chem. 276:53-61(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20510030; PubMed=11054574;
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuig J.,
 RA Moss P., Paepers B., Wang K.;
 RT "Sequencing and expression analysis of the serine protease gene
 cluster located in chromosome 19q13 region."
 RL Gene 257:119-130(2000).
 RN [3]
 RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=94289486; PubMed=8018728;
 RA Dhanich M.E., Splees M.;
 RT "A novel serine proteinase-like sequence from human brain."
 RL Biochim. Biophys. Acta 1218:225-228(1994).
 CC -1- FUNCTION: Protease whose physiological substrate is not yet known.
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1;
 CC IsoId=Q9H2R5-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9H2R5-2; Sequence=VSP_005405;
 CC Name=3;
 CC IsoId=Q9H2R5-3; Sequence=VSP_005406, VSP_005407;
 CC Name=4;
 CC IsoId=Q9H2R5-4; Sequence=VSP_005404;
 CC -1- TISSUE SPECIFICITY: Highest expression in the thyroid gland. Also
 CC expressed in the prostate, salivary, and adrenal glands and in the
 CC colon testis and kidney.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; AF242195; AAC09469.1; -;
 DR EMBL; AF242195; AAC09470.1; -;
 DR EMBL; AF242195; AAC09471.1; -;
 DR EMBL; AF242195; AAC09472.1; -;
 DR EMBL; AF243527; AAC33354.1; -;
 DR EMBL; X75363; CA53145.1; ALT_SEQ.
 DR HSBP; P00763; IDPO.
 DR MEROPS; S01.081; -;
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; FALSE_NG.
 KW Hydrolase; Serine protease; Glycoprotein; Signal; Zymogen;
 FT Alternative splicing. 16 POTENTIAL.

FT PROPER 17 21 ACTIVATION PEPTIDE (POTENTIAL).
 FT CHAIN 22 256 KALIKREIN 15.
 FT ACT_SITE 62 256 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 106 106 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 209 209 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 122 206 Missing (in isoform 4).
 FT VARSPLIC 122 256 /FTID-VSP_005404.
 FT VARSPLIC 161 161 Missing (in isoform 2).
 FT VARSPLIC 161 161 /FTID-VSP_005405.
 FT VARSPLIC 161 161 V -> G (in isoform 3).
 FT VARSPLIC 162 256 /FTID-VSP_005406.
 FT VARSPLIC 162 256 Missing (in isoform 3).
 FT CONFLICT 147 160 /FTID-VSP_005407.
 FT SEQUENCE 256 AA: 28087 MW: B5BF8D6022786B5 CRC64;
 SQ
 Alignment Scores:
 Pred. No.: 4.55e-38 Length: 256
 Score: 692.50 Matches: 129
 Percent Similarity: 65.50% Conservative: 40
 Best Local Similarity: 50.00% Mismatches: 74
 Query Match: 29.22% Indels: 15
 DB: 1 Gaps: 4
 US-09-856-320A-1 (1-1301) x KIKF_HUMAN (1-256)
 QY 215 ATTCGAGTTAACTCTGCTGCTGGCAACAGGGCTGTGAGGGAGAGACGAGATC 274
 DB 4 LeuLeuThrLeuSerPheLeuLeuAlaSerThrAlaAlaGlnAspGlyAsp---LysLeu 22
 QY 275 ATCAAGGGGCTGAGTGCAGAGCCCTGAGAGCCCTGAGAGCCCTGAGAGAG 334
 DB 23 LeuGlnGlyAspGlnCysAlaProHisSerGlnProTyrGlnValAlaLeuTyrGlnArg 42
 QY 335 ACGGGCTACTCTGTGGGGCCAGCTCATCCGCCAGATGGCTCTGTGACAGCCAC 394
 DB 43 GlyArgPheAsnCysGlyAlaSerLeuLeuSerProHisTyrValLeuSerAlaAlaHis 62
 QY 395 TGCCCTCAAGCCCGCTACATAGTTCACCTGGGGGCGCAACCTCCAGAGAGAGGGC 454
 DB 63 CysGlnSerArgPheMetArgValArgLeuGlnHisAsnLeuArgLysArgAspGly 82
 QY 455 TGTGAGCAGACCCGAGCAGCAGTGTCTCCGCCACCCCGGGCTGACACACAGCCTC 514
 DB 83 ProGlnGlnLeuArgThrThrSerArgValIleProHisProArgTyrGlu----- 99
 QY 515 CCCAACAAAGACCCGAGATGACATCATCTGCTGGAAGATGGCATCCGCTTCATC 574
 DB 100 ---AlaArgSerHisArgAsnAspIleMetLeuLeuArgValGlnProAlaArgLeu 118
 QY 575 ACCTGGGCTGTGCGACCCCTGCTCCTCAGCTGTGTGACAGTGTGCGACAGCTGC 634
 DB 119 AsnProGlnValArgProAlaValLeuProThrArgCysProHisProGlnGlnAlaCys 138
 QY 635 CTCATTCCGGCTGGGGGCGAGCAGCTC-----AGCCCC--- 667
 DB 139 ValValSerGlyTyrGlyLeuValSerHisAsnGlnProGlyThrAlaGlySerProArg 158
 QY 668 ---CAGTTACGCCCTGCTCAGACCTGTGGATGGCGGCACATCACCATTGAGACCAAG 724
 DB 159 SerGlnValSerLeuProAspThrLeuHisCysAlaAsnIleSerIleIleSerAspThr 178
 QY 725 AAGTGTGAGACGCTACCCGCGCAACATCAGACACAGATGGTGTGCGAGCTGAG 784
 DB 179 SerCysAspLysSerTyrProGlyArgLeuThrAsnThrMetValCysAlaGlyAlaGln 198
 QY 785 GAAGGGGCAAGACTCTGCGCAGGGTACTCCGGGGCCCTCTGGTGTGTAACCACTCT 844
 DB 199 GlyArgGlyAlaGlnSerCysGlyGlnLysPserGlyGlyProLeuValCysGlyGlyLe 218
 QY 845 CTTCAGAGCATTAATCTCTCTGGGGCGCAGATCCGTGTGCGATCACCCGAAAGCTGTGTC 904

DB 219 LeuGlnGlyIleValSerTyrPglAspValProCysAspAsnThrThrLysProGlyVal 238
 QY 905 TACAGGAAGTGTGCAATATATGACGTGATCCGAGACGATGAGAACAT 958
 DB 239 TyrThrLysValCysHisTyrLeuGlnTyrPglLeuArgGlnThrMetLysArgAsn 256
 RESULT 6
 KIKF_HUMAN
 ID KIKF_HUMAN STANDARD: PRT: 260 AA.
 AC 060259: Q9HCB3: Q9UII9: Q9UD47;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neutropin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Ovasin) (Serine
 DE protease TMDG-14) (Tumor-associated differentially expressed gene-14
 DE protein).
 GN KIKF OR PRSS19 OR TADG14 OR NRPN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Hippocampus;
 RX MEDLINE=98372070; PubMed=9714609;
 RA Yoshida S., Taniguchi M., Hirata A., Shiosaka S.;
 RT "Sequence analysis and expression of human neutropin cDNA and gene.";
 RL Eur. J. Biochem. 260:627-634(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Brain;
 RX MEDLINE=99203457; PubMed=10102990;
 RA Mitsui S., Tsuruoka N., Yamashiro K., Nakazato H., Yamaguchi N.;
 RT "A novel form of human neutropin, a brain-related serine protease, is
 RT generated by alternative splicing and is expressed preferentially in
 RT human adult brain.";
 RL Eur. J. Biochem. 260:627-634(1999).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Ovary;
 RX MEDLINE=99413504; PubMed=10485494;
 RA Underwood L.J., Yanamoto H., Wang Y., Shigemasa K., Parmley T.R.,
 RA O'Brien T.J.;
 RT "Cloning of tumor-associated differentially expressed gene-14, a novel
 RT serine protease overexpressed by ovarian carcinoma.";
 RL Cancer Res. 59:4435-4439(1999).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Gan L., Gellinas R., Gown A.M., Moss P., Smith R., Wang K.;
 RT "Molecular cloning and characterization of a novel serine protease,
 RT ovasin, a potential molecular marker for ovarian carcinomas.";
 RL Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=20510030; PubMed=11054574;
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
 RA Moss P., Paepel B., Wang K.;
 RT "Sequencing and expression analysis of the serine protease gene
 RT cluster located in chromosome 19q13 region.";
 RL Gene 257:119-130(2000).
 RN [6]
 RP SEQUENCE OF 1-164 FROM N.A. (ISOFORM 1).
 RA Lamerdin J.E., McCready P.M., Skowronski E., Vismathan V.,
 RA Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Ganes J.,
 RA Dangnan L., Briker A., Christensen M., Georgescu A., Avila J., Liu S.,
 RA Andreise T., Frankheim M., Altix C., Amico-Keller G., Coefield J.,
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
 RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 Olsen A.S., Carrano A.V.;
 RT "Sequence analysis of chromosome 19q13.4.";
 RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.

CC	-1- FUNCTION: SUGGESTED TO BE INVOLVED IN KINDLING EPILEPTOGENESIS AND HIPPOCAMPAL PLASTICITY.
CC	-1- CATABOLIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
CC	-1- SUBCELLULAR LOCATION: secreted.
CC	-1- ALTERNATIVE PRODUCTS:
CC	Event=Alternative splicing; Named isoforms-2;
CC	Name=1;
CC	Idoid=060259-1; Sequence=Displayed;
CC	Name=2;
CC	Idoid=060259-2; Sequence=VSP_005401;
CC	-1- TISSUE SPECIFICITY: ISOFORM 1 IS PREDOMINANTLY EXPRESSED IN THE PANCREAS WHILE ISOFORM 2 IS EXPRESSED IN ADULT BRAIN AND HIPPOCAMPI. BOTH FORMS ARE ALSO FOUND IN FETAL BRAIN AND PLACENTA. NOT DETECTED IN KIDNEY, SPLEEN, LIVER AND LUNG.
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
CC	-----
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CC	-----
DR	EMBL; AB009849; BAA38673.1; -
DR	EMBL; AB012761; BAA28676.1; -
DR	EMBL; AB010780; BAA88684.1; -
DR	EMBL; AB008390; BAA82665.1; -
DR	EMBL; AB008927; BAA82666.1; -
DR	EMBL; AF005982; AAD56050.1; -
DR	EMBL; AF005974; AAD25979.1; -
DR	EMBL; AF005974; AAD25979.1; -
DR	EMBL; AF243527; AAG33361.1; -
DR	EMBL; AC011473; AAG32354.1; -
DR	HSSP; Q61955; INPM.
DR	MEMOPS; S01.244; -
DR	GeneW; HGNC:6369; KLB8.
DR	GO; GO:0007399; P:neurogenesis; TMS.
DR	InterPro; IPR001314; Chymotrypsin.
DR	InterPro; IPR001254; Ser-protease_Try.
DR	Pfam; PF000089; trypsin; 1.
DR	PRINTS; PR00722; CHYMOTRYPSIN.
DR	SMART; SM00020; TRY_SPC; 1.
DR	PROSITE; PS00340; TRYPSIN_DOM; 1.
DR	PROSITE; PS00340; TRYPSIN_HIS; 1.
DR	PROSITE; PS00135; TRYPSIN_SER; 1.
KW	Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;
KW	Alternative splicing.
FT	SIGNAL 1 28
FT	PROPEP 29 32
FT	CHAIN 33 260
FT	ACR_SITE 73 73
FT	ACR_SITE 120 120
FT	ACR_SITE 212 212
FT	DISULFID 39 173
FT	DISULFID 58 74
FT	DISULFID 145 246
FT	DISULFID 152 218
FT	DISULFID 184 198
FT	DISULFID 208 233
FT	CARBOHYD 110 110
FT	VARSPLIC 23 23
SO	SEQUENCE 260 AA; 28048 MW; EF439E5BC83E660 CMC64; /FTid=VSP_005401.

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

6.63e-38

690.00

66.93%

49.21%

29.11%

Length:

Matches:

Conservative:

Mismatches:

Indels:

260

125

45

80

4

DB:	1	Gaps:	3
US-09-856-320A-1 (1-1301) x KIK8_HUMAN (1-260)			
QY	188 CGSTCCSTCCSCCAGGCAATGAGATTTGCAGTTAACTCTCTG-----GCTCTG		241
Db	3 ArgProArgProArgAlaAlaLysThrThrMetPheLeuLeuGlyValAlaTyr		22
QY	242 GCACACAGGCTTTAGGGGAGACACAGATCATCAAGGGTTGCGATGCGACAC		307
Db	23 AlaGlyHisSerArgAlaGlnGlySerValLeuGlyLysGlyLysGlyLysGlyLys		42
QY	302 TCCACACCCCGAGGAGCAGCCTGTCTCCAGAGACAGCCTGCTGGGCGACGCTG		361
Db	43 SerGlnProThrPheGlnAlaLeuPheGlnGlyGlnGlnLeuLeuGlyValLeu		62
QY	362 ATGCCCCCAGATGCTCTGACACAGCCCACTGCTCCAAAGCCCGCTACATAGTTC		421
Db	63 ValGlyLysThrThrValLeuThrAlaAlaHisCysLysLysProLysTyrThrValArg		82
QY	422 CTGGGCGAGACCAACTCCAGAAAGGAGGAGGCTGTGACAGACCCGGACAGCCAGAG		481
Db	83 LeuGlyAspHisSerLeuGlnAsnLysAspGlyProGlnGlnGlnThrProValGln		107
QY	482 TCTTCCCCCACCSCGGCTTCAACAACAGCTCCCAACAAAGACACCCCAATGATAC		541
Db	103 SerIleProHisIleProCysTyrLysAsnSer---AspValGluAspHisAsnHisAspLeu		121
QY	542 ATCTGTGTAAGATGGCATCTGGCAGATGCTCATCATCTGGGGCTGGTCCAGCCCTCACTC		601
Db	122 MetLeuLeuGlnLeuArgAspGlnAlaSerLeuGlySerLysValLysProIleSerLeu		141
QY	602 TCTCAAGCTGTGTCACTGCTGACACACAGCTCCTCATTTCCGGCTGGGAGACAGCTCC		661
Db	142 AlaAspHisCysThrGlnProGlyGlnLysCysThrValSerGlyTyrGlyThrValThr		161
QY	662 AGCCCCCAGTAAAGCTGCTGCTCAACCTTGAGAGCCGACCAACATCCATCATTTGACAC		721
Db	162 SerProArgGluAsnPheProAspThrLysAsnLysCysAlaGluValLysIlePheProGln		181
QY	722 CAGAACTGTAGAAAGCTTACCCCGGCAACATCAGACACACATGATGTGTGGCAGCGTG		781
Db	182 LysLysCysGluLysAspAlaTyrProGlyGlnIleThrAspGlyMetValCysAlaGlySer		201
QY	782 CAGGAAGGGGCAAGGATCTCTGCCAGGGTCACTCCGGGGCCCTGTGTTGATACAG		841
Db	202 SerLysGlyAla---AspThrCysGlnGlnLysAspSerGlyGlyProLeuValCysAspGly		220
QY	842 TCTCTTCAAGGAGATTAATCTCTGGGGGACAGATCGGTGGGATCACCACCGAAACCTGGT		901
Db	221 AlaLeuGlnGlyIleIleHisSerThrPheLysAspProCysGlyLysSerAspLysProGly		240
QY	902 GTCTACAGAAAGCTGCAAAATATGTGACTGGATTCACGAG		943
Db	241 ValTyrThrAsnIleCysArgTyrLeuAspThrIleLys		254
RESULT 7			
KIK8_HUMAN			
ID	KIK8_HUMAN	STANDARD:	PRT: 277 AA.
AC	Q9URK3; Q9Y433;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Kallikrein 13 precursor (EC 3.4.21.-) (Kallikrein-like protein 4)		
GN	KLK13 OR KLK14.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
FN	[1]		
XP	SEQUENCE FROM N.A.		
XP	MEDLINE=20229789; PubMed=10766816;		

RA	Yousef G.M., Chang A., Diamantis E.P. ;
RT	"Identification and characterization of KLR-14, a new kallikrein-like
RL	gene that appears to be down-regulated in breast cancer tissues.";
RN	J. Biol. Chem. 275:11891-11896(2000).
RM	[2]
RP	SEQUENCE FROM N.A.
RA	Lamerdin J.E., MCCready P.M., Skowronski E., Visanathan V.,
RB	Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stllwagen S.,
RC	Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Gaines J.,
RD	Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
RE	Dantrese T., Trankhim M., Altix C., Amico-Keller G., Coefield J.,
RF	Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
RG	Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RH	Olsen A.S., Carraro A.V. ;
RI	"Sequence analysis of chromosome 19q13.4."
RJ	Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.
RK	[3]
RP	SEQUENCE OF 1-180 FROM N.A.
RC	TISSUE=uterus;
RA	Ansoore W., Wirner U., Mewes H.-W., Gassenhuber J., Wiemann S. ;
RL	Submitted (MAY-1999) to the EMBL/Genbank/DBJ databaes.
CC	-1 SUBCELLULAR LOCATION: Secreted (Probable).
CC	-1 TISSUE SPECIFICITY: EXPRESSED IN PROSTATE, BREAST, TESTIS AND
CC	SALIVARY GLAND.
CC	-1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
CC	-----
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CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb-sib.ch/)
CC	or send an email to license@isb-sib.ch .
CC	-----
DR	EMBL; AF135024; AAD26425.2; -
DR	EMBL; AC011473; AAG32325.1; -
DR	EMBL; AL050220; CAB43320.1; ALT_INIT.
DR	HSSP; P00763; IDPO.
DR	MEROPS; S01.306; -
DR	Genev; HGNC:6361; KKLK13.
DR	MIM; 605505; -
DR	GO; GO:0005576; C:extracellular; NAS.
DR	GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
DR	InterPro; IPR001254; Ser.protease_Try.
DR	Pfam; PF00089; trypsin_1.
DR	SMART; SM0020; TRYP_SPC; 1.
DR	PROSITE; PSS0240; TRYPSIN_DOM; 1.
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.
DR	PROSITE; PS00135; TRYPSIN_SER; 1.
KW	Hydrolase; Serine protease; Glycoprotein; Signal.
FT	SIGNAL
FT	CHAIN
FT	ACT_SITE
FT	ACT_SITE
FT	DISULFID
FT	DISULFID
FT	DISULFID
FT	DISULFID
FT	DISULFID
FT	CARBOHYD
FT	CARBOHYD
FT	CONFLICT
SO	SEQUENCE
SA:	277 AA; 30570 MW; BA8A9B8DFB5D542 CRC64;
Alignment Scores:	
Pred. No.:	9.72e-38
Score:	687.50
Percent Similarity:	66.92%
Best local Similarity:	48.46%
Query Match:	29.01%
OB:	1
Length:	277
Matches:	126
Conservative:	48
Mismatches:	71
Gaps:	15
Indels:	3

[illegible]

"Purification, molecular cloning, and expression of a human stratum corneum trypsin-like serine protease with possible function in desquamation." J. Biol. Chem. 274:30033-30040(1999).

[2]

SEQUENCE FROM N.A.

RP MEDLINE=2018156; PubMed=10652563;

RA Yousef G.M., Luo L.-Y., Diamandis E.P.

RT "Identification of novel human kallikrein-like genes on chromosome 19q13.3-q13.4."

RL Anticancer Res. 19:2843-2852(1999).

[3]

SEQUENCE FROM N.A.

RP MEDLINE=20510030; PubMed=11054574;

RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Paepker B., Wang K.;

RT "Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region."

RL Gene 257:119-130(2000).

[4]

SEQUENCE FROM N.A.

RP TISSUE=Ovary;

RC MEDLINE=23388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Dlatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Kulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Feingold J., Hellmuth E., Kettman M., Madan A., Rodriques S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E., Jones S.U.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -1- FUNCTION: MAY BE INVOLVED IN DESQUAMATION.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN SKIN, BREAST, BRAIN AND TESTIS.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.

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EMBL: AF168768; AAF03101.1; -

EMBL: AF135028; AAD26429.1; -

EMBL: AF243327; AAG33358.1; -

EMBL: BC008036; AAH08036.1; -

HSSP: P00763; IDPO.

MEROPS: S01.017; -

Genew: HGNC:6366; KLK5.

DR MIM: 605643; -

DR GO: GO:0005615; C:extracellular space; TAS.

DR GO: GO:0008544; P:epidermal differentiation; TAS.

DR GO: GO:0006508; P:proteolysis and peptidolysis; NAS.

DR InterPro: IPR001254; Chymotrypsin.

DR InterPro: IPR001254; Ser_protease TRY.

DR Pfam: PF00089; trypsin; 1.

DR SMART: SMART:PRO0722; CHYMOTRYPSIN.

DR SMART: SMART:PRO0722; TRY-SPC; 1.

DR PROSITE: PS50240; TRYPSIN_DOM; 1.

DR PROSITE: PS00134; TRYPSIN_HIS; 1.

DR PROSITE: PS00135; TRYPSIN_SER; 1.

KW HydroLase; Serine protease; Glycoprotein; Signal.

FT SIGNAL 1

FT CHAIN 23

FT ACT_SITE 108

FT ACT_SITE 153

FT ACT_SITE 245

FT DISULFID 73

FT DISULFID 93

FT DISULFID 109

FT DISULFID 178

FT DISULFID 185

FT DISULFID 217

FT DISULFID 241

FT CARBOHYD 69

FT CARBOHYD 173

FT CARBOHYD 208

FT CARBOHYD 252

FT CONFLICT 25

SO SEQUENCE 293 AA; 32020 MW; D92C92F3609E5946 CRC64;

Alignment Scores:

Pred. No.:	2,55e-35	Length:	293
Score:	650.50	Matches:	118
Percent Similarity:	68.24%	Conservative:	41
Best Local Similarity:	50.64%	Mismatches:	67
Query Match:	27.45%	Indels:	7
DB:	1	Gaps:	4

US-09-856-320a-1 (1-1301) x KLK5_HUMAN (1-293)

QY 266 ACCGAGTATCATCAAGGGGCTCGAGTGCAGACCTTCACCCGCTGGAGGACCC--- 322

DB 65 SertrglllellsnglsnglserraspCysaspmetlthrlnprotrglnalalaileu 84

QY 323 CTGTTCGAGAAGACGCGCTACTCTGTGGGCGAGCTCATCGGCGCCAGATGGCTGCTG 382

DB 85 LeuleuargproaenglnleuTYRysglYAlaValleuValnlsproglnttrpleu 104

QY 383 ACAGACAGCCGCTGCTCAAGCCGCCGCTACATAGTTCACCTGGGCGACACACCTTCAG 442

DB 105 ThrAlaAlaHlsCysAlrgLysValPheArgValArgleuGlYHsTYRserleuSer 124

QY 443 AAG---GAGAGGGCTGTGACGACAGCCGACACCTAGTCTTCCACCCGCGC 499

DB 125 ProValTYRgluserglYnglnlmetPheglnglYallYserlIleproHlsproglY 144

QY 500 TTCACACACAGCCCTCCGACCAAGACCGGACGATGATTCATCGTGGAGATGGCA 559

DB 145 TYRser-----HlsproglYHlserrasnlspleuMetleuIleLysleuAsn 160

QY 560 TCCGCACTTCATCACTGAGGCTGTCGACCCCTCACCTTCCTTCACGCTGTGCACT 619

DB 161 ArgArgglleargproHlsrValAspValArgProIleAsnValserHlsCysproSer 180

QY 620 GCTGGACACAGCTGCTCATTTCCGGCTGGGCGACGATGCACCCCGAGTACGCTG 679

DB 181 AlagllYHlsrCysleuValserglYtrgglYThrTYRserlIleproglYnlsHlsPhe 200

QY 680 CCTCACACCTTGGAGTGGCGGACATCATCATGATGAGACACCAAGTGTGGAACGCC 739

DB 201 ProLysValleuIleCysleuAsnIleSerValleuSerGlYnlsArgCysgluAspAla 220

QY 740 TACCCGCGCAACATCAACACCATGATGTTGTCGACGCTGCAGAGAGGCGCAAGAG 799

DB 221 TYRProArglnlInleAspArHlmetPheCysAlagly---AspYsAlaaglYAlgaSp 239

QY 800 TCCTGCCAGGGTACTCTCGGGGCGCTGTGTTGTACACAGTCTCTTCAAGGCAATATC 859

DB 240 SerCysglnglYAspserglYglYProValIalCysAsnGlYserleuInglnlYleuVal 259

QY 860 TCCTGGGGCGCAGGATCGTGTGATCACCAGAAACCTGCTGTACACGAAGTCTGC 919


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OY 611 TGTGTCACTGCTGGACACAGCTGCTCATTTCCGGCTGGGGACAGACAGCCACCCAC 670
DB 145 GIDPRLYSLVGLYGLYSETHRYCSLEUALASERGLYTRPGYSETHRYLPSROLEUILL 164
OY 671 TTACGCGCTGCTGACACCTGTCGATGGCGCCACACATGACATGAGACAGAGTGT 730
DB 165 TRPLUHEPRDAPSPAPSPLEGLINCYSVALANSILLENHLSLEULEUSERASHGIDLYSCYS 184
OY 731 GAGACGCTTACCCCGGCGACATCATGACACATCATGCTGTGTGCGACGTCGAGAAAGG 790
DB 185 ILLEULALATRYLRYGLULYSVALTRHASPHEULEUCYSALAGLYGLULGULGLUCLY 204
OY 791 GGCAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 850
DB 205 GLYLYSPAPSPHRYCSYTHNGLYASPSEGLYGLYPROLEUCYSPSPGLYVALLEULN 224
OY 851 GGCATATATCTGCTGGGGCGACAGATCCGTCGATCCGACATCCGACGAGGCTGCTGCTACAG 910
DB 225 GLYILETHRSERTTRPGYSEVALPPOCYSAALALYSHRANMETPROVALAILETYRTHR 244
OY 911 AAGCTGCAAAATATGTGGACTGGATCCAGAGACATGAGAACAT 958
DB 245 LYSLEULELYSPHETHRSERTTRPLEYGLULVALMETLYSGULUAN 260
RESULF 12
KLK1_RAT STANDARD; PRT; 261 AA.
AC P00758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Glandular kallikrein, pancreatic 1 precursor (EC 3.4.21.35) (Tissue
DE kallikrein) (PS kallikrein) (RKG-1).
GN KLK1 OR KLK-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID-10116;
RN [1]
RP MEDLINE-83117659; PubMed-6961406;
RA Swift G.H., Dagorn J.-C., Ashley P.L., Cummings S.W., McDonald R.J.;
RT "Rat pancreatic kallikrein mRNA: nucleotide sequence and amino acid
RT sequence of the encoded preproenzyme.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:7263-7267(1982).
RN [2]
RP MEDLINE-86051477; PubMed-2998455;
RA Ashley P.L., MacDonald R.J.;
RT "Kallikrein-related mRNAs of the rat submaxillary gland: nucleotide
RT sequences of four distinct types including tonin.";
RL Biochemistry 24:4512-4520(1985).
RN [3]
RP MEDLINE-89214217; PubMed-2708383;
RA Wines D.R., Brady J.M., Pritchett D.B., Roberts J.L., MacDonald R.J.;
RT "Organization and expression of the rat kallikrein gene family.";
RL J. Biol. Chem. 264:7653-7662(1989).
RN [4]
RP MEDLINE-89214217; PubMed-2708383;
RA Wines D.R., Brady J.M., Pritchett D.B., Roberts J.L., MacDonald R.J.;
RT "Organization and expression of the rat kallikrein gene family.";
RL J. Biol. Chem. 264:7653-7662(1989).
RN [5]
RP MEDLINE-86131678; PubMed-3004582;
RA Gerald W.L., Chao J., Chao L.;
RT "Immunological identification of rat tissue kallikrein cDNA and

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RT Characterization of the kallikrein gene family.";
RL Biochim. Biophys. Acta 866:1-14(1986).
CC 1- FUNCTION: GLANDULAR KALLIKREINS CLEAVE MET-LYS AND ARG-SER BONDS
CC IN KININOGEN TO RELEASE LYS-BRADYKININ.
CC 1- CATALYTIC ACTIVITY: Preferential cleavage of Arg-I'-xaa bonds in
CC small molecule substrates. Highly selective action to release
CC kallidin (Lysyl-bradykinin) from kininogen involves hydrolysis of
CC Met-I'-xaa or Leu-I'-xaa.
CC 1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
CC -----
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CC -----
DR EMBL; J00758; -; NOT ANNOTATED_CDS.
DR EMBL; M11563; AAA41464.1; ALT_INIT.
DR EMBL; M23876; AAA41462.1; -;
DR EMBL; M23874; AAA41462.1; JOINED.
DR EMBL; M23875; AAA41462.1; JOINED.
DR EMBL; D00448; BAA00346.1; JOINED.
DR EMBL; D00446; BAA00346.1; JOINED.
DR EMBL; D00447; BAA00346.1; JOINED.
DR EMBL; X03560; CAA27247.1; -;
DR PIR; A00944; KORTP.
DR HSSP; P00757; 1SGF.
DR InterPro; IPR001254; Ser_Protease_Try.
DR pfam; PF00089; trypsin_1.
DR SMART; SM00020; TRYP-SPC; 1.
DR PROSITE; PS02040; TRYP-SIN_DOM; 1.
DR PROSITE; PS0134; TRYP-SIN_HIS; 1.
DR PROSITE; PS00135; TRYP-SIN_SER; 1.
KW Hydrolyase; Serine protease; Glycoprotein; Multigene family; Zymogen;
KW Signal.
FT SIGNAL 1 18 PROBABLE.
FT PROPEP 19 24 ACTIVATION PEPTIDE (PROBABLE).
FT CHAIN 25 261 GLANDULAR KALLIKREIN 1.
FT CHAIN 25 111 CHAIN 1.
FT CHAIN 112 261 CHAIN 2.
FT ACT_SITE 65 65 CHARGE RELAY SYSTEM.
FT ACT_SITE 120 120 CHARGE RELAY SYSTEM.
FT ACT_SITE 213 213 CHARGE RELAY SYSTEM.
FT DISULFID 31 173 BY SIMILARITY.
FT DISULFID 50 66 BY SIMILARITY.
FT DISULFID 152 219 BY SIMILARITY.
FT DISULFID 184 198 BY SIMILARITY.
FT DISULFID 209 234 BY SIMILARITY.
FT CARBOHYD 108 108 N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE 261 AA; 28852 MW; F2F99C0227A7882B CRC64;
Alignment Scores:
Pred. No.: 3.61e-33 Length: 261
Score: 617.50 Matches: 112
Percent Similarity: 62.50% Conservative: 48
Best local Similarity: 43.75% Mismatches: 85
Query Match: 26.05% Indels: 11
DB: 1 Gaps: 2
US-09-856-320A-1 (1-1301) x KLK1_RAT (1-261)
OY 224 TTATCTGCTGCTGCTGGACACAGGCTGTGAGGGGA-----GAGACACAG 271
DB 5 ILEULHEULALALALALALALALALALALALALALALALALALALALALALALALALAL 24
OY 272 ATCATCAAGGGGTTGATGAGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 331
DB 25 VALVALGLYGLYTRYSANCYSGLUMELANSEGLNPRORPGLNVALALALALALALALAL 44
OY 332 AAGACGGGCTACTCTGTGTGGGCGACGCTCATGCCCCCAGATGCTCTGACAGACCC 391

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Db      45 pHeGlygluTyrLeuGlyValLeuIleAspSerTrpPailIleHAlaIa 64
QY      392 CAGTCGCTCAAGCCCGCTACATAGTTCACTGGGGCAGACACCTCCAGAGAGAG 451
Db      65 HlSCyAlaIleThAspAsnTyrGlnValTrpLeuGlyAlaGAsnAsnLeuTyrGlnAspGlu 84
QY      452 GCGCTGAGACAGACCCGGACAGACCTAGTCTCCCGACCCCGGCTTCAACAAACGC 511
Db      85 ProPheAlaGlnHlAspLeuValSerGlnSerPheProHlIsProlGlyPheAsnGlnAsp 104
QY      512 CTC-----CCCAACAAAGACCCGCAATGACATCATGCTGGGG 550
Db      105 LeuIleTrpAsnHlThrAlaGlnProGlyAspAspTyrSerAsnAspLeuLeu 124
QY      551 AAGATGACATCCGACAGTCTCAACACCTGGGCTGGGCTCCGACCCCTCAACACGC 610
Db      125 HlAspSerGlnProHlAspIleThrAspGlyValLysValIleAspLeuProIleGlu 144
QY      611 TGTGTCACTGTGGACACAGTGTCTCATTTCCGGGTGGGGAGACAGTCCAGCCCGCAG 670
Db      145 GluProLysValGlySerThrCysLeuAlaSerGlyTyrGlySerIleThrProAspGly 164
QY      671 TTACGGCTGCTCACACCTGGGATGGGCAACATCATCATGAGCAGACCAAGATGT 730
Db      165 LeuGlnLeuSerAspAspLeuGlnCysValAsnIleAspLeuSerAsnGlnLysCys 184
QY      731 GAGAACGCTTACCCGGACACATGACAGACACCATGTTGTCGACGCTGACAGAGAG 790
Db      185 ValGluAlaHlAspGlnLysGlnValThrAspLeuMetLeuCysAlaGlyLysMetAspGly 204
QY      791 GGCAGGAGATCTGCGCAGGATGACATCGGGGGCCCTGTGGTGTACACAGTCTCTCAA 850
Db      205 GlyLysAspThrCysLysGlyAspSerGlyCylProLeuIleCysAsnGlyValLeuGln 224
QY      851 GGCATTATCTCTGGGGCAGGATCGGTGGGATGACCCGAAAGGCTGGTGTACAGAG 910
Db      225 GlyIleThrSerTrpGlyPheAsnProCysGlyGluProLysSerProGlyIleTyr 244
QY      911 AAGTCTGCAATATGTGACTGTGATCCAGAGACAGACCAACAT 958
Db      245 LysLeuIleLysPheThrProTrpIleLysGluValMetLysGlnAsn 260

RESULT 13
TRY3_CHICK STANDARD; PRT; 248 AA.
AC 090629;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trypsin II-P29 precursor (EC 3.4.21.4).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus
OX NCBI_TaxID=9031;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=95251611; PubMed=7733885;
RA Wang K., Gan L., Lee I., Hood L.E.;
RT Isolation and characterization of the chicken trypsinogen gene
family.*;
RL Biochem. J. 307:471-479(1995).
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg--|-Xaa, Lys-|-Xaa.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: HIGH LEVELS ARE SEEN IN THE PANCREAS WHILE
CC -1- LOWER LEVELS ARE FOUND IN THE LIVER, SPLEEN AND THYMUS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
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CC or send an email to license@isb-sib.ch).
DR EMBL: U15157; AAA79914.1; -.
DR PIR: S55066; S55066.
DR HSSP: P00763; IDPO.
DR MEROPS: S01.151; -.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin; 1.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS00240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; 1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
DR HydroLase: Serine protease; Digestion; Pancreas; Zymogen; Signal;
KW Multigene family.
KW Multi-subunit.
FT SIGNAL 1..16 BY SIMILARITY.
FT PROPEP 17..25 ACTIVATION PEPTIDE (BY SIMILARITY).
FT CHAIN 26..248 TRYPsin II-P29.
FT ACT_SITE 65..65 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 109..109 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 202..202 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 32..162 BY SIMILARITY.
FT DISULFID 50..66 BY SIMILARITY.
FT DISULFID 134..235 BY SIMILARITY.
FT DISULFID 141..208 BY SIMILARITY.
FT DISULFID 173..187 BY SIMILARITY.
FT DISULFID 198..222 BY SIMILARITY.
FT SITE 196..196 REQUIRED FOR SPECIFICITY (BY SIMILARITY).
SQ SEQUENCE 248 AA; 26622 MW; E5E1B07622B58E CRC64;

Alignment Scores:
Pred. No.: 8, 22e-33 Length: 248
Score: 612.00 Matches: 121
Percent Similarity: 63.35% Conservative: 38
Best Local Similarity: 48.21% Mismatches: 82
Query Match: 25.82% Indels: 10
DB: 1 Gaps: 5

US-09-856-320A-1 (1-1301) x TRY3_CHICK (1-248)
QY 209 ATGAGGATTCGTGAGTTAATCTG-----CTGTCTGTGCAACAGGCTTGAGGGGA 262
Db 1 MetLysPheLeuPheLeuIleLeuSerCysLeuGlyAlaAlaValAlaPheProGlyGly 20
QY 263 -----GACACAGATCATCAAGGGCTTCAGATGACACCTCATCTCCAGCCCTGGCAG 316
Db 21 AlaAspAspAspLysLysLysValGlyTyrThrCysProGlnHisSerValProTyrGln 40
QY 317 GCAGCCCTGTTCGAGAGACGGGGTACTCTGTGGGGCAGCGTCATCCGCCCGAGATGG 376
Db 41 ValSerLeu---AsnSerGlyTyrHisPheCysGlyGlySerLeuIleAsnSerGlnTrp 59
QY 377 CTCCTGACAGACAGCCCATCTGCTCAAGCCCGCTCAATAGTTTACCTGGGGCAGCAGAC 436
Db 60 ValLeuSerAlaAlaHisCysTyrLysSerArgLysGlnValAlaArgSerValIleLeuArgHisPro 79
QY 437 CTCGCAAGAGAGAGGGCTGTGAGCAGACCCGAGACGCCAGCAGAGTCCCTCCCGACCCGC 496
Db 80 IleAspValGlnGlnAspSerGlnValAlaArgSerSerValIleLeuArgHisPro 99
QY 497 GCGTTCACACAGACGCTCCCAACAAAGACCCGCAATGACATCATGCTGGTGAAGATG 556
Db 100 LysTyrSerSerIleThrLeuAsn-----AsnAspIleMetLeuLeuLysLeu 115
QY 557 GCATGCAAGTCTCATCACTCGGGCTGTGCGACCCCTCAACCTCTCTCAAGCTGTGTTC 616
Db 116 AlaSerAlaValAlaGlnTyrSerAlaAspIleGlnProIleAlaLeuProSerSerCysAla 135
QY 617 ACTGCGGACAGACAGGCTCATTTCCGGCTGGGGCAGAGAGCTCCAGCCCGCAGTTACGC 676
Db 136 LysAlaGlyThrGluCysLeuSerGlyTyrGlyAlaThrLeuSerAsnGlyTyrAsn 155

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OY 677 CTGCTCAGACCTGGATGCGCCACATCATTCATGAGCAGACAGTGTGAGAC 736
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 156 TyrProGluLeuGlnCysLeuAsnAlaProIleLeuSerAspGlnGlu 175
OY 727 GCGTACCCCGGCAATGACAGACACCATGGTGTGCGACCTGCAGAGGGGCGAG 796
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 176 AlaTyrProGlyAspIleThrSerAsnMetIleCysValGlyPheLeuGlnGly 195
OY 797 GACTCTCCAGAGGTGACTCCGGGGCCCTGTGTCTTAACAGTCTCTCAAGCAT 856
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 196 AspSerCysGlnGlyAspSerGlyGlyProValValCysAsnGlyGluLeuGlnGly 215
OY 857 ATCTCTGGGGCCAGATCCGTGTCGATCACCCGAAAGCCTGTGTCTACAGCAATC 916
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 216 ValSerTyrGlyIleGly---CysAlaLeuGlyGlyTyrProGlyValTyrThrIleVal 234
OY 917 TGCAATATGTGAGTGCATGATCCAGAGAGCATG 949
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 235 CysAsnTyrValAspTyrPheGlnGlnThrIle 245

RESULT 14
KLC_RAT
ID KLC_RAT STANDARD: PRT: 259 AA.
AC P36376:
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glandular kallikrein 12, submandibular/renal precursor (EC 3.4.21.35)
DE (Tissue kallikrein) (RSCG-3).
GN KLR12 OR KLR-12.
OS Rattus norvegicus (rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89088074; PubMed=2849988;
RA Chen Y.-P., Chao J., Chao L.;
RT "Molecular cloning and characterization of two rat renal kallikrein
RT genes."
RL Biochemistry 27:7189-7196(1988).
CC -1- FUNCTION: GLANDULAR KALLIKREINS CLEAVE MET-LYS AND ARG-SER BONDS
CC IN KININOGEN TO RELEASE LYS-BRADYKININ.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage of Arg-|-Xaa bonds in
CC small molecule substrates. Highly selective action to release
CC kallidin (Lysyl-bradykinin) from kininogen involves hydrolysis of
CC Met-|-Xaa or Leu-|-Xaa.
CC -1- TISSUE SPECIFICITY: KIDNEY AND SUBMANDIBULAR GLAND.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M19648; AAA51640.1; -.
DR EMBL: M22822; AAA51640.1; JOINED.
DR PIR: B31136; B31136.
DR HSSP: P00759; 1TON.
DR MEROPS: S01.160; -.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin_1.
DR SMART: SM00020; trypsin_1.
DR PROSITE: PS02440; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Glycoprotein; Multigene family; Zymogen;
FT SIGNAL 1 18 PROBABLE.

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FT PROPEP 19 24 ACTIVATION PEPTIDE (PROBABLE).
FT CHAIN 25 259 GLANDULAR KALLIKREIN 12,
FT ACT_SITE 63 63 SUBMANDIBULAR/RENAL.
FT ACT_SITE 118 118 CHARGE RELAY SYSTEM.
FT ACT_SITE 211 211 CHARGE RELAY SYSTEM.
FT DISULFID 31 171 BY SIMILARITY.
FT DISULFID 48 64 BY SIMILARITY.
FT DISULFID 150 217 BY SIMILARITY.
FT DISULFID 182 196 BY SIMILARITY.
FT DISULFID 207 232 BY SIMILARITY.
FT CARBOHYD 91 91 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 106 106 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 259 AA; 28759 MW; 535ABBE25435144F CRC64;

Alignment Scores:
Pred. No.: 8.9e-33 Length: 259
Score: 611.50 Matches: 112
Percent Similarity: 60.85% Conservative: 45
Best Local Similarity: 43.41% Mismatches: 88
Query Match: 25.80% Indels: 13
DB: 1 Gaps: 3

US-09-856-320A-1 (1-1301) x KLC_RAT (1-259)
OY 218 CTGCAGTTAATCTGCTTGTGTCGCAAGGCTTGAGGG-----GGAGAG 265
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3 LeuGlnIleLeuPheLeuValLeuSerValGlyIleAspAlaIleProIleGly 22
OY 266 ACCAGGATCATCAAGGGGTTGAGTGCAGAGCTTACCTCCAGCCCTGGAGAGCCCTG 325
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 23 SerAlaValAlaGlyGlyTyrCysGlnIleAsnSerGlnProTyrGlnAlaVal 42
OY 326 TTCGAGAAGAGCGGCTACTGTGTGGGCGAGCTCATCGCCCGCAGATGGCTGTGACA 385
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 43 Ile-----AsnAlaGlyTyrLeuGlyGlyValLeuLeuAspProSerTyrValIleThr 60
OY 386 GCAGCCCACTGCTCTCAAGCCCGCTACATAGTTCACCTGGGGCGAGCAACCTCCAGAG 445
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 AlaAlaIleCysTyrSerHisAsnTyrHisValLeuLeuGlyArgAsnAlaLeuPheLys 80
OY 446 GAGAGGGGCTGTGAGCAGACCCCGGACAGCCAGCTAGTCCTTCCCGCCCGGCTTAAC 505
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 81 AspIleProPheAlaGlnTyrAlaValAlaMetIleSerPheProHisProAspTyrAsn 100
OY 506 -----AACAGCCTCCCAACAAAGACCCAGCAATGACATCATG 544
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 101 ProPheMetLysAsnHisThrLeuPheProGlyAspAspHisSerAsnAspLeuMet 120
OY 545 CTGCTGAAGATGGCATGCCAGTCTCCATGACCTGGGCTGTGCGACCCCTACCCCTGCC 604
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 LeuLeuHisLeuSerGlnProAlaAspIleThrAspGlyValIleAspLeuPro 140
OY 605 TCAGCCTGTGACATGCTGTGGCAGCAGCTGCTCATTTCCGGCTGGGCGACAGCTCCAGC 664
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 141 ThrIleGlnProIleValGlySerThrCysLeuAlaSerIleTyrPheSerThrLysPro 160
OY 665 CCCAGTTAGCGCTGCTCCACACCTTGCAGATGGCCCAACATCCACCATTTGAGACACAG 724
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 161 LeuGlnTyrPheGlnPheProAspAspLeuGlnCysValAsnIleAsnIleLeuSerAsnGln 180
OY 725 AAGTGTGAGAACGCTTACCCCGGCAACATGACACACATGATGTTGCTGCAGCTGCAG 784
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 LysCysIleLysAlaHisThrGlnMetValThrAspValMetLeuCysAlaGlyGluLeu 200
OY 785 GAAGGGGCAAGAGCTCTGCGCAGAGTACTCCGGGGCCCTGTGCTGTAAACATCTP 844
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 201 GlnIleGlyLysAspThrCysAsnGlyAspSerGlyGlyProLeuLeuCysAspGlyVal 220
OY 845 CTTCAGAGCATTAATCTGCTGGGCGCAGATCCGTTGCTGATCAACCGCAAGCCGTGCTC 904
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 221 LeuGlnIleIleThrSerThrPheSerValProCysGlyGlnThrAsnArgProAlaIle 240

```


SO SEQUENCE 261 AA: 28998 MW: 4870748E174AF7C8 CRC64;

Alignment Scores:

Pred. No.:	8.91e-33	Length:	261
Score:	611.50	Matches:	110
Percent Similarity:	63.28%	Conservative:	52
Best Local Similarity:	42.97%	Mismatches:	83
Query Match:	25.80%	Indels:	11
DB:	1	Gaps:	2

US-09-856-320A-1 (1-1301) x KLR3_MOUSE (1-261)

```
OY 224 TTAATCCTGCTGCTGCTGGCAACAGGCTGTAGGGGA-----GAGACACAG 271
      ::::: |||||::: || :::
Db 5 IleuPheLeuAlaLeuSerLeuGlyGlyLeuAspAlaAlaProProValGlnSerArg 24
OY 272 ATCATCAAGGGGTTCGAGTCGACGCTCATGCCAGCTCCAGCCCTGGCAGGCGCCCTGTTCGAG 331
      ||::: |||||::: ||::: |||||::: |||||::: |||||:::
Db 25 IleValGlyGlyPheLeuGlyGlyLeuAsnSerGlnProTrpHisValAlaValTyrArg 44
OY 332 AAGACGGGCTACTCTGTGGGCGACGCTCATGCCAGATGCTCTGACAGCAGCC 391
      ||::: |||||::: ||::: || |||||::: |||||::: |||||:::
Db 45 TyrThrGlnTyrLeuGlyGlyValLeuLeuAsnProAsnTrpValLeuThrAlaAla 64
OY 392 CACTGCCCTCAAGCCCGCTACATAGTTCACCTGGGCGACACAACTCCAGAGAGAG 451
      ||||| ||||| ||||| |||||::: ||||| |||||::: |||||
Db 65 HisCysTyrAspAsnTyrLeuValTyrLeuGlyLeuAsnAsnLeuPheLeuAspGlu 84
OY 452 GGCTGTGAGCAGCCCGACAGCCAGCTGATGCTCCGCCAGCCCGGCTTCACACAGC 511
      || |||| ::::: |||||::: |||||::: |||||::: |||||
Db 85 ProSerAlaGlnHisArgPheValSerTyrAlaLeuProHisProGlyPheAsnMetSer 104
OY 512 CTCGCCAACA-----GACCACCGCAATGACATCATCTGTG 550
      |||| |||| ::::: |||||::: |||||::: |||||::: |||||
Db 105 LeuMetArgLysHisLeuArgPheLeuGlyTyrAspTyrSerAsnAspLeuMetLeu 124
OY 551 AAGATGGAGTCGACGCTCATCATCAGCTGGGCTGGCAGCCCTCACCTCTCTCAGC 610
      ::::: ||||| ||||| |||||::: |||||::: |||||::: |||||
Db 125 ArgLeuSerLysProIleAspIleThrAspThrValLysProIleThrLeuProThrGlu 144
OY 611 TGTTCTACATGCTGACACAGCTGCTCATTTCCGGCTGGGCGACAGCTCCAGCCCG 670
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||
Db 145 GluProLysLeuGlySerThrCysLeuAlaSerGlyTyrGlySerIleThrProThrLys 164
OY 671 TTACGCTGCTCACACCTTGCGATGCCCAACATCACCATCATTTGACACAGCAGAGTGT 730
      ::: |||| |||| |||||::: |||||::: |||||::: |||||
Db 165 PheGlnPheThrAspAspIleuTyrCysValAlaLeuLysLeuLeuProAsnGluAspCys 184
OY 731 GAGAACCCCTACCCCGGCAACATCACAGACACCATGGTGTGCCAGCTGCAGAGAGG 790
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||
Db 185 AlaLysAlaHisIleGlyLysValThrAspAlaMetLeuLysAlaGlyLysLeuAspGly 204
OY 791 GGCAAGACTCTGCTGAGGCTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 850
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||
Db 205 GlyLysAspThrCysLysGlyAspSerGlyGlyProLeuIleCysAspGlyValLeuGln 224
OY 851 GGCATTATCTCTGCGGCGCAGATCGCTGCGATCACCCGAAAGCCGTGCTGTACAG 910
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 225 GlyLeuSerSerThrGlyHisThrProCysGlyGlyProAspMetProGlyValTyrThr 244
OY 911 AAAGCTGCAAAATGTGCACTGATCCAGAGACGATGAAGAACAT 958
      ||||: ||||: |||||::: |||||::: |||||::: |||||
Db 245 LysLeuAsnLysPheThrSerTrpIleLysAspThrMetAlaLysAsn 260
```

Search completed: October 15, 2003, 20:20:54
Job time : 26.9416 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 15, 2003, 20:04:15 ; Search time 35.6662 Seconds
(without alignments)
7015.902 Million cell updates/sec

Title: US-09-856-320A-1
Perfect score: 2370
Sequence: 1 ctgccttgcctccacacctg.....aaaaaaaaaaaaaaaaaaaaa 1301

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 566616

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+n2p.model -DEV=xlp
-O=/cgn2.1/USPTO.spool.P/US09856320/r/unat_15102003.105640.8549/app.query.fasta_1.2318
-DB=PIR.76 -OFMT=fastan -SUFFIX=prp -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdt -LIST=45
-DOCALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=plot -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09856320@cgn.1.1.74@runat_15102003.105640.8549 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR.76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	698.5	29.5	260	2	I56559 neuropsin - mouse
2	618.5	26.1	261	2	A31136 tissue kallikrein
3	617.5	26.1	265	1	KORP tissue kallikrein
4	612	25.8	248	2	S55066 trypsin (EC 3.4.21
5	611.5	25.8	259	2	B31136 tissue kallikrein
6	611.5	25.8	261	1	NGMSG 7S nerve growth fa
7	604.5	25.5	263	2	S15686 tissue kallikrein
8	602.5	25.4	246	1	TRPRT2 trypsin (EC 3.4.21
9	601.5	25.4	261	2	A34079 tissue kallikrein
10	600.5	25.3	246	1	TRRT1 trypsin (EC 3.4.21
11	596.5	25.2	261	2	A29586 trypsin (EC 3.4.21
12	595.5	25.1	259	1	KORPtn tonin (EC 3.4.21.-
13	595	25.1	261	2	A29745 tissue kallikrein
14	594	25.1	238	2	S31779 trypsin (EC 3.4.21

15	591.5	25.0	261	2	S45303 tissue kallikrein
16	585.5	24.7	246	2	B25528 trypsin (EC 3.4.21
17	585	24.7	261	2	A25606 tissue kallikrein
18	580.5	24.5	261	1	KOMSI tissue kallikrein
19	580	24.5	231	1	TRPCTR trypsin (EC 3.4.21
20	580	24.5	262	1	KORH tissue kallikrein
21	578.5	24.4	244	2	A44284 tissue kallikrein
22	578	24.4	232	1	KOPC tissue kallikrein
23	576	24.3	247	1	TRDG trypsin (EC 3.4.21
24	572.5	24.2	257	2	S33772 tissue kallikrein
25	572.5	24.2	261	2	S01971 tissue kallikrein
26	571.5	24.1	253	2	A53968 serine proteinase
27	569	24.0	229	1	TRBOTR trypsin (EC 3.4.21
28	567	23.9	247	2	A27547 trypsin (EC 3.4.21
29	565	23.8	243	2	A35871 trypsin (EC 3.4.21
30	565	23.8	256	1	NGMSA 7S nerve growth fa
31	564.5	23.8	261	2	A41020 tissue kallikrein
32	564	23.8	259	2	A29746 tissue kallikrein
33	563	23.8	247	2	S13813 trypsin (EC 3.4.21
34	563	23.8	248	2	S55067 trypsin (EC 3.4.21
35	562.5	23.7	261	1	A32297 semenogelase (EC 3
36	559.5	23.6	261	1	S35711 trypsin (EC 3.4.21
37	559	23.6	242	2	S49489 trypsin (EC 3.4.21
38	559	23.6	247	2	S05494 trypsin (EC 3.4.21
39	558.5	23.6	259	2	D23863 tissue kallikrein
40	558.5	23.6	261	1	TRMSM5 tissue kallikrein
41	558	23.5	261	2	A24378 tissue kallikrein
42	557.5	23.5	304	2	S33496 trypsin (EC 3.4.21
43	556	23.5	246	1	TRDGC trypsin (EC 3.4.21
44	555.5	23.4	231	2	S31778 trypsin (EC 3.4.21
45	553	23.3	261	2	JE0236 tissue kallikrein

ALIGNMENTS

RESULT 1
I56559
neuropsin - mouse
C:Species: Mus musculus (house mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C:Accession: I56559
R:Chen, Z.L.; Yoshida, S.; Kato, K.; Momoto, Y.; Suzuki, J.; Tanaka, T.; Ito, J.; Nis
J. Neurosci. 15, 5088-5097, 1995
A:Title: Expression and activity-dependent changes of a novel limbic-serine protease
A:Reference number: I56559; MID:95348817; PMID:7623137
A:Accession: I56559
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-260 <RES>
A:Cross-references: GB:D30785; NID:91648847; PIDN:BA06451.1; PID:g1020091
A:Superfamily: trypsin; trypsin homology
F:33-252/Domain: trypsin homology <TRY>

Alignment Scores:

Pred. No.: 1.11e-38 Length: 260
Score: 698.50 Matches: 129
Percent Similarity: 66.13% Conservative: 35
Best Local Similarity: 52.02% Mismatches: 77
Query Match: 29.47% Indels: 7
Gaps: 3

US-09-856-320A-1 (1-1301) x I56559 (1-260)

QY	227	ATCCTGCTGCTCTGTGCAACAGGCGTGTGAGGGGAGAGCCAGG-----	271
DB	13	lleleuleuleuleuphemeteilyalatrpalagilyleuThArghlaInglyerlys	32
QY	272	ATCATCAAGGGTGTGAGTGCACAGCCTCACTCCAGCCCTGGACAGGACCCCTGTTGAG	331
DB	33	lleleuGLUGlyArgGluCysIleleprohIsseRginPtotrgInAlAlaleuupheIn	52
QY	332	AAAGACGGCTACTGTGTGGGGGAGACGCTCATGCCGCCAGATGGCTCTGTGACAGCC	391

Db 53 GLYGLNARGLEULEICYSGLYGLYValLeuValIAspArgTrpValIleuThrAlaAla 72
 QY 392 CACTGCCTCAAGCCCGCTACATATGTCACCTGGGCGACACAACTCCAGAGAGAG 451
 Db 73 HISCYSGLYSGLNGLYSGLYSerValArgLeuIleuIAspHisSerIleuSerArgAsp 92
 QY 452 GGCTGTAGAGCAGCAGCCGACGACGAGTCCTCCCGCCCGGGCTTCAACAGC 511
 Db 93 GLNProIleuGlnGluIleGlnValAlaIleuSerIleuGlnHisProCysTrpAsnAsnSer 112
 QY 512 CTCGCCAACAAGACACCCGATGATGATGATGATGATGATGATGATGATGATGATG 571
 Db 113 AsnPro---GluAspHisSerHisAspIleuIleuIleuIleuIleuIleuIleuIleu 131
 QY 572 ATCACTGGCTGTGGCAGCCCTGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 631
 Db 132 LeuIleuIAspLysValLysProValGlnLeuIleuIleuIleuIleuIleuIleuIleu 151
 QY 632 TGCTCATTTCCGGCTGGGCGACGATCCAGCCCGGATTAAGCCCTGCTCAACCTTG 691
 Db 152 CysIleIleSerGlyTrpGlyTrpGlyTrpValTrpSerProGlnGluAsnProAsnThrLeu 171
 QY 692 CGATGCCCAACATACCATCATGATGATGATGATGATGATGATGATGATGATGATG 751
 Db 172 AsnGlyAlaGluValLysIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 191
 QY 752 ATCAACAGACACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 811
 Db 192 IleThrGlnGluMetValCysAlaGly---SerSerAsnGlyAlaAspTrpHisGlnGly 210
 QY 812 GATCCCGGGGGCTGT 871
 Db 211 AspSerIleuGlyProLeuValCysAspGlyMetLeuIleuGlnGlyIleuIleuIleuIleu 230
 QY 872 GATCCGT 931
 Db 231 AspProCysGlyLysProGluLysProGlyValTrpThrLysIleuCysArgTrpThrThr 250
 QY 932 TGGATCCAGAGACGATGAAGAAC 955
 Db 251 TrpIleLysLysThrMetAspAsn 258
 Db
 RESULT 2
 A31136
 N: Alternate names: glandular prokallikrein 7, submandibular - rat
 C: Species: Rattus norvegicus (Norway rat)
 C: Date: 31-Mar-1990 #sequence.revision 31-Mar-1990 #text.change 22-Jun-1999
 C: Accession: A31136; S10698; S10699; D41429; B41429; S09315
 R: Chen, Y.P., Chao, J., Chao, L.
 Biochemistry 27, 7189-7196, 1988
 A: Title: Molecular cloning and characterization of two rat renal kallikrein genes.
 A: Reference number: A31136; MUID:89088074; PMID:2849988
 A: Accession: A31136
 A: Molecule type: DNA
 A: Residues: 1-261 <CHE>
 A: Cross-references: GB:M19647; GB:J02837; NID:9204999; PIDN:AAA41461.1; PID:9205000
 R: Elmoujahed, A.; Gutman, N.; Brillard, M.; Gauthier, F.
 FEBS Lett. 265, 137-140, 1990
 A: Title: Substrate specificity of two kallikrein family gene products isolated from the
 A: Reference number: S10698; MUID:90306305; PMID:2194829
 A: Accession: S10698
 A: Molecule type: protein
 A: Residues: 25-36 <ELM>
 A: Accession: S10699
 A: Molecule type: protein
 A: Residues: 112-139 <EL2>
 R: Kato, H.; Nakashima, E.; Enjiyoji, K.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.
 J. Biochem. 102, 1389-1404, 1987
 A: Title: Characterization of serine proteinases isolated from rat submaxillary gland: w1
 A: Reference number: A41429; MUID:88198057; PMID:3482210
 A: Accession: D41429
 A: Molecule type: protein

A: Residues: 112-133 <KAT>
 A: Accession: B41429
 A: Molecule type: protein
 A: Residues: 25-34, 'D', 36-45, 'S', 47-67, 'X', 69-75 <KA2>
 R: Brady, J.M.; MacDonald, R.J.
 Arch. Biochem. Biophys. 278, 342-349, 1990
 A: Title: The expression of two kallikrein gene family members in the rat kidney.
 A: Reference number: S09315; MUID:90225801; PMID:2183721
 A: Accession: S09315
 A: Status: not compared with conceptual translation
 A: Molecule type: mRNA
 A: Residues: 43-45, 'S', 47-114, 'A', 116-261 <BBA>
 C: Superfamily: trypsin; trypsin homology
 C: Keywords: hydrolase; serine proteinase
 F: 1-18/Domain: signal sequence #status predicted <SIG>
 F: 19-261/Product: tissue prokallikrein 7, submandibular #status predicted <MAT>
 F: 25-253/Domain: trypsin homology <TRY>
 F: 65,120,213/Active site: His, Asp, Ser #status predicted

Alignment Scores:

Pred. No.:	2,17e-33	Length:	261
Score:	618.50	Matches:	114
Percent Similarity:	62.11%	Conservative:	45
Best local Similarity:	44.53%	Mismatches:	86
Query Match:	26.10%	Indels:	11
DB:	2	Gaps:	2

US-09-856-320A-1 (1-1301) x A31136 (1-261)

QY 224 TTAATCCTGCTGT 271
 Db 5 IleuLeuLeuAspLeuSerLeuGlnIleuIleuIleuIleuIleuIleuIleuIleuIleu 24
 QY 272 ATCAACAGGGGT 331
 Db 25 ValIleuGlyTrpLysCysGlnLysAsnSerGlnProIleuIleuIleuIleuIleuIleu 44
 QY 332 AAGACGGCTACTCTGT 391
 Db 45 PheThrLysTrpLeuLysCysGlyGlyValLeuIleuIleuIleuIleuIleuIleuIleu 64
 QY 392 CACTGCCTCAAGCCCGCTACATATGATGATGATGATGATGATGATGATGATGATGATG 451
 Db 65 HisCysSerSerAsnAsnTrpGlnValTrpLeuGlyArgAsnAsnLeuLeuGlnAspGln 84
 QY 452 GGCTGTGACAGACCCGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 511
 Db 85 ProPheAlaGlnHisArgLeuValSerGlnSerPheProHisProAspTrpLysProPhe 104
 QY 512 CTC-----CCCAACAAAGACCACCGAATGATGATGATGATGATGATGATGATGATG 550
 Db 105 LeuMetArgAsnHisThrArgLysProGlyAspAspHisSerAsnAsnLeuMetLeuLeu 124
 QY 551 AAGATGACATGCCGACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 610
 Db 125 HisLeuSerIleuProIleuAspIleuHisAspGlyValIleuValIleuAspLeuProThrGln 144
 QY 611 TGCTGACCTGT 670
 Db 145 GlnProLysValIleuSerIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 164
 QY 671 TTACGCTGCTGACACCTTGCATGATGATGATGATGATGATGATGATGATGATGATGAT 730
 Db 165 TrpGlnProPheProAspAspLeuGlnCysValAsnIleuHisLeuLeuSerAsnGluLysCys 184
 QY 731 GAGAAAGCCTACCCCGGCAACATCAACAGACACCATGATGATGATGATGATGATGATGAT 790
 Db 185 IleLysAlaTrpLysGlnLysValTrpAspLeuMetLeuIleuIleuIleuIleuIleuIleu 204
 QY 791 GGCAAGACATCTGCCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 850
 Db 205 GlyLysAspThrCysThrGlyAspSerGlyGlyProLeuLeuLysAspGlyValLeuGln 224

QY 851 GGCAATATCTCTGGGGCCAGATCCGTGCGATACCCGAAAGCTGTCTACAG 910
DB 225 GYIIIEthSertPrpLysSerValProCysAlaLysThAsnMetProAlaIleYrThr 244
QY 911 AAGTCTGCAATATGCTGATCGATCGAGAGACATGACATGACAAAT 958
DB 245 LysLeuIleLysPheThrSertPrpIleLysGluValMetLysGluAsn 260

RESULT 3
KORTP
tissue kallikrein (EC 3.4.21.35) precursor - rat
N:Alternate names: glandular kallikrein; kininogenin; true tissue kallikrein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text-change 16-Jun-2000
C:Accession: A00944; A41429; A25137; JX0073; A23863; A33359
R:Smith, G.H.; Dagonn, J.C.; Ashley, P.L.; Cummings, S.W.; Macdonald, R.J.
Proc. Natl. Acad. Sci. U.S.A. 79, 7263-7267, 1982
A:Title: Rat pancreatic kallikrein mRNA: nucleotide sequence and amino acid sequence of
A:Reference number: A00944; MUID:83117659; PMID:6961406
A:Accession: A00944
A:Molecule type: mRNA
A:Residues: 1-265 <SMI>
A:Experimental source: pancreatic
R:Kato, H.; Nakanishi, E.; Enjoji, K.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.
J. Biochem. 102, 1389-1404, 1987
A:Title: Characterization of serine proteinases isolated from rat submaxillary gland: w
A:Reference number: A41429; MUID:88198057; PMID:3482210
A:Accession: A41429
A:Status: preliminary
A:Molecule type: protein
A:Residues: 29-53, 'X', 55-87 <KAT>
R:Gerald, W.L.; Chao, J.; Chao, L.
Biochem. Biophys. Acta 866, 1-14, 1986
A:Title: Immunological identification of rat tissue kallikrein cDNA and characterization
A:Reference number: A25137; MUID:86131678; PMID:3004582
A:Accession: A25137
A:Molecule type: mRNA
A:Residues: 115-265 <GER>
R:Pinou, H.; Fukui, K.; Miyake, Y.
J. Biochem. 105, 834-840, 1989
A:Title: Identification and structure of the rat true tissue kallikrein gene expressed i
A:Reference number: JX0073; MUID:89927211; PMID:2753879
A:Accession: JX0073
A:Molecule type: DNA
A:Residues: 1-265 <IND>
A:Cross-references: GB:D00448; NID:9220792; PIDN:BAA00346.1; PID:9220794
A:Experimental source: kidney
R:Ashley, P.L.; Macdonald, R.J.
Biochemistry 24, 4512-4520, 1985
A:Title: Kallikrein-related mRNAs of the rat submaxillary gland: nucleotide sequences of
A:Reference number: A23863; MUID:86051477; PMID:2998455
A:Accession: A23863
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-265 <ASB>
A:Cross-references: GB:M1563; NID:9205029; PIDN:AAA41464.1; PID:9205030
A:Experimental source: submaxillary gland
R:Wiles, D.R.; Brady, J.M.; Pritchett, D.B.; Roberts, J.L.; Macdonald, R.J.
J. Biol. Chem. 264, 7653-7662, 1989
A:Title: Organization and expression of the rat kallikrein gene family.
A:Reference number: A33359; MUID:89214217; PMID:2708383
A:Accession: A33359
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 5-265 <MIN>
A:Cross-references: GB:M23874; GB:J04701; GB:M23875; GB:M23876; NID:9205007; PIDN:AAA414
C:Comment: The kallikreins liberate lysyl-bradykinin, a vasoactive decapeptide, from kin
C:Comment: The protein presumably assumes the two-chain form by cleavage between residu
C:Comment: Tissue kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release 1
C:Genetics:
A:introns: 20/1; 73/2; 169/1; 214/3
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; pancreas; serine proteinase; zymogen

F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-28/Domain: activation peptide #status predicted <AP>
F:29-265/Product: tissue kallikrein, pancreatic #status predicted <MP>
F:29-257/Domain: trypsin homology <TRY>
F:35-177, 54-70, 156-223, 188-202, 213-238/Disulfide bonds: #status predicted
F:69,124,217/Active site: His, Asp, Ser #status predicted

Alignment Scores:

	Pred. No.:	2,53e-33	Length:	265
Score:	617.50	Matches:	112	
Percent Similarity:	62.508	Conservative:	48	
Best Local Similarity:	43.758	Mismatches:	85	
Query Match:	26.058	Indels:	11	
DB:	1	Gaps:	2	

US-09-856-320A-1 (1-1301) x KORTP (1-265)

QY 224 TTAATCTCTCTGCTGCGAACAGGGCTGTGAGGGGA-----GAGACGAG 271
DB 9 ILeuPheLeuAlaLeuSertPrpLysValArgAsnAspAlaAlaProProValGlnSertArg 28
QY 272 ATCATCAAGGGGTGAGTGCAGAGCTCACTCCAGCCCTGGAGGAGCAGCCCTGTCGAG 331
DB 29 ValValGlyGlyTyrAsnGlyMetAsnSerGlnProTPrpValAlaValTyrTyr 48
QY 332 AAGACGGGCTACTCTGTGGGGGAGCTCATCGCCCGGAGATGGCTCTGCAGACGAGC 391
DB 49 PheGlyGlyTyrLeuGlyGlyValLeuIleAspProSertPrpAlaIleThrAlaIle 68
QY 392 CACTGCTCAAGCCCGGCTACATATGTCACCTGGGGGACACACACCTCCAGAGAGAG 451
DB 69 HisCysAlaThrAspAsnTyrGlnValTPrpLeuGlyArgAsnAsnLeuTyrGluAsn 88
QY 452 GGCTGTGACAGACCCGAGACGAGCAGCTGATGATGCTCCCGCCAGCCGGCTCAACAGAC 511
DB 89 ProPheAlaGlnHisArgLeuValSerGlnSerPheProHisProIlePheAsnGlnAsp 108
QY 512 CTC-----CCCAACAAAGACACCGGCAATGACATGATGCTGTG 550
DB 109 LeuIleTPrpAsnHisThrArgGlnProGlyAspAspTyrSerAsnAspLeuLeu 128
QY 551 AAGATGGCATCGCCGATCTCCATCACCTGGCTGTGGACCCCTACCTCTCTCAGCG 610
DB 129 HisLeuSerGlnProAlaAspIleThrAspGlyValIleValIleAspLeuProIleGln 148
QY 611 TGTGTCACTGTGGACGACGAGCTTCATTCGCTGGGGGAGACGACGACGACCCGAG 670
DB 149 GluProLysValGlySertPrpCysLeuAlaSerGlyTPrpGlySertPrpProAspGly 168
QY 671 TTACGCTGCTCTCACACCTTGGATGCGCCACATCACCATCATGATGAGCAGAGAGTGT 730
DB 169 LeuGluLeuSerAspAspLeuGlnCysValAsnIleAspLeuLeuSerAsnGlyCys 188
QY 731 GAGAACGCTACCCGCGGCAACATCACAGACACCATGCTGTGGCCAGCGTGCAGAGAG 790
DB 189 ValGluAlaHisLysGluGluValThrAspLeuMetLeuCysAlaGlyLysMetAspGly 208
QY 791 GGCAAGAGCTCTGCGACGAGGTGACATCCGCGGCGGCTGTGTAACAGATCTGTCA 850
DB 209 GlyLysAspThrCysLysLysAspSerGlyGlyProLeuIleLysAsnLysValLeuGln 228
QY 851 GGCAATATCTCTGGGGCCAGATCCGTGCGATACCCGAAAGCTGTCTACAG 910
DB 229 GYIIIEthSertPrpLysSerValProCysAlaLysThAsnMetProAlaIleYrThr 248
QY 911 AAGTCTGCAATATGCTGATCGATCGAGAGACATGACATGACAAAT 958
DB 249 LysLeuIleLysPheThrProTPrpIleLysGluValMetLysGluAsn 264

RESULT 4
S55066
trypsin (EC 3.4.21.4) II precursor, pancreatic (clone 2-P29) - chicken
N:Alternate names: trypsinogen II


```

Db      121 LeuLeuHisLeuSerGluProAlaAspIleThrAspGlyValIlyValIleAspLeuPro 140
QY      605 TCACGCTGTGTCAGCTGCTGCACACAGCTCCATTCCTCGGCTGGGGCAGCACGTCACAC 664
      ::::: ||||| ||||| ||||| ||||| |||||
Db      141 ThrGluGluProLysValIleGlySerThrCysLeuAlaSerGlyTyrPheSerThrAspPro 160
QY      665 CCCAGTTACGGCTGGCTGCACACCTTGCGATCGCCCAACATCACTCATTTGAGCCAG 724
      ::::: ||| ||||| ||||| ||||| |||||
Db      161 LeuGluTyrGluPheProAspAspLeuGlnCysValAsnIleAsnIleLeuSerAsnGln 180
QY      725 AAGTGTGAGAACGCTTACCCCGGCAACATCACAGACACACCTGGTGTGCTCCAGCTGCAG 784
      ||||| ||||| ||||| ||||| ||||| |||||
Db      181 LysCysIleLeuAlaHisThrGlnMetValIleThrAspValMetLeuCysAlaGlyIleLeu 200
QY      785 GAAGGGGCGACAGACTCTGTCACAGGTCAGTCCGGGGCCCTGCTGTGTATGACCACTGT 844
      ||||| ||||| ||||| ||||| ||||| |||||
Db      201 GluGlyGlyLysAspThrCysAsnGlyAspSerGlyGlyProLeuLeuCysAspGlyVal 220
QY      845 CTTCAAGGATATATCTCCCTGGGGCCAGATCCGTGTGCATCACCCGAAAGCTGGTGTTC 904
      ||||| ||||| ||||| ||||| ||||| |||||
Db      221 LeuGlnGlyIleThrSerThrPheSerValProCysGlyGluThrAsnArpProAlaIle 240
QY      905 TACAGCAAGCTGTGCAATATATGTGACATGATCAGAGACAGACATGAAGAACAAT 958
      ||||| ||||| ||||| ||||| ||||| |||||
Db      241 TyrThrLysLeuIleLysPheThrSerTrpIleLysGluValMetLysGluAsn 258

```

RESULT 6

```

NGMSG
7S nerve growth factor gamma chain (BC 3.4.21.-) precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Dec-1981 #sequence revision 17-May-1985 #text change 18-Jun-1999
C:Accession: A91005; A90949; A93510; A92341; A00942; A21093; A22705
R:Evans, B.A.; Richards, R.I.
EMBO J. 4, 133-138, 1985
A:Title: Genes for the alpha and gamma subunits of mouse nerve growth factor are contiguous
A:Reference number: A91005; MUID:85257431; PMID:3848399
A:Accession: A91005
A:Molecule type: DNA
A:Residues: 1-261 <EVA>
R:Ullrich, A.; Gray, A.; Wood, W.I.; Hayflick, J.; Seeburg, P.H.
DNA 3, 387-392, 1984
A:Title: Isolation of a cDNA clone coding for the gamma-subunit of mouse nerve growth fa
A:Reference number: A90949; MUID:85076169; PMID:6548955
A:Accession: A90949
A:Molecule type: mRNA
A:Residues: 1-261 <UL>
A:Cross-references: GB:X01389; NID:953373; PIDN:CAA25645.1; PID:953374
R:Howles, P.N.; Dickinson, D.P.; DiCaprio, L.L.; Woodworth-Gutai, M.; Gross, K.W.
Nucleic Acids Res. 12, 2791-2805, 1984
A:Title: Use of a cDNA recombinant for the gamma-subunit of mouse nerve growth factor to
A:Reference number: A93510; MUID:84169573; PMID:620835
A:Accession: A93510
A:Molecule type: mRNA
A:Residues: 127-202, 'E', 204-261 <HON>
A:Cross-references: GB:X00472; NID:954260; PIDN:CAA25154.1; PID:954261
A:Experimental source: Inbred strain DBA/2J
R:Thomas, K.A.; Baglan, N.C.; Bradshaw, R.A.
J. Biol. Chem. 256, 9156-9166, 1981
A:Title: The amino acid sequence of the gamma-subunit of mouse submaxillary gland 7 S ne
A:Reference number: A92341; MUID:81264363; PMID:7263706
A:Accession: A92341
A:Molecule type: protein
A:Residues: 25-107, 112-261 <THO>
A:Experimental source: outbred strain Swiss Webster
C:Comment: 7S nerve growth factor is composed of two alpha chains, a beta dimer composed
C:Comment: The active form of the gamma chain occurs naturally as combinations of either
C:Genetic:
A:Map position: 7
A:Introns: 16/1; 69/2; 165/1; 210/3
A:Superfamily: trypsin, trypsin homology
C:Keywords: glycoprotein; growth factor; hydrolase; serine proteinase; submandibular gla
F:1-18/Domain: signal sequence #status predicted <SIS>
F:25-253/Domain: trypsin homology <TRY>

```

```

F:25-107/Domain: segment B1 <GB1>
F:25-107,112-261/Product: nerve growth factor gamma chain (active form) #status exper
F:112-261/Domain: segment A <GAA>
F:112-164/Domain: segment C <GCC>
F:165-261/Domain: segment B2 <GB2>
F:31-173,50-66,152-219,184-198,209-234/Disulfide bonds: #status predicted
F:55,120,213/Active site: His, Asp, Ser #status predicted
F:102/Binding site: carbohydrate (Asn) (covalent) #status experimental

```

Alignment Scores:

	Pred. No.:	Length:	Matches:
Score:	6,31e-33	261	611/50
Percent Similarity:	63.288		Conservative: 52
Best Local Similarity:	42.978		Mismatches: 83
Query Match:	25.808		Indels: 11
DB:	1	Gaps:	2

US-09-856-320A-1 (1-1301) x NGMSG (1-261)

```

QY      224 TTAATCTGCTGTGCTGTGCGAACAGGGCTGTAGGGGA-----GAGACAGG 271
      ::::: ||||| ||||| ||||| ||||| |||||
Db      5 IleuPheLeuAlaLeuSerLeuGlyIleAspAlaIleProProValGlnSerArg 24
QY      272 ATCATCAAGGGGTGAGTGCAGAGCTCACTCCAGCCCTGGCAGGACGCTGTTCAG 331
      ||||| ||||| ||||| ||||| ||||| |||||
Db      25 IleValGlyLysPheLysCysGlyLysAsnSerGlnProTrpHisValAlaValTyrArg 44
QY      332 AAGAGCGGCTACTGCTGTGGGGGAGAGCGCTACATCCGCCAGATGGCTGCTGCAGACGC 391
      ||||| ||||| ||||| ||||| ||||| |||||
Db      45 TyrThrGlnTyrLeuLysGlyValIleLeuAspProAsnTrpValLeuTrpAlaIle 64
QY      392 CACTGCTCAAGGCCCGCTACATATGTCACCTGGGCGACACAACTCCAGAGAGAG 451
      ||||| ||||| ||||| ||||| ||||| |||||
Db      65 HisCysTyrAspAspAsnTyrLysValTyrLeuGlyLysAsnLeuPheLysAspGlu 84
QY      452 GCGTGTGACAGACCGCGGACAGGACTGAGTCTTCCGCCACCCCGGCTTCAACAACG 511
      ||||| ||||| ||||| ||||| ||||| |||||
Db      85 ProSerAlaGlnHisArgPheValSerLysAlaIleProHisProLysPheAsnMetSer 104
QY      512 CTCGCCAACAAA-----GACCACCGCAATGACATGATGCTGTCG 550
      ||||| ||||| ||||| ||||| ||||| |||||
Db      105 LeuMetArgLysHisIleArgPheLeuGluTyrAspTyrSerAsnAspLeuMetLeuLeu 124
QY      551 AAGATGCGATCGCCACTGTCATCACCCTGGCTGGAGACCCCTCCTCCTCAGCG 610
      ::::: ||||| ||||| ||||| ||||| |||||
Db      125 ArgLeuSerLysProAlaAspIleThrAspThrValLysProIleThrProThrGlu 144
QY      611 TGTGTACATGCTGGGACAGCTGCTCATTTCCGCTGGGGGACAGCACGTCAGCCCGCAG 670
      ||||| ||||| ||||| ||||| ||||| |||||
Db      145 GluProLysLeuGlySerThrCysLeuAlaSerGlyTyrGlySerIleThrProThrLys 164
QY      671 TTACGCTGCTGCACACCTTGCATCGGCGACACATCACATGATGAGCAGAGTGT 730
      ::::: ||||| ||||| ||||| ||||| |||||
Db      165 PheGlnPheThrAspAspLeuTyrCysValAsnLeuLysLeuLeuProAsnGlnLysCys 184
QY      731 GAGAACGCTTACCCCGGCAACATCACAGACACCATGCTGTGTCAGCGAGAGGG 790
      ||||| ||||| ||||| ||||| ||||| |||||
Db      185 AlaLysAlaHisIleGluLysValIleThrAspAlaMetLeuCysAlaGlyIleMetAspGly 204
QY      791 GGCAGGATCTCTGCGAGGCTGACTCCGGGGGCCCTCTGCTGTATACCACTGTCTTCA 850
      ||||| ||||| ||||| ||||| ||||| |||||
Db      205 GlyLysAspThrCysLysGlyAspSerGlyGlyProLeuIleCysAspGlyValLeuGln 224
QY      851 GGCATATCTGCTGGGGGAGGATCGCTGTCGATCACCCGAAAGCTGTGTCACAG 910
      ||||| ||||| ||||| ||||| ||||| |||||
Db      225 GlyIleThrSerTrpLysIleThrProCysGlyGluProAspMetProLysValTyrThr 244
QY      911 AAGTCTGCAATATGTGAGTGCATGATCAGAGACATGAAGAACAAT 958
      ||||| ||||| ||||| ||||| ||||| |||||
Db      245 LysLeuAsnLysPheThrSerTrpIleLysAspThrMetAlaLysAsn 260

```

RESULT 7
S1586

Db 99 PheAspArgLysThrLeuAsn-----AsnAspIleMetLeuIleLysLeuSer 114
 QY 560 TCGCCAGTCTCCATCATCCTGGCGCTGCGACCCCTCACCTCTCTCCACGCTGTGCTCACT 619
 Db 115 SerProValLysLeuAsnAlaArgValAlaThrValAlaLeuProSerSerCysAlaPro 134
 QY 620 GCTGGCACCAGCTGCTCATTTCCGGCTGGGACAGACCTCCAGCCCCAGTTACGGCTG 679
 Db 135 AlaGlyThrGlnCysLeuIleSerGlyAsnThrLeuSerSerGlyAlaAsnGln 154
 QY 680 CCTCACACCTGCGATGGCGCCCAACATCACCATTCATGACACAGAGAGTGAAGAAGCC 739
 Db 155 ProAspLeuLeuGlnCysLeuAsnAlaProLeuLeuProGlnAlaAspCysGlnAlaSer 174
 QY 740 TACCCCGGCACATCATCAGACACACATGCTGTGCTGCAGCGTGCAGAAAGGGGCAAGAC 799
 Db 175 TyrProGlyLysIleThrAspAsnMetValCysValGlyPheLeuGlnGlyLysAsp 194
 QY 800 TCCTGCGCAGGCTGACTCCGGGGGCCCTCTGGTCTGTACCACTCTCTTCAAGCATATTC 859
 Db 195 SerCysGlnGlyAspSerGlyGlyProValValCysAsnGlyLeuLeuGlnGlyLeuVal 214
 QY 860 TCCTGGGGCCAGAGTCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 919
 Db 215 SerTyrGlyTyrGly----CysAlaLeuProAspAsnProGlyValTyrThrLysValCys 233
 QY 920 AATATGTGACTGATCCAGACGAGACGATGAAGAACAAT 958
 Db 234 AsnTyrValAspTyrPrlIleGlnAspThrIleAlaIleAsn 246

RESULT 9
 A:34079
 tissue kallikrein (EC 3.4.21.35) P1 precursor - rat
 A:Alternate names: kallikrein-related proteinase k8
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 22-Jun-1999
 C:Accession: A34079; S10700
 R:Brady, J.M.; Wines, D.R.; Macdonald, R.J.
 Biochemistry 28, 5203-5210, 1989
 A:Title: Expression of two kallikrein gene family members in the rat prostate.
 A:Reference number: A34079; MUID:89352606; PMID:2765531
 A:Accession: A34079
 A:Status: preliminary
 A:Molecule type: DNA; mRNA
 A:Molecule type: protein
 A:Residues: 1-261 <BNA>
 A:Cross-references: GB:M27215; GB:M27216; GB:M27217; NID:g206638; PIDN:AAA42036.1; PID:g
 A:Experimental source: prostate
 R:Elmoujeh, A.; Gutman, N.; Brillard, M.; Gauthier, F.
 FEBS Lett. 265, 137-140, 1990
 A:Title: Substrate specificity of two kallikrein family gene products isolated from the
 A:Reference number: S10698; MUID:90306305; PMID:2194829
 A:Accession: S10700
 A:Molecule type: protein
 A:Residues: 25-43;112-138 <ELM>
 A:Experimental source: submaxillary gland
 A>Note: 125-Lys was also found
 C:Superfamily: trypsin; trypsin homology
 C:Keywords: hydrolase; serine proteinase
 F:25-111/Domain: trypsin homology <TRY>
 F:25-111/Product: tissue kallikrein P1 light chain #status experimental <MAT1>
 F:112-261/Product: tissue kallikrein P1 heavy chain #status experimental <MAT2>
 F:65;120;213/Active site: His, Asp, Ser #status predicted

Alignment Scores:

Pred. No.: 2,89e-32 Length: 261
 Score: 601.50 Matches: 111
 Percent Similarity: 60.85% Conservative: 46
 Best Local Similarity: 43.02% Mismatches: 90
 Query Match: 25.38% Gaps: 11
 DB: 2 Gaps: 2

US-09-856-320A-1 (1-1301) x A34079 (1-261)

QY 218 CTGCAATTAACTCTGCTGCTGCGACAGGG-----CTTGTAAGGGAGAG 265
 Db 3 LeuLeuIleLeuPheLeuIleLeuSerLeuGlyTyrPasnAspAlaAlaProProGlnGln 22
 QY 266 ACCAGGATCATCAAGGGCTTCAGATGCAAGCCTCACTCCAGCCCTGGGAGGACCCCTG 325
 Db 23 SerArgIleIleGlyLysPheAsnGlyLysAsnSerGlnProTyrPrlValAlaVal 42
 QY 326 TTGGAAGAAGACCGGCTACTCTGTGGGGGAGCGAGCTATGCGCCCGAGATGGGCTCCGAGA 385
 Db 43 TyrHisPheAsnGlnProGlnCysGlyValLeuIleHisProSerTyrPrlIleHis 62
 QY 386 GCAGGCGACCTGCTCAAGCCCGCTACATAGTTCATCTGGGCGAGACACCACTCCAGAG 445
 Db 63 AlaAlaHisCysTyrSerValAsnTyrGlnValTyrPrlGlyArgAsnAsnLeuGln 82
 QY 446 GAGAGAGGCTGTGACAGACACCGGACAGGACGACGATGATCTTCCCGACCCCGGCTTCAAC 505
 Db 83 AspGlyProPheAlaGlnHisArgLeuValSerGlnSerPheProHisProGlyPheAsn 102
 QY 506 AACACGCTC-----CCCAACAAAGACACCGCAATGACATCATG 544
 Db 103 LeuAspIleIleLysAsnHisThrArgLysProGlyAsnAspTyrSerAsnAspLeuMet 122
 QY 545 CTGTGAAGATGACATCGGCACTCTCATACCTGGGCTGCGAACCCCTCACTCTCC 604
 Db 123 LeuLeuHisLeuLysThrProAlaAspIleThrAspGlyValLysValIleAspLeuPro 142
 QY 605 TCACGCTGTGTCATGCTGGACACACGACGCTCTCATTTCCGGCTGGGCGACAGCTCCAGC 664
 Db 143 ThrGlnGluProLysValGlySerThrCysLeuThrSerGlyTyrPrlSerIleThrPro 162
 QY 665 CCCGAGTTACGCGCTGCTGCACACCTTGCGATCGGCAACATCAACATCATGATGACGAC 724
 Db 163 LeuLysTyrPrlGluPheProAspAspLeuGlnCysValAsnHisLeuLeuSerAsnGln 182
 QY 725 AAGTGTGACAGCGCTTACCCCGGCAACATCACAGACACCATGCTGTGTCAGCGTGCAG 784
 Db 183 LysCysIleLysAlaTyrAsnAspGluValThrAspValMetLeuCysAlaGlyLysMet 202
 QY 785 GAAGGGCGCAAGACTCTCGCAGAGGTATCCGGGGGCCCTCTGTGCTGTACCACTGT 844
 Db 203 AspGlyGlyLysAspIleCysLysGlyAspSerGlyGlyProLeuIleLysAspGlyVal 222
 QY 845 CTTCAGGCAATATCTCCCTGGGCGCAGATCCGTCGTCGATCAACCGAAGACCTGGTGC 904
 Db 223 LeuGlnGlyIleThrSerTyrPrlSerMetProCysGlyLysProAsnLysProSerVal 242
 QY 905 TACACGAAGAATGTGCAATATGTGACTGATCCAGAGACGATGAAGAACAAT 958
 Db 243 TyrThrLysLeuIleLysPheThrSerTyrPrlMetLysValMetLysGlnAsn 260

RESULT 10

TRRT1
 trypsin (EC 3.4.21.4) I precursor - rat
 N:Alternate names: trypsinogen I
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 24-Sep-1999
 C:Accession: B22657; A00948
 R:Crataik, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; Macdonald, R.J.; Rutter, W.J.
 J. Biol. Chem. 259, 14255-14264, 1984
 A:Title: Structure of two related rat pancreatic trypsin genes.
 A:Reference number: A22657; MUID:85054880; PMID:6094547
 A:Accession: B22657
 A:Molecule type: DNA

A:Residues: 1-246 <CRA>
 A:Cross-references: GB:J00779; NID:g206507; PIDN:AAA98518.1; PID:g206508
 A>Note: the authors translated the codon ATC for residue 6 as Leu and GAC for residue
 R:Macdonald, R.J.; Stary, S.J.; Stary, G.H.
 J. Biol. Chem. 257, 9724-9732, 1982
 A:Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences
 A:Reference number: A00948; MUID:82265624; PMID:6896710
 A:Accession: A00948

A:Molecule type: mRNA
 A:Residues: 1-246 <MAC>
 A:Cross-references: GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508
 C:Genetics:
 A:introns: 14/1; 67/2; 152/1; 197/3
 C:Superfamily: trypsin; trypsin homology
 C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:16-23/Domain: activation peptide #status predicted <APT>
 F:24-246/Product: trypsin I #status predicted <ENZY>
 F:24-239/Domain: trypsin homology <TRY>
 F:30-160,48-64,133-233,139-206,171-185/Disulfide bonds: #status predicted
 F:63,107,200/Active site: His, Asp, Ser #status predicted
 F:75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Alignment Scores:
 Pred. NO.: 3.38e-32 Length: 246
 Score: 600.50 Matches: 118
 Percent Similarity: 62.45% Conservative: 40
 Best Local Similarity: 46.64% Mismatches: 88
 Query Match: 25.34% Indels: 7
 Gaps: 4

US-09-856-320a-1 (1-1301) x TRRN1 (1-246)

OY 200 CTCACGCGCATGAGATTCTGACATTATCTGCTGCTGCGCAACAGGCGTTGTAGCG 259
 Db 1 MetSerAlaLeuLeuIleLeuAlaLeuValGlyAlaAlaValAlaPheProLeu---Glu 19

OY 260 GGAGAGACAGCATCAACAGGGGTTCAGTGCAGAACGCTCCAGCCCTGGCAGCA 319
 Db 20 AspaSapbpySlIeValGlyGlyTyrThrcysProGlnHisSerValProTyrGlnVal 39

OY 320 GCCCTGTTTCGAGAAGCGGCTACTCTGTGGGGCGAACCTATGCCGCCAGATGGCTC 379
 Db 40 SerLeu---AsnSerGlyTyrHisPheCysGlyGlySerLeuIleAsnAspGlnTyrVal 58

OY 380 CTGACGACAGCCCTGCTCTCAACGCCCTACATAGTTCACCTGGGGCAGCAACCTC 439
 Db 59 ValSerAlaAlaHisCysTyrTyrLeuSerArgTleGlnValAlaGlyLeuGlnHisAsnIle 78

OY 440 CAGAGAAGAGGGCTGTGACGACAGCCGCGACGCCACTGCTCCGCCCGCCCGGC 499
 Db 79 AsnValIleuGlnGlyAspGlnPheIleAsnAlaAlaGlyIleIleLysHisProAsn 98

OY 500 TTCAACAACAAGCCTCCCAACAAGAACCCGCAATGATCATGTGTGAAGATGCA 559
 Db 99 TyrSerSerTyrPheLeuAsn-----AsnAspIleMetLeuIleLysLeuSer 114

OY 560 TCGCAGTCTGCATCACCCTGGGCTGTGGACCCCTCAACCTCTCTCCAGCTGTGACT 619
 Db 115 SerProValIlyLeuAsnAlaArgValAlaProValAlaLeuProSerAlaCysAlaPro 134

OY 620 GCTGGACACAGCTCTCATTTTCGGCTGGGGGAGCAGCTCCAGCCCGCATGTGCGCTG 679
 Db 135 AlagIlythrGlnCysLeuIleSerGlyTyrPglYAsnThrLeuSerAanGlyValAsnAsn 154

OY 680 CCTCAACACTTGGCATGCGCCCAACATCATCATCTTGAAGCAACGAAAGTGTGAACGCC 739
 Db 155 ProAspLeuLeuGlnCysValAspAlaProValIleuSerGlnAlaAspCysGlnAlaAla 174

OY 740 TACCCGCGCAACATCAACAGACACATGATGTGTGCCAGCTGCAGGAAGGGGGCAAGAC 799
 Db 175 TyrProGlyGlnIleThrSerSerMetIleCysValGlyPheLeuGlnGlyGlyLysAsp 194

OY 800 TCGTCCAGAGGTGACTCCGGGGGCGCTGTGTTGTAAACAGTCTTCAAGGATATC 859
 Db 195 SerCysGlnIlyAspSerGlyGlyProValCysAsnGlyGlnLeuGlnGlyIleVal 214

OY 860 TCGTGGGCGAGATCCGTGTGCATCACCCGAAAGCGTGTGTCTACAGAAAGTGTGC 919
 Db 215 SerTyrPglYtyrGly---CysAlaLeuProAspAsnProGlyValTyrThrLysValCys 233

OY 920 AATATGTGACGTGCATCCAGACAGCATGAAACAAT 958
 Db 234 AsnDheValGlyTyrPleGlnAspThrIleAlaAlaAsn 246

RESULT 11
 A29586
 Locus kallikrein (EC 3.4.21.35) hK-1 precursor - human
 N:Alternate names: glandular kallikrein
 C:Species: Homo sapiens (man)
 C:Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 22-Jun-1999
 R:Schmedlich, L.J.; Bennetts, B.H.; Morris, B.J.
 DNA 6, 429-437, 1987
 A:Title: Primary structure of a human glandular kallikrein gene.
 A:Reference number: A29586; MUID:88054467; PMID:2824146
 A:Accession: A29586
 A:Molecule type: DNA
 A:Residues: 1-261 <SCCH>
 A:Cross-references: GB:M18157; NID:g186640; PIDN:AAA74454.1; PID:g386842
 A:Note: the authors translated the codon TAC for residue 43 as Trp
 C:Genetics:
 A:introns: 16/1; 69/2; 165/1; 210/3
 C:Superfamily: hydrolase; trypsin homology
 C:Keywords: hydrolase; serine proteinase
 F:25-253/Domain: trypsin homology <TRI>
 F:65,120,213/Active site: His, Asp, Ser #status predicted

Alignment Scores:
 Pred. NO.: 6.2e-32 Length: 261
 Score: 596.50 Matches: 111
 Percent Similarity: 62.11% Conservative: 48
 Best Local Similarity: 43.36% Mismatches: 86
 Query Match: 25.17% Indels: 11
 Gaps: 2

US-09-856-320a-1 (1-1301) x A29586 (1-261)

OY 224 TTAATCCTGCTGTGCTGCGCAACAGGCGTTGTAGGGGA-----GAGACCGAG 271
 Db 5 ValIleuSerIleAlaLeuSerValGlyCysThrGlyAlaValProLeuIleGlnSerArg 24

OY 272 ATATCAAGGGGTTGCGTGCAGAACCCCTACCTCCAGCCCTGGCAGCAGCAGCCCTTCGAG 331
 Db 25 IleValIleGlyTyrPglCysGlyGlyHisSerGlnProTyrPglValAlaValTyrSer 44

OY 332 AAGACGGGCTACTCTGTGGGGGAGCGCTGATGCCGCCAGATGGCTCTGACAGAGCC 391
 Db 45 HisGlyTyrPheAlaHisCysGlyGlyValIleValHisProGlnTyrPheValIleThrAlaAla 64

OY 392 CACTGGCTCAAGCCCGCTCATAGTTTACCTGGGGCAGCAACCTCCAGAAAGAGAG 451
 Db 65 HisCysLeuLysLysAsnSerGlnValTyrPleGlnGlyArgHisAsnLeuPheGlnProGln 84

OY 452 GCGTGTAGAGAACCCGCGACAGCAGTACTCTCCGCCCGCCGCTTCACAAACAGC 511
 Db 85 AspThrGlyGlnIlyValProValSerHisSerPheThrIleProLeuTyrAsnMetSer 104

OY 512 CTC-----CCCAACAAGACCCGCGCATGATCATCATCTTCCTCAGC 550
 Db 105 LeuLeuLysHisGlnSerLeuArgProAspGlnAspSerSerHisAspLeuMetLeu 124

OY 551 AAGATGGCATGCCAGTCTCATACCTGGGCTGTGGACCCCTCAACCTCTCTCAGC 610
 Db 125 ArgLeuSerGlnProAlaLysIleThrAspValIlyValIleuGlyLeuProThrGln 144

OY 611 TGTGTACTCTGTGCGACACACTGCTCATATTCGGGCTGGGGCAGCAGTCCAGCCAG 670
 Db 145 GluProAlaLeuIlyThrThrCysTyrAlaSerGlyTyrPglSerIleGlnProGlnGln 164

OY 671 TTACGCGCTGCTCAACCTTGATGGCGCAACATGATCATCTTGAAGCAACGAGTGT 730
 Db 165 PheLeuArgProArgSerLeuGlnCysValSerLeuHisLeuLeuSerAsnAspMetCys 184

QY 731 GAGAACGCTACCCGGGACATCAACACACACATGCTGTCCAGCGTCAAGAGG 790
 Db 185 AATAGTATATySerGluValThrGluPheMetLeuCysAlaGlyLeuThrPrtyrGly 204
 QY 791 GGCAGAGACTCTCCAGGAGTACTCCGGGGCCCTGCTGTGTATACAGTCTGTCA 850
 Db 205 GtlyAspPrthCysGlyGlyAspSerGlyGlyProLeuValCysAsnGlyValLeuGln 224
 QY 851 GGCATTATCTCTGGGGCCAGATCCGTGTGCGATCACCCGAAGCCTGTGTACAG 910
 Db 225 GlyIleThrSerTrpGlyProGluProCysAlaLeuProGluLysProAlaValThr 244
 QY 911 AAGCTGCAATATGTGACCTGATCCAGAGAGAGAGAGAGAGAGAT 958
 Db 245 LysValValHisTyArgLysTrpIleLysAspPrthIleAlaAlaAsn 260
 RESULT 12
 KORTN
 tonin (EC 3.4.21.-) precursor - rat
 N:Alternate names: esterase 1
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 25-Feb-1985 #sequence revision 02-Dec-1994 #text change 18-Jun-1999
 C:Accession: B33359; A32340; C23863; A93323; A94635; A34050; A30971; A00945
 R:Wines, D.R.; Brady, J.M.; Pritchett, D.B.; Roberts, J.L.; MacDonald, R.J.
 J. Biol. Chem. 264, 7653-7662, 1989
 A:Title: Organization and expression of the rat kallikrein gene family.
 A:Reference number: A33359; MUID:89214217; PMID:2708383
 A:Accession: B33359
 A:Molecule type: DNA
 A:Residues: 1-259 <MIN>
 A:Cross-references: GB:M2877; GB:J04702; GB:M2878; NID:9207411; PIDN:AAA42259.1; PID:9
 R:Shal, S.Y.; Woodley-Miller, C.; Chao, J.; Chao, L.
 Biochemistry 28, 5334-5343, 1989
 A:Title: Characterization of genes encoding rat tonin and a kallikrein-like serine prote
 A:Reference number: A32340; MUID:89375248; PMID:5550051
 A:Accession: A32340
 A:Molecule type: DNA
 A:Residues: 1-259 <SHA>
 A:Cross-references: GB:M26533; NID:9206775; PIDN:AAA42081.1; PID:9206776; GB:J02860
 R:Ashley, P.L.; Macdonald, R.J.
 Biochemistry 24, 4512-4520, 1985
 A:Title: Kallikrein-related mRNAs of the rat submaxillary gland: nucleotide sequences of
 A:Reference number: A23863; MUID:86051477; PMID:2998455
 A:Accession: C23863
 A:Molecule type: mRNA
 A:Residues: 1-259 <ASH>
 A:Cross-references: GB:M11565; NID:9205033; PIDN:AAA41466.1; PID:9205034
 R:Lazure, C.; Leduc, R.; Seidah, N.G.; Thibault, G.; Genest, J.; Chretien, M.
 Nature 307, 555-558, 1984
 A:Title: Amino acid sequence of rat submaxillary tonin reveals similarities to serine pr
 A:Reference number: A93323; MUID:84117504; PMID:6320014
 A:Accession: A93323
 A:Molecule type: protein
 A:Residues: 25-259 <LAI>
 R:Lazure, C.
 submitted to the Protein Sequence Database, March 1985
 A:Reference number: A94635
 A:Contents: carbohydrate-binding site; revisions
 A:Accession: A94635
 A:Molecule type: protein
 A:Residues: 104-119 <LA2>
 R:Kanada, M.; Furukata, N.; Yamaguchi, T.; Ikeita, M.; Kizuki, K.; Moriya, H.
 Biochem. Biophys. Res. Commun. 166, 231-237, 1990
 A:Title: Observation of tissue prokallikrein activation by some serine proteases, argini
 A:Reference number: A34050; MUID:90147705; PMID:2302205
 A:Accession: A34050
 A:Molecule type: protein
 A:Residues: 25-30,'X',32-34 <KAN>
 R:Lazure, C.; Leduc, R.; Seidah, N.G.; Thibault, G.; Genest, J.; Chretien, M.
 Biochem. Cell Biol. 65, 321-337, 1987
 A:Title: The complete amino acid sequence of rat submaxillary gland tonin does contain t
 A:Reference number: A30971; MUID:87271223; PMID:3038148
 A:Accession: A30971

A:Molecule type: protein
 A:Residues: 25-259 <LA2>
 C:Comment: This protein is found in submaxillary gland. It has both trypsin- and chym
 C:Genetics:
 A:Introns: 16/1; 67/2; 163/1; 208/3
 C:Superfamily: trypsin; trypsin homology
 C:Keywords: glycoprotein; hydrolase; serine proteinase
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:18-24/Domain: propeptide #status predicted <PRO>
 F:25-259/Product: tonin #status experimental <MAT>
 F:31-171,48-64,150-217,182-196,207-232/Dissulfide bonds: #status predicted
 F:63,118,211/Active site: His, Asp, Ser #status predicted
 F:106,189/Binding site: carbohydrate (Asn) (covalent) #status experimental

Alignment Scores:

Pred. No.:	7,22e-32	Length:	259
Score:	595.50	Matches:	109
Percent Similarity:	62.02%	Conservative:	51
Best Local Similarity:	42.25%	Mismatches:	85
Query Match:	25.13%	Indels:	13
DB:	1	Gaps:	3

US-09-856-320A-1 (1-1301) x KORTN (1-259)

QY 218 CTGCAAGTTAACTCTGCTGCTGCTGCAACAGGGCTTGAGG-----GGAGG 265
 Db 3 LeuGlnIleLeuSerLeuValLeuSerValGlyArgIleAspAlaAlaProProGlyGln 22
 QY 266 ACCAGATCATCAGAGGGCTTGAGTGCAGAGCTCATCTCCAGCCTGCGAGGACCCGCT 325
 Db 23 SerArgIleValGlyGlyTyLysCysGlyLysAsnSerGlnProTrpGlnValAlaVal 42
 QY 326 TTGCAAGAGAGCGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 385
 Db 43 IleAsnGlu-----TyrLeuCysGlyGlyValLeuIleAspProSerTrpAlaIleThr 60
 QY 386 GCAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 445
 Db 61 AlaAlaHisCysTyrSerAsnAsnTyrglnValLeuGlyArgAsnAsnLeuPheLys 80
 QY 446 GAGGAGGGCTGAGACACAGCCGAGACAGCTAGTCTTCCACCCCGGCTTC---502
 Db 81 AspGluProPheAlaGlnArgLysValAlaArgLysSerPheArgHisProAspTyrIle 100
 QY 503 -----AACAAAGCCCTCCCAACAAAGCCGCAAGCCGCAAGCAATGATCATG 544
 Db 101 ProLeuIleValThrAsnAspPrthGluGlnProValHisAspHisSerAsnAspLeuMet 120
 QY 545 CTGTTGAAGATGATCGCATCGCATCTGCATCAGCTGGGCTGCGACCCCTCAGCTGCC 604
 Db 121 LeuLeuHisLeuSerGluProAlaAspPrthGlyGlyValIleValIleLeuSerPro 140
 QY 605 TCACCTGTGTATCTGCTGCGACACAGCTGCTCATTTCCGGTGGGAGACAGCTGCAGC 664
 Db 141 ThrLysGluProLysValGlySerThrCysLeuAlaSerGlyTyrGlySerThrAsnPro 160
 QY 665 CCCGAGTTAAGCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 724
 Db 161 SerGluMetValValSerHisAspLeuGlnCysValAsnIleHisLeuLeuSerAsnGlu 180
 QY 725 AAGTTGAGAAAGCCTACCCCGCAACATCAAGACAGACACATGCTGTGCGAGCTGCAG 784
 Db 181 LysCysIleGluThrTyrLysAspAsnValThrAspValMetLeuCysAlaGlyLysIleMet 200
 QY 785 GAAGGGGCAAGAGCTCTGCGAGGATCTCGGGGGCCCTGTGCTGTATACCAAGTCT 844
 Db 201 GluGlyGlyLysAspPrthCysAlaGlyAspSerGlyGlyProLeuIleCysAspGlyVal 220
 QY 845 CTTCAGGAGTATCTCTGCGGAGGAGATCGGTGCGAGACCCGAAAGCCTGTGCTGCTG 904
 Db 221 LeuGlnGlyIleThrSerGlyGlyAlaThrProCysAlaLysProLysThrProAlaIle 240

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 15, 2003, 16:00:49 ; Search time 475.114 Seconds
(without alignments)
7105.351 Million cell updates/sec

Title: US-09-856-320A-1

Perfect score: 1301
Sequence: 1 ctgccttgcctccacacctg.....aaaaaaaaaaaaaaaaaaaa 1301

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1731049 seqs, 1297405648 residues

Total number of hits satisfying chosen parameters: 3462098

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1271.4	97.7	1292	12	US-09-933-767-189 Sequence 189, App
2	1271.4	97.7	1292	14	US-10-023-282-189 Sequence 189, App
3	1198	92.1	1204	11	US-09-946-374-169 Sequence 169, App
4	1198	92.1	1204	12	US-10-015-387A-169 Sequence 169, App
5	1198	92.1	1204	12	US-10-137-870-505 Sequence 505, App
6	1198	92.1	1204	12	US-10-140-018-505 Sequence 505, App
7	1198	92.1	1204	12	US-10-140-021-505 Sequence 505, App
8	1198	92.1	1204	12	US-10-140-274-505 Sequence 505, App
9	1198	92.1	1204	12	US-10-140-471-505 Sequence 505, App
10	1198	92.1	1204	12	US-10-140-807-505 Sequence 505, App
11	1198	92.1	1204	12	US-10-140-922-505 Sequence 505, App
12	1198	92.1	1204	12	US-10-140-924-505 Sequence 505, App
13	1198	92.1	1204	12	US-10-140-926-505 Sequence 505, App
14	1198	92.1	1204	12	US-10-141-698-505 Sequence 505, App
15	1198	92.1	1204	12	US-10-141-702-505 Sequence 505, App
16	1198	92.1	1204	12	US-10-141-704-505 Sequence 505, App

17	1198	92.1	1204	12	US-10-142-421-505 Sequence 505, App
18	1198	92.1	1204	12	US-10-142-432-505 Sequence 505, App
19	1198	92.1	1204	12	US-10-142-767-505 Sequence 505, App
20	1198	92.1	1204	12	US-10-143-033-505 Sequence 505, App
21	1198	92.1	1204	12	US-10-144-994-505 Sequence 505, App
22	1198	92.1	1204	12	US-10-145-628-505 Sequence 505, App
23	1198	92.1	1204	12	US-10-145-631-505 Sequence 505, App
24	1198	92.1	1204	12	US-10-145-633-505 Sequence 505, App
25	1198	92.1	1204	12	US-10-145-746-505 Sequence 505, App
26	1198	92.1	1204	12	US-10-145-748-505 Sequence 505, App
27	1198	92.1	1204	12	US-10-145-823-505 Sequence 505, App
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38	1198	92.1	1204	12	US-10-147-506-505 Sequence 505, App
39	1198	92.1	1204	12	US-10-147-510-505 Sequence 505, App
40	1198	92.1	1204	12	US-10-147-511-505 Sequence 505, App
41	1198	92.1	1204	12	US-10-147-529-505 Sequence 505, App
42	1198	92.1	1204	12	US-10-153-397-505 Sequence 505, App
43	1198	92.1	1204	12	US-10-153-586-505 Sequence 505, App
44	1198	92.1	1204	12	US-10-158-783-505 Sequence 505, App
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ALIGNMENTS

RESULT 1
US-09-933-767-189
Sequence 189, Application US/09933767
Publicatation No. US20030181692A1
GENERAL INFORMATION:
APPLICANT: NI et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P2
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: PCT/US01/05614
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/184,836
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/193,170
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 09/205,258
PRIOR FILING DATE: 1998-12-04
PRIOR APPLICATION NUMBER: PCT/US98/11422
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/048,885
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049,375
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,881
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,880
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,896
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049,020
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,876
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PRIOR APPLICATION NUMBER: 60/048,894

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 ; PRIOR FILING DATE: 1997-12-18
 ; PRIOR APPLICATION NUMBER: 60/073,160
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: 60/073,159
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 ; PRIOR APPLICATION NUMBER: 60/085,925
 ; PRIOR FILING DATE: 1998-05-18
 ; PRIOR APPLICATION NUMBER: 60/085,921
 ; PRIOR FILING DATE: 1998-05-18

; PRIOR APPLICATION NUMBER: 60/085,923
 ; PRIOR FILING DATE: 1998-05-18
 ; PRIOR APPLICATION NUMBER: 60/085,922
 ; PRIOR FILING DATE: 1998-05-18
 ; PRIOR APPLICATION NUMBER: 60/092,921
 ; PRIOR FILING DATE: 1998-07-15
 ; PRIOR APPLICATION NUMBER: 60/094,657
 ; PRIOR FILING DATE: 1998-07-30
 ; NUMBER OF SEQ ID NOS: 1245
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 189
 ; LENGTH: 1292
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-933-767-189

Query Match 97.7%; Score 1271.4; DB 12; Length 1292;
 Best Local Similarity 99.58; Pred. No. 0;
 Matches 1282; Conservative 4; Mismatches 0; Indels 3; Gaps 1;

QY 1 CTGCTTGTCTCCACACCTGTGTCAGGAGAGAGGAGAAAGCCAGGAGGACCTTA 60
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 Db 2 CTGCTTGTCTCCACACCTGTGTCAGGAGAGAGGAGAAAGCCAGGAGGACCTTA 58
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QY 61 ACTGAACAAACAAAGCTGGAGAGAGAGAGATCTGCTCGGCTCCGATGACAG 120
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 Db 59 ACTGAACAAACAAAGCTGGAGAGAGAGAGATCTGCTCGGCTCCGATGACAG 118
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QY 121 GTTGAAGTGGCTGGGAGCTGGAATCATGCGGAGAGGCTCTACACGACCAAGAAC 180
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 Db 119 GTTGAAGTGGCTGGGAGCTGGAATCATGCGGAGAGGCTCTACACGACCAAGAAC 178
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QY 181 TGGGGCCGCTCTCTCCCTCCAGGCCATGAGATTCGACATTAATCTGCTCT 240
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 Db 179 TGGGGCCGCTCTCTCCCTCCAGGCCATGAGATTCGACATTAATCTGCTCT 238
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QY 241 GGCACAGGCTTGTAGGGGAGAGACAGATCATTAAGGGTTCAGATGCAAGCTCA 300
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 Db 239 GGCACAGGCTTGTAGGGGAGAGACAGATCATTAAGGGTTCAGATGCAAGCTCA 298
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QY 301 CTCCACGCTTGGAGAGACCCCTGTCGAAAGACGCGCTACTGTGGGGGACGCT 360
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 Db 299 CTCCACGCTTGGAGAGACCCCTGTCGAAAGACGCGCTACTGTGGGGGACGCT 358
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QY 361 CATCGCCCCAGATGCTCTGACAGAGCCCACTGCTCAAGCCCGCTACATAGTTCA 420
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 Db 359 CATCGCCCCAGATGCTCTGACAGAGCCCACTGCTCAAGCCCGCTACATAGTTCA 418
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QY 421 CTTGGGGGACACAACTCCAGAAAGAGAGGCTGTGACAGACACCCGACACCTGA 480
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 Db 419 CTTGGGGGACACAACTCCAGAAAGAGAGGCTGTGACAGACACCCGACACCTGA 478
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QY 481 GTCCCTTCCCCACCCCGCTTAAACAACACCTTCCCAAAAGACCAAGCAATGACAT 540
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 Db 479 GTCCCTTCCCCACCCCGCTTAAACAACACCTTCCCAAAAGACCAAGCAATGACAT 538
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QY 541 CATCTGTGTGAAGATGCGATGCCAGTCTCATACCTGGGCTGTGGACCCCTACACCT 600
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 Db 539 CATCTGTGTGAAGATGCGATGCCAGTCTCATACCTGGGCTGTGGACCCCTACACCT 598
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QY 601 CTCTCAGCTGTGTGATCAGTGTGACACCACTGCTCATTTCCGGTGGGGGACGACGTC 660
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QY 661 CAGCCCCCAAGTACGCTGCTTACACCTTGCATGCGGCAATCATCATTTAGCA 720
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QY 721 CCAGAACTGTGAAGACCTTACCCCGCAACATCACAGACCAATGGTGTGTCAGCGT 780
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QY 781 GCAGGAAGGGGCAAGACTCTGACAGGCTGACCTCGGGGGCCCTCTGTGTTAACCA 840


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Qy 1081 GCACCTACAGAGAGACTCTGTCACTTAATTAATCAACCTGGGGTTCGAAATCAGTACCTG 1140
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Qy 1201 TTTTGTATCCCGAGCCCAAGACAGCTCTGGCCATATATCAATGTTCAATAATAT 1260
Db 1199 TTTTGTATCCCGAGCCCAAGACAGCTCTGGCCATATATCAATGTTCAATAATAT 1258
Qy 1261 TGCTAAATGAAAAAATGAAAAAATGAAAAA 1289
Db 1259 TGCTAAATGAAAAAATGAAAAAATGAAAAA 1287

RESULT 2
US-10-023-282-189
; Sequence 189, Application US/10023282
; Publication No. US20030092893a1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007p1
; CURRENT APPLICATION NUMBER: US/10/023,282
; CURRENT FILING DATE: 2001-12-20
; EARLIER APPLICATION NUMBER: 09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
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; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 189
; LENGTH: 1292
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-023-282-189

Query Match 97.7%; Score 1271.4; DB 14; Length 1292;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 182; Conservative 4; Mismatches 0; Indels 3; Gaps 1;

Qy 1 CTGCTTCTCTCCACCTGCTGTCAGGGAGAGAGGAGGAGAAAGCCAGGAGGAGCCTA 60
Db 2 CTGCTTCTCTCCACCTGCTGTCAGGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 58
Qy 61 ACTGAAACAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
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Db 59 ACTAAAAACAACAGCTGGAGAGACGAGATCTGGCTCGGCTTCGCGAGATGACAG 118
Qy 121 GTTAGAGTGGCTGGCGGAGTGAAGTATCGGGGAGAGTCTCACAGACGCAAGAAC 180
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Qy 181 TGGGGCCCGCTCTCCCTCCAGGCGCATGAGATCTGCAATTCCTGCTGCTCT 240
Db 179 TGGGGCCCGCTCTCCCTCCAGGCGCATGAGATCTGCAATTCCTGCTGCTCT 238
Qy 241 GGCACAGAGGCTTAGGGGAGAGACGAGATCATGAAGGGTTCGAGTCAAGCCCA 300
Db 239 GGCACAGAGGCTTAGGGGAGAGACGAGATCATGAAGGGTTCGAGTCAAGCCCA 298
Qy 301 CTCCAGCCCTGGAGGAGCCCTGTTGAGAGAGCGCGCTACTCTGTGGGGGAGCGCT 360
Db 299 CTCCAGCCCTGGAGGAGCCCTGTTGAGAGAGCGCGCTACTCTGTGGGGGAGCGCT 358
Qy 361 CATGCGCCCGAGATGGTCTCTGAGAGAGCCACTGCTCAAGCCCGCTACATAGTTCA 420
Db 359 CATGCGCCCGAGATGGTCTCTGAGAGAGCCACTGCTCAAGCCCGCTACATAGTTCA 418
Qy 421 CCTGGGCGAGACAACTCCAGAGAGAGGCGCTGAGAGAGACCGGAGAGCGACTGA 480
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Db 599 CTCTCAAGCTGTGCTACTGCTGGGAGAGGCTGCTGCTGCTGCTGGGAGAGAGTGC 658
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RESULT 3
US-09-946-374-169
Sequence 169, Application US/09946374
Publication No. US20030073129A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830P1C1
CURRENT APPLICATION NUMBER: US/09/946,374
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
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PRIOR FILING DATE: 1998-09-01
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PRIOR FILING DATE: 1998-09-02
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;; PRIOR FILING DATE: 1998-09-17
;; PRIOR APPLICATION NUMBER: 60/100848
;; PRIOR FILING DATE: 1998-09-18
;; PRIOR APPLICATION NUMBER: 60/100849
;; PRIOR FILING DATE: 1998-09-18
;; PRIOR APPLICATION NUMBER: 60/100919
;; PRIOR FILING DATE: 1998-09-17
;; PRIOR APPLICATION NUMBER: 60/100930
;; PRIOR FILING DATE: 1998-09-17
;; PRIOR APPLICATION NUMBER: 60/101014
;; PRIOR FILING DATE: 1998-09-18
;; PRIOR APPLICATION NUMBER: 60/101068
;; PRIOR FILING DATE: 1998-09-18
;; PRIOR APPLICATION NUMBER: 60/101071
;; PRIOR FILING DATE: 1998-09-18
;; PRIOR APPLICATION NUMBER: 60/101279
;; PRIOR FILING DATE: 1998-09-22
;; PRIOR APPLICATION NUMBER: 60/101471
;; PRIOR FILING DATE: 1998-09-23
;; PRIOR APPLICATION NUMBER: 60/101472
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;; PRIOR APPLICATION NUMBER: 60/101474
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;; PRIOR APPLICATION NUMBER: 60/101475
;; PRIOR FILING DATE: 1998-09-23
;; PRIOR APPLICATION NUMBER: 60/101476
;; PRIOR FILING DATE: 1998-09-23
;; PRIOR APPLICATION NUMBER: 60/101477
;; PRIOR FILING DATE: 1998-09-23
;; PRIOR APPLICATION NUMBER: 60/101479
;; PRIOR FILING DATE: 1998-09-23
;; PRIOR APPLICATION NUMBER: 60/101738
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101741
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101743
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101915
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101916
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/102207

;; PRIOR FILING DATE: 1998-09-29
;; PRIOR APPLICATION NUMBER: 60/102240
;; PRIOR FILING DATE: 1998-09-29
;; PRIOR APPLICATION NUMBER: 60/102307
;; PRIOR FILING DATE: 1998-09-29
;; PRIOR APPLICATION NUMBER: 60/102330
;; PRIOR FILING DATE: 1998-09-29
;; PRIOR APPLICATION NUMBER: 60/102331
;; PRIOR FILING DATE: 1998-09-29
;; PRIOR APPLICATION NUMBER: 60/102484
;; PRIOR FILING DATE: 1998-09-30
;; PRIOR APPLICATION NUMBER: 60/102487
;; PRIOR FILING DATE: 1998-09-30
;; PRIOR APPLICATION NUMBER: 60/102570
;; PRIOR FILING DATE: 1998-09-30
;; PRIOR APPLICATION NUMBER: 60/102571
;; PRIOR FILING DATE: 1998-09-30
;; PRIOR APPLICATION NUMBER: 60/102684
;; PRIOR FILING DATE: 1998-10-01
;; PRIOR APPLICATION NUMBER: 60/102687
;; PRIOR FILING DATE: 1998-10-01
;; PRIOR APPLICATION NUMBER: 60/102965
;; PRIOR FILING DATE: 1998-10-02
;; PRIOR APPLICATION NUMBER: 60/103258
;; PRIOR FILING DATE: 1998-10-06
;; PRIOR APPLICATION NUMBER: 60/103314
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103315
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103328
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103395
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103396
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103401
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103449
;; PRIOR FILING DATE: 1998-10-06
;; PRIOR APPLICATION NUMBER: 60/103633
;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: 60/103678
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;; PRIOR APPLICATION NUMBER: 60/103679
;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: 60/103711
;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: 60/104257
;; PRIOR FILING DATE: 1998-10-14
;; PRIOR APPLICATION NUMBER: 60/104987
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105000
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105002
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105104
;; PRIOR FILING DATE: 1998-10-21
;; PRIOR APPLICATION NUMBER: 60/105169
;; PRIOR FILING DATE: 1998-10-22
;; PRIOR APPLICATION NUMBER: 60/105266
;; PRIOR FILING DATE: 1998-10-22
;; PRIOR APPLICATION NUMBER: 60/105693
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105694
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105807

Query Match 92.1%; Score 1198; DB 11; Length 1204;
Best Local Similarity 100.0%; Pred. No. 8.8e-312;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 104 GTTCGCGAGATGACAGAGTTGAGGTGGCTGCGGAGCTGGAAGTCAATCGGCGAGAGCTGTC 163
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Db 1 GTTCCGAGATGACAGAGTTGAGTGGCTGGGGAGCTGGAAGTATCGGGCAGAGTCTC 60
QY 164 ACACGACCCGAAGAACTGGGGCCGCTCTCCGCCCTCCAGGCCATGAGATTCTGCAG 223
Db 61 ACACGACCCGAAGAACTGGGGCCGCTCTCCGCCCTCCAGGCCATGAGATTCTGCAG 120
QY 224 TTATCTGCTGCTCTGGGCAACAGGGCTTGTAGGGGAGAGACAGGATCATCAAGGG 283
Db 121 TTTAATCTGCTGCTGGGCAACAGGGCTTGTAGGGGAGAGACAGGATCATCAAGGG 180
QY 284 TTGAGAGTGAAGCTCACTCCACGCCCTGGCAGGAGAGCCGTTGGAAGAACGCGGCTA 343
Db 181 TTGAGAGTGAAGCTCACTCCACGCCCTGGCAGGAGAGCCGTTGGAAGAACGCGGCTA 240
QY 344 CTGTGGGGGCGAGCTCATCGCCCAAGATGGCTCTGACAGCAGCCCATGCTCTCAG 403
Db 241 CTGTGGGGGCGAGCTCATCGCCCAAGATGGCTCTGACAGCAGCCCATGCTCTCAG 300
QY 404 CCCCCTACATAGTTCACTGGGGGAGCAGCAACTCCAGAAAGAGAGGGCTGTGAGCAG 463
Db 301 CCCCCTACATAGTTCACTGGGGGAGCAGCAACTCCAGAAAGAGAGGGCTGTGAGCAG 360
QY 464 ACCCGGACAGCAGTGAAGTCTCCACGCCGCTTCAACACAGAGCCTCCCAACAAA 523
Db 361 ACCCGGACAGCAGTGAAGTCTCCACGCCGCTTCAACACAGAGCCTCCCAACAAA 420
QY 524 GACCAACCGCAATGACATCATGCTGGTGAAGATGAGCATCGCCAGTCTCATCACTGGGCT 583
Db 421 GACCAACCGCAATGACATCATGCTGGTGAAGATGAGCATCGCCAGTCTCATCACTGGGCT 480
QY 584 GTGGACCCCTCAACCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 643
Db 481 GTGGACCCCTCAACCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 644 GGGTGGGGGCGAGCACTGCTCAGCCCACTGACCTGCTGCTGCTGCTGCTGCTGCTGCT 703
Db 541 GGGTGGGGGCGAGCACTGCTCAGCCCACTGACCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 704 ATCAACCATCATGAGACCAAGAGTGTGAGAACGCTTACCCCGGCAACATCACAGACCC 763
Db 601 ATCAACCATCATGAGACCAAGAGTGTGAGAACGCTTACCCCGGCAACATCACAGACCC 660
QY 764 ATGATGTGTGCGAGCGGTGCGAGGAAGGGGGAAGAGTCTGCGAGGGTGTGCTGCGGG 823
Db 661 ATGATGTGTGCGAGCGGTGCGAGGAAGGGGGAAGAGTCTGCGAGGGTGTGCTGCGGG 720
QY 824 CTTCTGTGTGTAAACAGTCTCTTCAAGGCAATATCTCTGCGGGGCGAGATCCGTGCG 883
Db 721 CTTCTGTGTGTAAACAGTCTCTTCAAGGCAATATCTCTGCGGGGCGAGATCCGTGCG 780
QY 884 ATCAACCCGAAGAGCTGTGTCTACAGAAAGTGTGCAAAATATGTGAGCTGAGTCCAGAG 943
Db 781 ATCAACCCGAAGAGCTGTGTCTACAGAAAGTGTGCAAAATATGTGAGCTGAGTCCAGAG 840
QY 944 ACAGTGAAGAACTTGTGAGTGTGAGCCACACAGCCAGCCATCAACCTCATTTCCACT 1003
Db 841 ACAGTGAAGAACTTGTGAGTGTGAGCCACACAGCCAGCCATCAACCTCATTTCCACT 900
QY 1004 TGGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1063
Db 901 TGGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 1064 CATTTCTTTGGGCTCTCTGGGAGTACAGAGAGTGTGTCTGCTGCTGCTGCTGCTGCT 1123
Db 961 CATTTCTTTGGGCTCTCTGGGAGTACAGAGAGTGTGTCTGCTGCTGCTGCTGCTGCT 1020
QY 1124 GAATATGATGAGACCTGATATCAATTTGCTGAAATATTTGAGCTGCGGGAATGACA 1183
Db 1021 GAATATGATGAGACCTGATATCAATTTGCTGAAATATTTGAGCTGCGGGAATGACA 1080
QY 1184 ACACCTGGTTTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1243
Db 1081 ACACCTGGTTTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140

QY 1244 AGTTTCATATAATATTTGCTAAATGAAAAA 1301
Db 1141 AGTTTCATATAATATTTGCTAAATGAAAAA 1198
RESULT 4
US-10-015-387A-169
; Sequence 169, Application US/10015387A
; Publication No. US20030135034A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C54
; CURRENT APPLICATION NUMBER: US/10/015.387A
; PRIORITY FILING DATE: 2001-12-12
; PRIOR Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 169
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-387A-169
Query Match 92.1%; Score 1198; DB 12; Length 1204;
Best Local Similarity 100.0%; Pred. No. 8.8e-312;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 104 GTTCCGAGATGACAGAGTTGAGTGGCTGGGGAGCTGGAAGTATCGGGCAGAGTCTC 163
Db 1 GTTCCGAGATGACAGAGTTGAGTGGCTGGGGAGCTGGAAGTATCGGGCAGAGTCTC 60
QY 164 ACACGACCCGAAGAACTGGGGCCGCTCTCCGCCCTCCAGGCCATGAGATTCTGCAG 223
Db 61 ACACGACCCGAAGAACTGGGGCCGCTCTCCGCCCTCCAGGCCATGAGATTCTGCAG 120
QY 224 TTATCTGCTGCTCTGGGCAACAGGGCTTGTAGGGGAGAGACAGGATCATCAAGGG 283
Db 121 TTTAATCTGCTGCTGGGCAACAGGGCTTGTAGGGGAGAGACAGGATCATCAAGGG 180
QY 284 TTGAGAGTGAAGCTCACTCCACGCCCTGGCAGGAGAGCCGTTGGAAGAACGCGGCTA 343
Db 181 TTGAGAGTGAAGCTCACTCCACGCCCTGGCAGGAGAGCCGTTGGAAGAACGCGGCTA 240
QY 344 CTGTGGGGGCGAGCTCATCGCCCAAGATGGCTCTGACAGCAGCCCATGCTCTCAG 403
Db 241 CTGTGGGGGCGAGCTCATCGCCCAAGATGGCTCTGACAGCAGCCCATGCTCTCAG 300
QY 404 CCCCCTACATAGTTCACTGGGGGAGCAGCAACTCCAGAAAGAGAGGGCTGTGAGCAG 463
Db 301 CCCCCTACATAGTTCACTGGGGGAGCAGCAACTCCAGAAAGAGAGGGCTGTGAGCAG 360
QY 464 ACCCGGACAGCAGTGAAGTCTCCACGCCGCTTCAACACAGAGCCTCCCAACAAA 523
Db 361 ACCCGGACAGCAGTGAAGTCTCCACGCCGCTTCAACACAGAGCCTCCCAACAAA 420
QY 524 GACCAACCGCAATGACATCATGCTGGTGAAGATGAGCATCGCCAGTCTCATCACTGGGCT 583
Db 421 GACCAACCGCAATGACATCATGCTGGTGAAGATGAGCATCGCCAGTCTCATCACTGGGCT 480

QY 584 GTGCGACCCCTCAACCTCTCTCCTCAGCCTGTGTCTACTGTCTGGACCAAGCTGCTCATTTCC 643
DB 481 GTGCGACCCCTCAACCTCTCTCCTCAGCCTGTGTCTACTGTCTGGACCAAGCTGCTCATTTCC 540
QY 644 GGTGGGGGAGACGTCGACGAGCCCGGTTACGCTGCTCCACACCTTGGAGCCGCGAAC 703
DB 541 GGTGGGGGAGACGTCGACGAGCCCGGTTACGCTGCTCCACACCTTGGAGCCGCGAAC 600
QY 704 ATCACCATTATTGAGCACCAGAAAGTGTGAAAGCGCTACCCGGCAACATCAAGACACC 763
DB 601 ATCACCATTATTGAGCACCAGAAAGTGTGAAAGCGCTACCCGGCAACATCAAGACACC 660
QY 764 ATGTGTGTGTGCGACGCTGCGAGAAAGGGGGCAAGAGACTCTGCGAGGGTACTCCGCGGGC 823
DB 661 ATGTGTGTGTGCGACGCTGCGAGAAAGGGGGCAAGAGACTCTGCGAGGGTACTCCGCGGGC 720
QY 824 CCTGTGTGTGTGTACCAAGTCTCTCAAGGCAATTATCTCTGGGGCCAGATCCGTGTGCG 883
DB 721 CCTGTGTGTGTGTACCAAGTCTCTCAAGGCAATTATCTCTGGGGCCAGATCCGTGTGCG 780
QY 884 ATCACCAGCAAGCCTGTGTGTGTACAGAAAGTCTGCAATATGTGTGACTGTGATCCAGAG 943
DB 781 ATCACCAGCAAGCCTGTGTGTGTGTACAGAAAGTCTGCAATATGTGTGACTGTGATCCAGAG 840
QY 944 ACGATGAGAGACAATTAGACTGTGAGCCACCCACACAGCCCATTCACCTTCATTCACCT 1003
DB 841 ACGATGAGAGACAATTAGACTGTGAGCCACCCACACAGCCCATTCACCTTCATTCACCT 900
QY 1004 TGGT 1063
DB 901 TGGT 960
QY 1064 CATCTTTTGGGCTCTCTGT 1123
DB 961 CATCTTTTGGGCTCTCTGT 1020
QY 1124 GAAATCAGTGAACCTGTGATTTCAAAATTTGCTGAAATTTGTGACTGTGGAAATGACA 1183
DB 1021 GAAATCAGTGAACCTGTGATTTCAAAATTTGCTGAAATTTGTGACTGTGGAAATGACA 1080
QY 1184 AACCGGTTTGT 1243
DB 1081 AACCGGTTTGT 1140
QY 1244 AGGTTTCAATTAATTTGCTTAATGTAAAAAATTTGTGTGTGTGTGTGTGTGTGTGTGTGT 1301
DB 1141 AGGTTTCAATTAATTTGCTTAATGTAAAAAATTTGTGTGTGTGTGTGTGTGTGTGTGTGT 1198

RESULT 5
US-10-137-870-505
; Sequence 505, Application US/10137870
; Publication No. US20030138883A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P330R1C15
; CURRENT APPLICATION NUMBER: US/10/137,870
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-137-870-505

Query Match 92.1%; Score 1198; DB 12; Length 1204;
Best Local Similarity 100.0%; Pred. No. 8.8e-312;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 GTTCCGACATGTCAGAGGTTGAGGTGTGCGGGAGTGTGAAGTATCGGGCAGAGGTCTTC 163
DB 1 GTTCCGACATGTCAGAGGTTGAGGTGTGCGGGAGTGTGAAGTATCGGGCAGAGGTCTTC 60
QY 164 ACAGCAGCCAGAGAACTGGGCGCGCTCTCCGCCCTCCAGGCCATGAGGATTTCTGAC 223
DB 61 ACAGCAGCCAGAGAACTGGGCGCGCTCTCTCCGCCCTCCAGGCCATGAGGATTTCTGAC 120
QY 224 TTATCTCTCTTGT 283
DB 121 TTATCTCTCTTGT 180
QY 284 TTGAGTGTGAGGCTGT 343
DB 181 TTGAGTGTGAGGCTGT 240
QY 344 CTCTGT 403
DB 241 CTCTGT 300
QY 404 CCCCCTTACATGT 463
DB 301 CCCCCTTACATGT 360
QY 464 ACCCGGAGCAGCTGAGT 523
DB 361 ACCCGGAGCAGCTGAGT 420
QY 524 GACACCGCAATGACATGT 583
DB 421 GACACCGCAATGACATGT 480
QY 584 GTGCGACCCCTCAACCTCTCTCCTCAGCCTGTGTCTACTGTGTGACACAGCTGCTCATTTTC 643
DB 481 GTGCGACCCCTCAACCTCTCTCCTCAGCCTGTGTCTACTGTGTGACACAGCTGCTCATTTTC 540
QY 644 GGTGGGGGAGACGTCGACGAGCCCGGTTACGCTGCTCCACACCTTGGAGCCGCGAAC 703
DB 541 GGTGGGGGAGACGTCGACGAGCCCGGTTACGCTGCTCCACACCTTGGAGCCGCGAAC 600
QY 704 ATCACCATTATTGAGCACCAGAAAGTGTGAAAGCGCTACCCGGCAACATCAAGACACC 763
DB 601 ATCACCATTATTGAGCACCAGAAAGTGTGAAAGCGCTACCCGGCAACATCAAGACACC 660
QY 764 ATGTGTGTGTGCGACGCTGCGAGAAAGGGGGCAAGAGACTCTGCGAGGGTACTCCGCGGGC 823
DB 661 ATGTGTGTGTGCGACGCTGCGAGAAAGGGGGCAAGAGACTCTGCGAGGGTACTCCGCGGGC 720
QY 824 CCTGT 883
DB 721 CCTGT 780
QY 884 ATCACCAGCAAGCCTGT 943
DB 781 ATCACCAGCAAGCCTGT 840
QY 944 ACGATGAGAGACAATTAGACTGTGAGCCACCCACACAGCCCATTCACCTTCATTCACCT 1003

Db 841 ACGATGAAGAAACAAATTAAGCTGAGACCCACCCACACACCCATCCATTCATTTCCACT 900
QY 1004 TGGTGTGGTTCCTGCTCAGCTGTGTATTAAGAAACCCCTAAGCCAGACCCCTACGAA 1063
Db 901 TGGTGTGGTTCCTGCTCAGCTGTGTATTAAGAAACCCCTAAGCCAGACCCCTACGAA 960
QY 1064 CATTCCTTGGGCGCTCTGAGCTACAGAGATGCTGTCACTTAATTAATCAACCTGGGGTTC 1123
Db 961 CATTCCTTGGGCGCTCTGAGCTACAGAGATGCTGTCACTTAATTAATCAACCTGGGGTTC 1020
QY 1124 GAAATCAGTAGAGACCTGATCAATTCCTGCTGAATTAATGTGACCTGGGAATGACA 1183
Db 1021 GAAATCAGTAGAGACCTGATCAATTCCTGCTGAATTAATGTGACCTGGGAATGACA 1080
QY 1184 ACACCTGGTTCCTGCTGTTGTATCCCGACCCCAAGACAGCTCTGGCCATATATCA 1243
Db 1081 ACACCTGGTTCCTGCTGTTGTATCCCGACCCCAAGACAGCTCTGGCCATATATCA 1140
QY 1244 AGGTTTCAATTAATTTGCTAAATGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1301
Db 1141 AGGTTTCAATTAATTTGCTAAATGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1198

RESULT 6

US-10-140-018-505
; Sequence 505, Application US/10140018
; Publication No. US20030138885A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C158
; CURRENT APPLICATION NUMBER: US/10/140,018
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

Query Match 92.1%; Score 1198; DB 12; Length 1204;
Best Local Similarity 100.0%; Pred. No. 8.8e-312;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 104 GTTCCGAGATGACAGAGTTGAGTGGCTGGCGAGCTGAGATCATCGGGCAGAGGCTTC 163
Db 1 GTTCCGAGATGACAGAGTTGAGTGGCTGGCGAGCTGAGATCATCGGGCAGAGGCTTC 60
QY 164 ACACGACGCAAGAACCTGGGGCCGCTCTCCCTCCCTCCAGGCGCATGAGATTCTGCAG 223
Db 61 ACACGACGCAAGAACCTGGGGCCGCTCTCCCTCCCTCCAGGCGCATGAGATTCTGCAG 120
QY 224 TTATCTGCTGCTGTGGCAACGAGGCTGTGAGGGGAGAGACAGATCATTAAGGGG 283
|||||

Db 121 TTATCTGCTGCTGTGGCAACGAGGCTGTGAGGGGAGAGACAGATCATTAAGGGG 180
QY 284 TTGAGTGAAGACCTCACTCCACGCGCTGGCAGGAGCCGTTGCGAAGAGCGGCTA 343
Db 181 TTGAGTGAAGACCTCACTCCACGCGCTGGCAGGAGCCGTTGCGAAGAGCGGCTA 240
QY 344 CTCTGTGGGGGAGCGCTCATGCCCCAGATGAGCTCTGACAGGACCCATGCTTCAG 403
Db 241 CTCTGTGGGGGAGCGCTCATGCCCCAGATGAGCTCTGACAGGACCCATGCTTCAG 300
QY 404 CCCCCGTACATAGTTCACCTGCGGCGACACACCTCCAGAAAGGAGGGCTGTGACAG 463
Db 301 CCCCCGTACATAGTTCACCTGCGGCGACACACCTCCAGAAAGGAGGGCTGTGACAG 360
QY 464 ACCCGGACGACGACCTGAGTCTTCCCGACCCCGCTTCAACAACACGCTCCCAACAA 523
Db 361 ACCCGGACGACGACCTGAGTCTTCCCGACCCCGCTTCAACAACACGCTCCCAACAA 420
QY 524 GACCAACGCAATGACATCATGCTGTGAAAGATGGCATGCGCATCTCCATCACCTGGGCT 583
Db 421 GACCAACGCAATGACATCATGCTGTGAAAGATGGCATGCGCATCTCCATCACCTGGGCT 480
QY 584 GTGGAGCCCTCAGCCCTCTCTCAAGCTGTGCTACGCTGTGGACACGACCTGCTATTTC 643
Db 481 GTGGAGCCCTCAGCCCTCTCTCAAGCTGTGCTACGCTGTGGACACGACCTGCTATTTC 540
QY 644 GGCCTGGGGGACGACGCTCCAGCCCGCAGTTCAGCCCTGCTCACACCTTGGCGAGCCAC 703
Db 541 GGCCTGGGGGACGACGCTCCAGCCCGCAGTTCAGCCCTGCTCACACCTTGGCGAGCCAC 600
QY 704 ATCAACATCATTTGACACACAGAAAGTGTGAGAAAGCCTACCCCGGCAACATCACAGACCC 763
Db 601 ATCAACATCATTTGACACACAGAAAGTGTGAGAAAGCCTACCCCGGCAACATCACAGACCC 660
QY 764 ATGCTGTGCGCAACGCGGACGAGAAAGGGGAGAGAGTCTCCAGAGCTGACTCGGGGGC 823
Db 661 ATGCTGTGCGCAACGCGGACGAGAAAGGGGAGAGAGTCTCCAGAGCTGACTCGGGGGC 720
QY 824 CCTCTGTGCTGTAACAGCTCTTCAAGGATTAATTCCTGGGGCGAGATCCGTGCGG 883
Db 721 CCTCTGTGCTGTAACAGCTCTTCAAGGATTAATTCCTGGGGCGAGATCCGTGCGG 780
QY 884 ATCAACGCAAGACCTGCTGTCTACAGAAAGTGTGCAATTAATGTGAGCTGATCCAGAG 943
Db 781 ATCAACGCAAGACCTGCTGTCTACAGAAAGTGTGCAATTAATGTGAGCTGATCCAGAG 840
QY 944 ACGATGAAGAAACAAATTAAGCTGAGACCCACACACGACCCATCACCCTCATTTCCACT 1003
Db 841 ACGATGAAGAAACAAATTAAGCTGAGACCCACACACGACCCATCACCCTCATTTCCACT 900
QY 1004 TGGTGTGGTTCCTGCTGTTCACTGTATTAAGAAACCCCTAAGCCAGACCCCTACGAA 1063
Db 901 TGGTGTGGTTCCTGCTGTTCACTGTATTAAGAAACCCCTAAGCCAGACCCCTACGAA 960
QY 1064 CATTCCTTGGGCGCTCTGAGCTACAGAGATGCTGTCACTTAATTAATCAACCTGGGGTTC 1123
Db 961 CATTCCTTGGGCGCTCTGAGCTACAGAGATGCTGTCACTTAATTAATCAACCTGGGGTTC 1020
QY 1124 GAAATCAGTAGAGACCTGATCAATTCCTGCTGAATTAATGTGACCTGGGAATGACA 1183
Db 1021 GAAATCAGTAGAGACCTGATCAATTCCTGCTGAATTAATGTGACCTGGGAATGACA 1080
QY 1184 ACACCTGGTTCCTGCTGTTGTATCCCGACCCCAAGACAGCTCTGGCCATATATCA 1243
Db 1081 ACACCTGGTTCCTGCTGTTGTATCCCGACCCCAAGACAGCTCTGGCCATATATCA 1140
QY 1244 AGGTTTCAATTAATTTGCTAAATGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1301
Db 1141 AGGTTTCAATTAATTTGCTAAATGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1198

RESULT 7

US-10-140-021-505

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Sequence 505, Application US/10140021
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C167
CURRENT APPLICATION NUMBER: US/10/140,021
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 505
LENGTH: 1204
TYPE: DNA
ORGANISM: Homo Sapien
US-10-140-021-505
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Query Match 92.1%; Score 1198; DB 12; Length 1204;
Best Local Similarity 100.0%; Pred. No. 8,8e-312;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 104 GTTCCGAGAGTCAAGAGTGTGAGTGGCTGCGGAGCTGAGATCATCGGCGAGAGGCTTC 163
DB 1 GTTCCGAGAGTCAAGAGTGTGAGTGGCTGCGGAGCTGAGATCATCGGCGAGAGGCTTC 60
QY 164 ACAGAGCGCAAGAGAGCTGGGGGCGCGCTCCCGCCCGCCAGCCATGAGATTTCTGCAG 223
DB 61 ACAGAGCGCAAGAGAGCTGGGGGCGCGCTCCCGCCCGCCAGCCATGAGATTTCTGCAG 120
QY 224 TTATCTCTGCTGCTCTGCGCAACAGGGCTTGTAGGGGAGAGACCAGATCATCAAGGGG 283
DB 121 TTATCTCTGCTGCTCTGCGCAACAGGGCTTGTAGGGGAGAGACCAGATCATCAAGGGG 180
QY 284 TTGAGTGTCAAGCTCTACTCCAGCCCTGGCGAGGAGCCCTGTTGAGAGAGAGGGGCTTA 343
DB 181 TTGAGTGTCAAGCTCTACTCCAGCCCTGGCGAGGAGCCCTGTTGAGAGAGAGGGGCTTA 240
QY 344 CTCTGTGGGGGAGAGCTATGCCCCCAGATGGCTCTGACAGGAGCCCATGCTCTCAAG 403
DB 241 CTCTGTGGGGGAGAGCTATGCCCCCAGATGGCTCTGACAGGAGCCCATGCTCTCAAG 300
QY 404 CCCCCTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 463
DB 301 CCCCCTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 464 ACCCGAGAGAGCCATGAGTCTTCCCAACCCCGGGCTTCACAGAGCCCTCCCAACAAA 523
DB 361 ACCCGAGAGAGCCATGAGTCTTCCCAACCCCGGGCTTCACAGAGCCCTCCCAACAAA 420
QY 524 GACCAACCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 583
DB 421 GACCAACCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 584 GTGCGACCCCTGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 643
DB 481 GTGCGACCCCTGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
```

```
QY 644 GGCTGGGGGAGAGAGCTGCAGCCGCCAGGTTAGCGCTGCTCTACAGCCTTGGAGTGGCCAAAC 703
DB 541 GGCTGGGGGAGAGAGCTGCAGCCGCCAGGTTAGCGCTGCTCTACAGCCTTGGAGTGGCCAAAC 600
QY 704 ATCACCATTATGAGAGCAGCAGAAAGTGTGAAACGCTTACCCGGGCAACATCAGAGACCC 763
DB 601 ATCACCATTATGAGAGCAGCAGAAAGTGTGAAACGCTTACCCGGGCAACATCAGAGACCC 660
QY 764 ATGTTGTGTGCCAGCGCTGAGAGAAAGGGGCGCAAGAGATCTCTGCGAGGCTGATCCGGGGGC 823
DB 661 ATGTTGTGTGCCAGCGCTGAGAGAAAGGGGCGCAAGAGATCTCTGCGAGGCTGATCCGGGGGC 720
QY 824 CCTGTGTGTGTATACCAAGTCTCTTCAAGGCAATTAATCTCTGGGGCCAGAGTCCGTGTGCG 883
DB 721 CCTGTGTGTGTATACCAAGTCTCTTCAAGGCAATTAATCTCTGGGGCCAGAGTCCGTGTGCG 780
QY 884 ATCACCAGGAAAGCCGTGTGTCTACACGAAAGTGTGAAATATGTGAGCTGTGATCCAGAGG 943
DB 781 ATCACCAGGAAAGCCGTGTGTCTACACGAAAGTGTGAAATATGTGAGCTGTGATCCAGAGG 840
QY 944 ACAGTGAAGAAATATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1003
DB 841 ACAGTGAAGAAATATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 900
QY 1004 TGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1063
DB 901 TGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
QY 1064 CATTTCTTTGGGCTCTCTGAGCTACAGAGAGATGCTGCTATTAATCAACTGGGGTTC 1123
DB 961 CATTTCTTTGGGCTCTCTGAGCTACAGAGAGATGCTGCTATTAATCAACTGGGGTTC 1020
QY 1124 GAATCAGTGAAGCTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1183
DB 1021 GAATCAGTGAAGCTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1080
QY 1184 ACACCTGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1243
DB 1081 ACACCTGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
QY 1244 AGTTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1301
DB 1141 AGTTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1198
```

RESULT 8
US-10-140-274-505
Sequence 505, Application US/10140274
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C161
CURRENT APPLICATION NUMBER: US/10/140,274
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 550
SEQ ID NO 505
LENGTH: 1204
TYPE: DNA
ORGANISM: Homo Sapien
US-10-140-274-505

Query Match 92.1%; Score 1198; DB 12; Length 1204;
Best Local Similarity 100.0%; Pred. No. 8.8e-312;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 104 GTTCGCGAGATGACAGAGTTGAGTGGCTGCGGAGCTGAAGTCAATGCGGAGAGGTTTC 163
    |||||||
DB 1 GTTCGCGAGATGACAGAGTTGAGTGGCTGCGGAGCTGAAGTCAATGCGGAGAGGTTTC 60
OY 164 ACAGAGCCAAAGAACTGGGGCCGCTCCCTCCCTCCAGGCCATGAGATTCTGCAG 223
    |||||||
DB 61 ACAGAGCCAAAGAACTGGGGCCGCTCCCTCCCTCCAGGCCATGAGATTCTGCAG 120
OY 224 TTATCTCTGCTGCTCTGGCAACAGGGCTTTAGGGGGAGAGACAGATCATCAAGGG 283
    |||||||
DB 121 TTATCTCTGCTGCTCTGGCAACAGGGCTTTAGGGGGAGAGACAGATCATCAAGGG 180
OY 284 TTGAGTGCAGACCTCACTCCAGCCCTGGCAGAGCCCTGTTGAGAAAGAGCGGCTA 343
    |||||||
DB 181 TTGAGTGCAGACCTCACTCCAGCCCTGGCAGAGCCCTGTTGAGAAAGAGCGGCTA 240
OY 344 CTGTGTGGGGGCGAGCTTCATCCGCCAGATGGCTCTGACAGAGCCCATGCTCAAG 403
    |||||||
DB 241 CTGTGTGGGGGCGAGCTTCATCCGCCAGATGGCTCTGACAGAGCCCATGCTCAAG 300
OY 404 CCGCGCTACATAGTTCACTCTGGGCGACACAACTCCAGAAAGAGGGGCTGTGACAG 463
    |||||||
DB 301 CCGCGCTACATAGTTCACTCTGGGCGAGACAACTCCAGAAAGAGGGGCTGTGACAG 360
OY 464 ACCGCGACAGCCATGAGTCTCTCCCGACCCCGCTTCAACAACAGCCCTCCCAACAA 523
    |||||||
DB 361 ACCGCGACAGCCATGAGTCTCTCCCGACCCCGCTTCAACAACAGCCCTCCCAACAA 420
OY 524 GACCAACCGCAATGACATCATCTGTGTGAAGATGGCATTCGCCAGTCTCCATCTGG 583
    |||||||
DB 421 GACCAACCGCAATGACATCATCTGTGTGAAGATGGCATTCGCCAGTCTCCATCTGG 480
OY 584 GTGGACCCCTCACCTCTCTCTACGGCTGTGACGCTGTGACACAGTGGCTCATTTCC 643
    |||||||
DB 481 GTGGACCCCTCACCTCTCTCTCTACGGCTGTGACGCTGTGACACAGTGGCTCATTTCC 540
OY 644 GGCTGGGGCAGCAGCTCCAGCCCGCAGTTACGCTGTGCTACACCTTGCATGGCCAAC 703
    |||||||
DB 541 GGCTGGGGCAGCAGCTCCAGCCCGCAGTTACGCTGTGCTACACCTTGCATGGCCAAC 600
OY 704 ATCAACCATCATTTGACACACAGAACTGTGAGAACGCTTACCCCGCAACATCACAGAC 763
    |||||||
DB 601 ATCAACCATCATTTGACACACAGAACTGTGAGAACGCTTACCCCGCAACATCACAGAC 660
OY 764 ATGGTGTGTGCGACGTCGACAGAGGGGGGAGGAGTCTGCGGAGGTTGACTCCGGGGG 823
    |||||||
DB 661 ATGGTGTGTGCGACGTCGACAGAGGGGGGAGGAGTCTGCGGAGGTTGACTCCGGGGG 720
OY 824 CCTGTGTGTGTAACAGTCTCTTCAAGGCAATTAATCTCTGGGGCAGAGATCCGTGTG 883
    |||||||
DB 721 CCTGTGTGTGTAACAGTCTCTTCAAGGCAATTAATCTCTGGGGCAGAGATCCGTGTG 780
OY 884 ATCAACCCGAAAGCTGTGTCTACACAAAGTGTGCAAAATATGTGAGATTCAGAGAG 943
    |||||||
DB 781 ATCAACCCGAAAGCTGTGTCTACACAAAGTGTGCAAAATATGTGAGATTCAGAGAG 840
OY 944 ACGATGAAGAACAATTAAGTGCAGCAACCAACCAAGCCCATCAATCTTCAACT 1003
    |||||||
DB 841 ACGATGAAGAACAATTAAGTGCAGCAACCAACCAAGCCCATCAATCTTCAACT 900
OY 1004 TGGTGTGTGCTCTGCTTCACTGTATTAAGAAACCTTAAGCCATGACCTCTACGAA 1063
    |||||||
```

```
DB 901 TGGTGTGTGCTCTGCTTCACTGTATTAAGAAACCTTAAGCCAAAGACCTCTACGAA 960
OY 1064 CATTCCTTTGGGCTCTCTGAGTACAGAGATGCTGTCAATTAATCAACTGGGGTTC 1123
    |||||||
DB 961 CATTCCTTTGGGCTCTCTGAGTACAGAGATGCTGTCAATTAATCAACTGGGGTTC 1020
OY 1124 GAAATCAGTGAAGCTTGATTTCAATTTCTGCTTGAATATTTGACTGTGGAAATGACA 1183
    |||||||
DB 1021 GAAATCAGTGAAGCTTGATTTCAATTTCTGCTTGAATATTTGACTGTGGAAATGACA 1080
OY 1184 ACACCTGATTTGTTCTCTGTTGATCCCAAGCCCAAGACAGCTCCTGGCCATTAATCA 1243
    |||||||
DB 1081 ACACCTGATTTGTTCTCTGTTGATCCCAAGCCCAAGACAGCTCCTGGCCATTAATCA 1140
OY 1244 AGGTTCAATTAATTAATTTGCTTAATGAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1301
    |||||||
DB 1141 AGGTTCAATTAATTAATTTGCTTAATGAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1198

RESULT 9
US-10-140-471-505
: Sequence 505, Application US/10140471
: Publication No. US2003013887A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: Deforge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3330R1C163
: CURRENT APPLICATION NUMBER: US/10/140,471
: PRIOR APPLICATION DATE: 2002-05-06
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 505
: LENGTH: 1204
: TYPE: DNA
: ORGANISM: Homo Sapien
: US-10-140-471-505

Query Match 92.1%; Score 1198; DB 12; Length 1204;
Best Local Similarity 100.0%; Pred. No. 8.8e-312;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



```
QY 344 CTCTGTGGGGCGACGCTCATCGCCCCCAATAGGCTCTGTACAGCAGCCCACTGCTCAAG 403
DB 241 CTCTGTGGGGCGACGCTCATCGCCCCCAATAGGCTCTGTACAGCAGCCCACTGCTCAAG 300
QY 404 CCCCCGTACATAGTTTACCTGGGGGCGACCAACCTCCAGAGGAGGAGGCTGTGACAG 463
DB 301 CCCCCGTACATAGTTTACCTGGGGGCGACCAACCTCCAGAGGAGGAGGCTGTGACAG 360
QY 464 ACCCGGACAGCAGCTAGTCTCTCCCAACCCCGGCTTCAACAAAGCTCCCAACAA 523
DB 361 ACCCGGACAGCAGCTAGTCTCTCCCAACCCCGGCTTCAACAAAGCTCCCAACAA 420
QY 524 GACACCGCAATGACATCATGCTGTGAAGATGGCATCCAGTCTCATACACTGGCT 583
DB 421 GACACCGCAATGACATCATGCTGTGAAGATGGCATCCAGTCTCATACACTGGCT 480
QY 584 GTGGGACCCCTCACCCTCCTCAGCCTGTGACAGTGTGACAGCAGCTGCTCATTTCC 643
DB 481 GTGGGACCCCTCACCCTCCTCAGCCTGTGACAGTGTGACAGCAGCTGCTCATTTCC 540
QY 644 GGCTGGGGGACAGCTCCAGCCCGGATTAGGCTCTCAGACCTTGGATGGCCCAAC 703
DB 541 GGCTGGGGGACAGCTCCAGCCCGGATTAGGCTCTCAGACCTTGGATGGCCCAAC 600
QY 704 ATACCATCATTTGAGACACCAAGATGTGAAAGCCCTACCCCGGCAATCACAGACAC 763
DB 601 ATACCATCATTTGAGACACCAAGATGTGAAAGCCCTACCCCGGCAATCACAGACAC 660
QY 764 ATGGGTGTGGCAGGTGTGAGAAAGGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 823
DB 661 ATGGGTGTGGCAGGTGTGAGAAAGGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
QY 824 CCTGTGTCTGTACACAGTCTCTCAAGGATTTATCTCTGGGGGAGGAGTCCGTGTGG 883
DB 721 CCTGTGTCTGTACACAGTCTCTCAAGGATTTATCTCTGGGGGAGGAGTCCGTGTGG 780
QY 884 ATACCCCGCAAGCCTGTGTGTACACGAAAGTGTGCAATATGTGAGCTGTATCCAGAG 943
DB 781 ATACCCCGCAAGCCTGTGTGTACACGAAAGTGTGCAATATGTGAGCTGTATCCAGAG 840
QY 944 AGGATGAAGACAAATTTAGAGTGTGAGCCACCCAGCCAGCCCAACCCCTCAATTCAC 1003
DB 841 AGGATGAAGACAAATTTAGAGTGTGAGCCACCCAGCCAGCCCAACCCCTCAATTCAC 900
QY 1004 TGGTGTGTGTCTGTCTGTCTGTCTGTATTAAGAAACCTTAAGCAAGACCTCTACGA 1063
DB 901 TGGTGTGTGTCTGTCTGTCTGTCTGTATTAAGAAACCTTAAGCAAGACCTCTACGA 960
QY 1064 CATTTCTTTGGGCTCTGTGACTACAGAGAGTGTCTCACTTAATTAACACTGGGGTTC 1123
DB 961 CATTTCTTTGGGCTCTGTGACTACAGAGAGTGTCTCACTTAATTAACACTGGGGTTC 1020
QY 1124 GAATACAGTGAAGACCTGGAATTCGAAATTCGAAATTTGTGACTGTGGAAATGACA 1183
DB 1021 GAATACAGTGAAGACCTGGAATTCGAAATTTGTGACTGTGGAAATGACA 1080
QY 1184 ACACCTGTTTGTCTGTGTGTATCCCGAGCCCAAGACAGCTCTGGCCATATATCA 1243
DB 1081 ACACCTGTTTGTCTGTGTGTATCCCGAGCCCAAGACAGCTCTGGCCATATATCA 1140
QY 1244 AGGTTTCAATTAATTTTGTCTTAATGAAAAAATTTTGTCTTAATGAAAAAATTTT 1301
DB 1141 AGGTTTCAATTAATTTTGTCTTAATGAAAAAATTTTGTCTTAATGAAAAAATTTT 1198
```

RESULT 10
US-10-140-807-505

; Sequence 505, Application US/10140807
; Publication No. US20030134354A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen

```
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C174
CURRENT APPLICATION NUMBER: US/10/140,807
PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION REMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 505
LENGTH: 1204
TYPE: DNA
ORGANISM: Homo Sapien
US-10-140-807-505
```

Query Match 92.1%; Score 1198; DB 12; Length 1204;
Best Local Similarity 100.0%; Pred. No. 8,8e-312; Indels 0; Gaps 0;
Matches 1198; Conservative 0; Mismatches 0;

```
QY 104 GTTCCGAGATGACAGAGTTGAGGTGCTGCGGAGTGGAAATCATCGGAGAGGATTC 163
DB 1 GTTCCGAGATGACAGAGTTGAGGTGCTGCGGAGTGGAAATCATCGGAGAGGATTC 60
QY 164 ACAGCAGCCAGAGAACTGGGGCCGCTCTCCCTCCAGGATGAGATTTCTGAC 223
DB 61 ACAGCAGCCAGAGAACTGGGGCCGCTCTCCCTCCAGGATGAGATTTCTGAC 120
QY 224 TTAATCTCTGCTGTGTGCAACAGGGGCTGTGAGGGGAGAACAGAGATTCATCAAGGG 283
DB 121 TTAATCTCTGCTGTGTGCAACAGGGGCTGTGAGGGGAGAACAGAGATTCATCAAGGG 180
QY 284 TTGAGTGTCAACCTCTACCTCCAGCCTGGAGGAGAGCCCTTGTGAGAGAGGGGCTA 343
DB 181 TTGAGTGTCAACCTCTACCTCCAGCCTGGAGGAGAGCCCTTGTGAGAGAGGGGCTA 240
QY 344 CTCTGTGGGGGACGCTCATATGCCCCAGATGGCTCTGTGACAGACGCCCATGCTCAAG 403
DB 241 CTCTGTGGGGGACGCTCATATGCCCCAGATGGCTCTGTGACAGACGCCCATGCTCAAG 300
QY 404 CCGCGCTCATATGTTCACTGTGGGAGACCAACCTCCAGAAAGAGAGGGGCTGTGACAG 463
DB 301 CCGCGCTCATATGTTCACTGTGGGAGACCAACCTCCAGAAAGAGAGGGGCTGTGACAG 360
QY 464 ACCCGGACAGCAGTGTCTCTCCCAACCCCGGCTTCAACAAAGCTCTCCCAACAA 523
DB 361 ACCCGGACAGCAGTGTCTCTCCCAACCCCGGCTTCAACAAAGCTCTCCCAACAA 420
QY 524 GACACCGCAATGACATCATGCTGTGAAGATGGCATCCAGTCTCATACACTGGGCT 583
DB 421 GACACCGCAATGACATCATGCTGTGAAGATGGCATCCAGTCTCATACACTGGGCT 480
QY 584 GTGGGACCCCTCACCCTCCTCAGCCTGTGACAGTGTGACAGCAGCTGCTCATTTCC 643
DB 481 GTGGGACCCCTCACCCTCCTCAGCCTGTGACAGTGTGACAGCAGCTGCTCATTTCC 540
QY 644 GGCTGGGGGACAGCTCCAGCCCGGATTAGGCTCTCAGACCTTGGATGGCCCAAC 703
DB 541 GGCTGGGGGACAGCTCCAGCCCGGATTAGGCTCTCAGACCTTGGATGGCCCAAC 600
QY 704 ATACCATCATTTGAGACACCAAGATGTGAAAGCCCTACCCCGGCAATCACAGACAC 763
```


OY	1124	GAAATTCAGTGGACCTGGATTCAAAATTCGCTTGGAATATTGGACGTGGGAATGACA	1183
Db	1021	GAAATTCAGTGGACCTGGATTCAAAATTCGCTTGGAATATTGGACGTGGGAATGACA	1080
OY	1184	ACACCTGGTTTGTTCTCGTTGTATPCCCAAGCCCCAAGAAGACGTCGCCCATATATNACA	1243
Db	1081	ACACCTGGTTTGTTCTCGTTGTATPCCCAAGCCCCAAGAAGACGTCGCCCATATATNACA	1140
OY	1244	AGCTTTCATTAATAATTGCTTAATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1301
Db	1141	AGCTTTCATTAATAATTGCTTAATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1198

```

RESULT 12
US-10-140-924-505
; Sequence 505, Application US/10140924
; Publication No. US20030134355A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R01C177
; CURRENT APPLICATION NUMBER: US/10/140,924
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-140-924-505

```

Query Match	92.1%;	Score 1198;	DB 12;	Length 1204;
Best Local Similarity	100.0%;	Pred. No. 8.8e-312;		
Matches 1196;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	104	GTWCCGACAGATGCAGAGGTTGAGGTGCGTGGGACATGGAATCATCGGACAGAGTTC	163	
Db	1	GTTCGGACAGATGCAGAGGTTGAGGTGCGTGGGACATGGAATCATCGGACAGAGTTC	60	
QY	164	ACAGACGCCAAGGAACCTGGGGCCCGCTCTCCCTCTCAGGCCATGAGATTCTGCAG	223	
Db	61	ACAGACGCCAAGGAACCTGGGGCCCGCTCTCTCCCTCTCAGGCCATGAGATTCTGCAG	120	
QY	224	TTTAATCTGCTGCTGTGCGCAACAGGGCTTTGAGGGGAGAGACCGAGTATCAAGGGG	283	
Db	121	TTTAATCTGCTGCTGTGCGCAACAGGGCTTTGAGGGGAGAGACCGAGTATCAAGGGG	180	
QY	284	TTTCGAGTGCAGAGCTCACTCCACACCCTGGGAGGCAAGCCCTGTTGAGAAACGCGGCTA	343	
Db	181	TTTCGAGTGCAGAGCTCACTCCACACCCTGGGAGGCAAGCCCTGTTGAGAAACGCGGCTA	240	
QY	344	CTCTGTGGGGGAGAGTCATGAGCCCGACAGATGGTCTCGAAGAGAGCCCACTGGCTCAAG	403	
Db	241	CTCTGTGGGGGAGAGTCATGAGCCCGACAGATGGTCTCGAAGAGAGCCCACTGGCTCAAG	300	

QY	404	CCCCGCTACAAATGATTTACCTCTGGGGGACAGACAACCTCCGAAAGAGAGAGGGCTGTAGAG	463
Db	301	CCCCGCTACAAATGATTTACCTCTGGGGGACAGACAACCTCCGAAAGAGAGAGGGCTGTAGAG	360
QY	464	ACCCGGACAGCACTGAGTGAATCTTCCCCACCCGGCTTCAACAAACAGCTCCCAACAA	523
Db	361	ACCCGGACAGCACTGAGTGAATCTTCCCCACCCGGCTTCAACAAACAGCTCCCAACAA	420
QY	584	GTGGACCCCTCACCCCTCTCTCTCAAGCTGTATCACTGCTGGACACAGCTGGCTCAATTTCC	643
Db	481	GTGGACCCCTCACCCCTCTCTCTCTCAAGCTGTATCACTGCTGGACACAGCTGGCTCAATTTCC	540
QY	644	GGCTGGGGGACAGAGTGTCCAGGCCCAAGTACGCTGCTCTACACCTTGGCATGGGGCAAC	703
Db	541	GGCTGGGGGACAGAGTGTCCAGGCCCAAGTACGCTGCTCTACACCTTGGCGATGGGGCAAC	600
QY	704	ATCACATCATTTGAGCACACAGAAATGTGTAGAAGCCTTACCCGGCAACATACAGACACC	763
Db	601	ATCACATCATTTGAGCACACAGAAATGTGTAGAAGCCTTACCCGGCAACATACAGACACC	660
QY	764	ATGGTGTGTGCACAGCTGTGCAGGAAGGGGGCAGGACCTTCGACAGGTTAGTCCGGGGGC	823
Db	661	ATGGTGTGTGCACAGCTGTGCAGGAAGGGGGCAGGACCTTCGACAGGTTAGTCCGGGGGC	720
QY	824	CCCTGGTCTGTATCCAGCTCTCTTCAAGGCAATTTATTCCTGGGGCCAGATCCGTTGTCG	883
Db	721	CCCTGGTCTGTATCCAGCTCTCTTCAAGGCAATTTATTCCTGGGGCCAGATCCGTTGTCG	780
QY	884	ATCACCCGAAAGCCTGGTGTCTTACACGAAATGTGTGAATTTGTGAGCTGATCCAGAG	943
Db	781	ATCACCCGAAAGCCTGGTGTCTTACACGAAATGTGTGAATTTGTGAGCTGATCCAGAG	840
QY	944	ACGATGAAGAACAATTAGACTGGACCCACACAGACCCATCACCTCCATTTCCACT	1003
Db	841	ACGATGAAGAACAATTAGACTGGACCCACACAGACCCATCACCTCCATTTCCACT	900
QY	1004	TGGGTGTTGGTTCCTGTTCACCTCTGTTAATTAAGAAACCTTAAGCAGAACCTCTACGAA	1063
Db	901	TGGGTGTTGGTTCCTGTTCACCTCTGTTAATTAAGAAACCTTAAGCAGAACCTCTACGAA	960
QY	1064	CATTCTTTGGGCTCTCTGAGCTACAGAGATGCTGTCACTTAATTAATCACCTGGGGTTC	1123
Db	961	CATTCTTTGGGCTCTCTGAGCTACAGAGATGCTGTCACTTAATTAATCACCTGGGGTTC	1020
QY	1124	GAATTCAGTGAAGACTGGATTCAAATCTTGCTTGAATATATTGATCTGGGAATGACA	1183
Db	1021	GAATTCAGTGAAGACTGGATTCAAATCTTGCTTGAATATATTGATCTGGGAATGACA	1080
QY	1184	ACAACCTGGTTTGTCTCTGTTGTATCCCAAGCCCAAGACAGCTCTGGCCATATATCA	1243
Db	1081	ACAACCTGGTTTGTCTCTGTTGTATCCCAAGCCCAAGACAGCTCTGGCCATATATCA	1140
QY	1244	AGGTTTCAATTAATTAATTTGCTTAATTGAAAAAATTTAAAAAATTTAAAAAATTTAAAAA	1301
Db	1141	AGGTTTCAATTAATTAATTTGCTTAATTGAAAAAATTTAAAAAATTTAAAAAATTTAAAAA	1198

```

RESULT 13
US-10-140-926-505
: Sequence 505, Application US/10140926
: Publication No. US20030134356A1
: GENERAL INFORMATION:
:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: DeForge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.

```

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Collin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P33081C187
CURRENT APPLICATION NUMBER: US/10/140, 926
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 505
LENGTH: 1204
TYPE: DNA
ORGANISM: Homo Sapien
US-10-140-926-505

Query Match 92.1% Score 1198; DB 12; Length 1204;
Best Local Similarity 100.0%; Pred. No. 8.8e-312;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 GTTCCGAGATGACAGAGTTGAGGTGCTGGGAGCTGGAATCATGCGGAGAGTCTC 163
1 GTTCCGAGATGACAGAGTTGAGGTGCTGGGAGCTGGAATCATGCGGAGAGTCTC 60
DB 164 ACAGACACCAAGAGAACTGGGGCCCTCTCCCTCCAGGCTATGAGATTTCTGAG 223
61 ACAGACACCAAGAGAACTGGGGCCCTCTCCCTCCAGGCTATGAGATTTCTGAG 120
DB 224 TTAATCTGCTGTGCTGGCAACAGGGCTGTAGGGGAGAGACAGATCATCAAGGG 283
121 TTAATCTGCTGTGCTGGCAACAGGGCTGTAGGGGAGAGACAGATCATCAAGGG 180
QY 284 TTGAGTGAAGCCCTCACTCCAGCCCTGGAGGAGACCCCTGTTGGAAGACGGCTA 343
181 TTGAGTGAAGCCCTCACTCCAGCCCTGGAGGAGACCCCTGTTGGAAGACGGCTA 240
DB 344 CTCTGTGGGGGAGAGCTCATGCGCCCAAGATGCTCTGACAGAGACCCACTGCTTAAG 403
241 CTCTGTGGGGGAGAGCTCATGCGCCCAAGATGCTCTGACAGAGACCCACTGCTTAAG 300
QY 404 CCCGCTACATAGTTCACTGGGGGACAGACAACCTCCAGAAAGAGAGGGCTGTGACAG 463
301 CCCGCTACATAGTTCACTGGGGGACAGACAACCTCCAGAAAGAGAGGGCTGTGACAG 360
DB 464 ACCGGAAGCCCACTGAGCTTCCACCCCGGGCTTTCACAAACAGCCTTCCCAACAA 523
361 ACCGGAAGCCCACTGAGCTTCCACCCCGGGCTTTCACAAACAGCCTTCCCAACAA 420
QY 524 GACACCGCAATGACATGCTGGTGAAGATGGATGCGCAGCTGCTCACTACCTGGGCT 583
421 GACACCGCAATGACATGCTGGTGAAGATGGATGCGCAGCTGCTCACTACCTGGGCT 480
DB 584 GTGGAGCCCTCACTCTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 643
481 GTGGAGCCCTCACTCTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 644 GGGTGGGGGAGAGCTGCAAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 703
541 GGGTGGGGGAGAGCTGCAAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
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601 ATGACCATATGAGAGCAAGAGTGTGAAGAGCCCTACCCCGGCAACATCAAGAGACC 660
QY 764 ATGATGTGCTGCAAGCTGCAAGAGGGGAGAGACTCTGCGAGGGTGACTCCGGGGGG 823
|||||

DB 661 ATGATGTGCTGCAAGCTGCAAGAGGGGAGAGACTCTGCGAGGGTGACTCCGGGGGG 720
QY 824 CCTGTGCTGTATACAGAGCTCTTCAAGGATATATCTCTGGGGCCAGATTCGGTGGC 883
DB 721 CCTGTGCTGTATACAGAGCTCTTCAAGGATATATCTCTGGGGCCAGATTCGGTGGC 780
QY 884 ATGACCCGAAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 943
DB 781 ATGACCCGAAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 944 AGATGGAAGAAATGAGCTGAGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCT 1003
DB 841 AGATGGAAGAAATGAGCTGAGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCT 900
QY 1004 TGTGTGTTGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1063
DB 901 TGTGTGTTGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 1064 CATCTTTGGGCTCTCTGAGTACAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1123
DB 961 CATCTTTGGGCTCTCTGAGTACAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1124 GAAATCAGTGAAGCTGATTCAAATTCGCTGGAATATGAGTCTGAGGAAATGACA 1183
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QY 1184 ACACCTGTTGTTCTCTGTTGATCCAGCCCAAGAGAGCTCTGCGCATATATCA 1243
DB 1081 ACACCTGTTGTTCTCTGTTGATCCAGCCCAAGAGAGCTCTGCGCATATATCA 1140
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RESULT 14

US-10-141-698-505
Sequence 505, Application US/10141698
Publication No. US20030134357A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Collin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P33081C187
CURRENT APPLICATION NUMBER: US/10/141, 698
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 505
LENGTH: 1204
TYPE: DNA
ORGANISM: Homo Sapien
US-10-141-698-505

Query Match 92.1% Score 1198; DB 12; Length 1204;
Best Local Similarity 100.0%; Pred. No. 8.8e-312;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 GTTCCGCAATGCAGAGGTTGAGGTGGCTGCGGAGCTGGAAGTCATCGGCGAGAGGCTTC 163
DB 1 GTTCCGCAATGCAGAGGTTGAGGTGGCTGCGGAGCTGGAAGTCATCGGCGAGAGGCTTC 60
QY 164 ACAGCAGCCAAAGAACTGGGGGCGCTCTCCCGCTCCAGGCGCATGAGAAATTCGCGAG 223
DB 61 ACAGCAGCCAAAGAACTGGGGGCGCTCTCCCGCTCCAGGCGCATGAGAAATTCGCGAG 120
QY 224 TTAAATCCTGCTGCTCTGCGCAACAGGGCTTGTAGGGGAGAGACAGATTCATCAAGGGG 283
DB 121 TTAAATCCTGCTGCTCTGCGCAACAGGGCTTGTAGGGGAGAGACAGATTCATCAAGGGG 180
QY 284 TTGAGTGCAGAGCTTCACTCCAGCCCTGGCAGGAGAGCCCTGTTGAGAAAGCGGGCTA 343
DB 181 TTGAGTGCAGAGCTTCACTCCAGCCCTGGCAGGAGAGCCCTGTTGAGAAAGCGGGCTA 240
QY 344 CTCTGTGGGGGAGCGCTCATGCGCCCGCCAGATGGCTCTCAACAGAGCCCAAGCTCCCAAG 403
DB 241 CTCTGTGGGGGAGCGCTCATGCGCCCGCCAGATGGCTCTCAACAGAGCCCAAGCTCCCAAG 300
QY 404 CCCCCTACATAGTTACCTGGGGGAGCACAACCTTCAGAGAGAGAGGGCTGTGAGCAG 463
DB 301 CCCCCTACATAGTTACCTGGGGGAGCACAACCTTCAGAGAGAGAGGGCTGTGAGCAG 360
QY 464 ACCCGGACAGCAGTGAAGTCTTCCCAACCCCGGCTTCAGACAGAGCTCCCAACAAA 523
DB 361 ACCCGGACAGCAGTGAAGTCTTCCCAACCCCGGCTTCAGACAGAGCTCCCAACAAA 420
QY 524 GACCAACCGCAATGACATGCTGTGGAAGATGGGATGCGGAGTCCATCCATCACTGGGT 583
DB 421 GACCAACCGCAATGACATGCTGTGGAAGATGGGATGCGGAGTCCATCCATCACTGGGT 480
QY 584 GTGCGACCCCTCAGCCCTCTCTCAGAGCTGTGTCACTGTGCGGAGCAGAGCTGCTCAATTC 643
DB 481 GTGCGACCCCTCAGCCCTCTCTCAGAGCTGTGTCACTGTGCGGAGCAGAGCTGCTCAATTC 540
QY 644 GGCTGGGGGAGCAGCTCCAGGCGCCCAAGTTAGGCTGCTCAACCTTGGAGTGGCGCAAC 703
DB 541 GGCTGGGGGAGCAGCTCCAGGCGCCCAAGTTAGGCTGCTCAACCTTGGAGTGGCGCAAC 600
QY 704 ATCACCATCATGAGACAGCAGAAAGTGTGGAAGAGGCTACCCGGCAACATCAACAGACAC 763
DB 601 ATCACCATCATGAGACAGCAGAAAGTGTGGAAGAGGCTACCCGGCAACATCAACAGACAC 660
QY 764 ATGAGTGTGCGCAGGCTGCGAGAGAGGGGCAAGAGACTCTGCCAGGGGTACTCCGGGGGC 823
DB 661 ATGAGTGTGCGCAGGCTGCGAGAGAGGGGCAAGAGACTCTGCCAGGGGTACTCCGGGGGC 720
QY 824 CCTGTGCTGTACCAAGTCTCTTCAAGGCAATATCTCTGGGGCCAGGATCCGTGTGCG 883
DB 721 CCTGTGCTGTACCAAGTCTCTTCAAGGCAATATCTCTGGGGCCAGGATCCGTGTGCG 780
QY 884 ATCACCAGCAAGCCTGGTGTCTCAACAGAAAGTCTGAATATGTGAGAGGATTCAGAGAG 943
DB 781 ATCACCAGCAAGCCTGGTGTCTCAACAGAAAGTCTGAATATGTGAGAGGATTCAGAGAG 840
QY 944 ACAGTAGAAGAAATTTAGACTGGACCCACCAAGCCATCAACCTCCATTTCCACT 1003
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DB 901 TGGTGTGCTGCTGCTGCTGCTGTAAATTAAGAAACCTTAAGCCAGAGCCTTACGAA 960
QY 1064 CATTTGTTGGGCTCTCTGAGTACAGAGAGATGCTGCTTAATATCAAACTGGGGTTC 1123
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QY 1124 GAATACAGTGAAGCTGATTCAAATTTCTGCTTGAATATTTGTCACTCTGGGAATGACA 1183
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QY 1184 ACACCTGGTTGTCTCTGTGTATGCCAGACCCCAAGAAAGACGCTCTGGCCATATATCA 1243
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DB 1141 AGTTTCAATTAATATTTGCTTAATAGAAAAAATTTGCTTAATAGAAAAAATTTGCTTA 1198

RESULT 15
US-10-141-702-505
; Sequence 505, Application US/10141702
; Publication No. US20030134358A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P330R1C208
; CURRENT APPLICATION NUMBER: US/10/141, 702
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-141-702-505

Query Match 92.1%; Score 1198; DB 12; Length 1204;
Best Local Similarity 100.0%; Pred. No. 8.8e-312;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 GTTCCGCAATGCAGAGGTTGAGGTGGCTGCGGAGCTGGAAGTCATCGGCGAGAGGCTTC 163
DB 1 GTTCCGCAATGCAGAGGTTGAGGTGGCTGCGGAGCTGGAAGTCATCGGCGAGAGGCTTC 60
QY 164 ACAGCAGCCAAAGAACTGGGGGCGCTCTCCCGCTCCAGGCGCATGAGAAATTCGCGAG 223
DB 61 ACAGCAGCCAAAGAACTGGGGGCGCTCTCCCGCTCCAGGCGCATGAGAAATTCGCGAG 120
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DB 121 TTAAATCCTGCTGCTCTGCGCAACAGGGCTTGTAGGGGAGAGACAGATTCATCAAGGGG 180
QY 284 TTGAGTGCAGAGCTTCACTCCAGCCCTGGCAGGAGAGCCCTGTTGAGAAAGCGGGCTA 343
DB 181 TTGAGTGCAGAGCTTCACTCCAGCCCTGGCAGGAGAGCCCTGTTGAGAAAGCGGGCTA 240
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DB 241 CTCTGTGGGGGAGCGCTCATGCGCCCGCCAGATGGCTCTCAACAGAGCCCAAGCTCCCAAG 300
QY 404 CCCCCTACATAGTTACCTGGGGGAGCACAACCTTCAGAGAGAGAGGGCTGTGAGCAG 463
DB 301 CCCCCTACATAGTTACCTGGGGGAGCACAACCTTCAGAGAGAGAGGGCTGTGAGCAG 360
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QY	584	GTGCACCCCTTACCCTCTCCTCAAGCTGTGTCACTGGTGGACACAGTGGCTCATTTCC	643
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QY	644	GGCTGGGGCAGCAGCTCCAGGCCCGCAGTTAGCGCTCGCTCAACCTTGCGATGCGCCAC	703
Db	541	GGCTGGGGCAGCAGCTCCAGGCCCGCAGTTAGCGCTCGCTCAACCTTGCGATGCGCCAC	600
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Db	601	ATCACCATCATTTGAGCACACAGAGTGTAGAAAGCCTTACCCCGGCAATCAGACAGACC	660
QY	764	ATGGTGTGGCAGCGTGCCAGGAAGGGGGCAAGACCTCTGCGAGGGTGAATCCGGGGGC	823
Db	661	ATGGTGTGGCAGCGTGCCAGGAAGGGGGCAAGACCTCTGCGAGGGTGAATCCGGGGGC	720
QY	824	CCTCGTGTCTGTAAACAGTCTCTTAAAGCAATTATCTCTGGGGCAGAGATCCGTTGCG	883
Db	721	CCTCGTGTCTGTAAACAGTCTCTTAAAGCAATTATCTCTGGGGCAGAGATCCGTTGCG	780
QY	884	ATCACCCGAAGACCGTGGTGTCTACACGAAAGTCTGCAATATGTGGACTGATCCAGAG	943
Db	781	ATCACCCGAAGACCGTGGTGTCTACACGAAAGTCTGCAATATGTGGACTGATCCAGAG	840
QY	944	ACGATGAAGAACAATTAACATGAGGAGACCCACACACACCATCATCCTCCATTTCCACT	1003
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QY	1124	GAATCAGTGAAGACTGGATTCAAATTTGCTCTGAAATATTTGTGACTCTGGGAATGACA	1183
Db	1021	GAATCAGTGAAGACTGGATTCAAATTTGCTCTGAAATATTTGTGACTCTGGGAATGACA	1080
QY	1184	ACACCTGGTTGTCTCTGTGTATCCCAAGCAAGAGACAGTCCCTGGGCATATATACA	1243
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QY	1244	AGGTTTCATTAATATTTGCTTAATGAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTT	1301
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GenCore version 5.1.6
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Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1283.4	98.6	1314	3	US-09-025-059-2 Sequence 2, Appl
2	1271.4	97.7	1192	4	US-09-205-258-189 Sequence 189, App
3	1114.4	85.7	1192	3	US-08-944-483-8 Sequence 8, Appl
4	1063	81.7	1166	3	US-08-944-483-7 Sequence 7, Appl
5	1029.2	79.1	1146	4	US-09-205-258-247 Sequence 247, App
6	673.2	51.7	833	2	US-08-790-137-2 Sequence 2, Appl
7	662.4	50.9	1052	4	US-09-386-642-10 Sequence 10, Appl
8	551.8	42.4	662	4	US-09-702-705-109 Sequence 109, App
9	551.8	42.4	662	4	US-09-736-457-109 Sequence 109, App
10	478.8	36.8	618	4	US-09-280-116-3 Sequence 3, Appl
11	441.8	34.0	472	4	US-09-280-116-136 Sequence 136, App
12	409	31.4	409	4	US-09-702-705-1109 Sequence 1109, App
13	409	31.4	409	4	US-09-736-457-1109 Sequence 1109, App
14	368.4	28.3	406	3	US-08-944-483-6 Sequence 6, Appl
15	262	20.1	262	3	US-08-944-483-5 Sequence 5, Appl
16	250	19.2	250	3	US-08-944-483-4 Sequence 4, Appl
17	237.4	18.2	239	3	US-08-944-483-3 Sequence 3, Appl
18	228	17.5	994	3	US-09-008-271A-19 Sequence 19, Appl
19	224.8	17.3	944	3	US-09-070-526-1 Sequence 1, Appl
20	224	17.2	1049	4	US-09-386-642-9 Sequence 9, Appl
21	196.4	15.1	1570	4	US-09-996-243-308 Sequence 308, App
22	191.4	14.7	825	3	US-09-120-582-1 Sequence 1, Appl
23	188.8	14.5	897	2	US-08-956-267A-1 Sequence 1, Appl
24	187	14.4	1476	2	US-08-824-874-2 Sequence 2, Appl
25	187	14.4	1476	2	US-09-210-084-2 Sequence 2, Appl
26	187	14.4	1476	4	US-09-764-762-2 Sequence 2, Appl
27	182.6	14.0	732	1	US-08-361-395-2 Sequence 2, Appl

28	180.4	13.9	1341	4	US-08-983-075D-6 Sequence 6, Appl
29	180.4	13.9	1358	4	US-08-983-075D-8 Sequence 8, Appl
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31	178.8	13.7	766	3	US-08-767-820A-9 Sequence 9, Appl
32	178.8	13.7	766	3	US-08-622-046B-6 Sequence 6, Appl
33	178.8	13.7	766	3	US-08-622-046B-17 Sequence 17, Appl
34	178.8	13.7	766	3	US-09-100-264-6 Sequence 6, Appl
35	178.8	13.7	766	4	US-08-843-076D-6 Sequence 6, Appl
36	178.8	13.7	822	3	US-09-100-264-8 Sequence 8, Appl
37	178.8	13.7	832	3	US-08-768-859A-5 Sequence 5, Appl
38	178.8	13.7	832	3	US-08-768-859A-20 Sequence 20, Appl
39	178.8	13.7	832	3	US-08-767-820A-5 Sequence 5, Appl
40	178.8	13.7	832	3	US-08-767-820A-20 Sequence 20, Appl
41	178.8	13.7	832	3	US-08-622-046B-4 Sequence 4, Appl
42	178.8	13.7	832	3	US-08-622-046B-15 Sequence 15, Appl
43	178.8	13.7	832	4	US-08-843-076D-4 Sequence 4, Appl
44	178.2	13.7	760	3	US-08-768-859A-7 Sequence 7, Appl
45	178.2	13.7	760	3	US-08-767-820A-7 Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-025-059-2
; Sequence 2, Application US/09025059
; Patent No. 6075136
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,059
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0481 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1314 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGITUT10
; CLONE: 2723646
; US-09-025-059-2
Query Match 98.6%; Score 1283.4; DB 3; Length 1314;
Best Local Similarity 99.9%; Pred. No. 4.2e-315;

Matches 1284; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTTGCTCCACACCTGTGTAGAGGAGAGAGGAGAAAGCCAAAGGAGGACCTA 60
DB 16 CTGCTTGCTCCACACCTGTGTAGAGGAGAGAGGAGAAAGCCAAAGGAGGACCTA 75
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DB 76 ACTGAAACAAACAGCTGGGAGAGAGAGAGATCTGCGCTGGGTCCGAGATGACAG 135
QY 121 GTTGAAGTGGCTGGGAGAGAGAGATCTGCGGAGAGAGATCTGCGAGAGAGAGAG 180
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QY 181 TGGGAGCCGCTCTCTCCCTCCAGAGCATGAGATCTGCAAGTAACTCTGCTGCT 240
DB 196 TGGGAGCCGCTCTCTCCCTCCAGAGCATGAGATCTGCAAGTAACTCTGCTGCT 255
QY 241 GGCACACAGGCTTTAGGAGAGAGAGAGATCATCAAGGGGTTCCAGTGCAGAGCTCA 300
DB 256 GGCACACAGGCTTTAGGAGAGAGAGAGATCATCAAGGGGTTCCAGTGCAGAGCTCA 315
QY 301 CTCCAGAGCTGGGAGAGAGAGCTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGCT 360
DB 316 CTCCAGAGCTGGGAGAGAGAGAGCTGTTGAGAGAGAGAGAGAGAGAGAGAGAGCT 375
QY 361 CATGCCCCAGATGAGCTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTCA 420
DB 376 CATGCCCCAGATGAGCTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTCA 435
QY 421 CCTGGGAGAGACAACTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTCA 480
DB 436 CCTGGGAGAGACAACTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTCA 495
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DB 496 GTCTTCCCCCAGAT 555
QY 541 CATGCTGGTGAAGATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 600
DB 556 CATGCTGGTGAAGATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 615
QY 601 CTCTCAAGCTGTGTCACTGTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 660
DB 616 CTCTCAAGCTGTGTCACTGTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 675
QY 661 CAGCCCCAGATGAGCTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 720
DB 676 CAGCCCCAGATGAGCTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 735
QY 721 CCAGAGTGTGAGT 780
DB 736 CCAGAGTGTGAGT 795
QY 781 GCAGT 840
DB 796 GCAGT 855
QY 841 GTCTCTCAAGAGCTTTATCTCTGGGAGAGAGATCTGTCGATTCACAGAGAGAGT 900
DB 856 GTCTCTCAAGAGCTTTATCTCTGGGAGAGAGATCTGTCGATTCACAGAGAGAGT 915
QY 901 TGTCTACAGAAAGTGTGCAAAATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGATTA 960
DB 916 TGTCTACAGAAAGTGTGCAAAATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGATTA 975
QY 961 GACGTGAGT 1020
DB 976 GACGTGAGT 1035
QY 1021 TCACTGTGTAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 1080
DB 1036 TCACTGTGTAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 1095

QY 1081 GGAATACAGAGAGATGCTGTCACTTAATATCAACCTGGGTTGCAAAATCAATGAGACCTG 1140
DB 1096 GGAATACAGAGAGATGCTGTCACTTAATATCAACCTGGGTTGCAAAATCAATGAGACCTG 1155
QY 1141 GATTCAAATTTGCTTGAATATTTGACTCTGGAGATGACAAACACCTGGTTGTTCTC 1200
DB 1156 GATTCAAATTTGCTTGAATATTTGACTCTGGAGATGACAAACACCTGGTTGTTCTC 1215
QY 1201 TGTGTATCCCAACCCCAAGAGAGCTCTGGCATATATCAAGTTCAATTAATAT 1260
DB 1216 TGTGTATCCCAACCCCAAGAGAGCTCTGGCATATATCAAGTTCAATTAATAT 1275
QY 1261 TGTCTAAATGAAAAAAAAAAAAA 1285
DB 1276 TGTCTAAATGAAAAAAAAAAAAA 1300

RESULT 2
US-09-205-258-189
Sequence 189, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205, 258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048, 885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049, 375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049, 020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049, 019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048, 972

Query Match	97.7%	Score 1271.4	DB 4	Length 1292
Best Local Similarity	99.5%	Pred. No. 4.4e-312		
Matches 1282	Conservative	4	Mismatches 0	Indels 3
				Gaps 1
QY	1	CTGCCTTGCATCAACCTGTCACAGGGGAGAGGGGAGAAAGCCAAAGGAAGGACCTTA	60	
Db	2	CTGCCTTGCATCAACCTGTCACAGGGGAGAGGGGAGAAAGCCAAAGGAAGGACCTTA	58	
QY	61	ACTGAAAACAACAAGCTGGGAGAGCAGAACTGCGCTCGGGTTCCGAGATGACAGAG	120	
Db	59	ACTGAAAACAACAAGCTGGGAGAGCAGAACTGCGCTCGGGTTCCGAGATGACAGAG	118	
QY	121	GTTGAGGTGGCTGGGGGACGTGGAAGTCAATCGGCGAGAGGTTCCACAGCAGCCAAAGAAC	180	
Db	119	GTTGAGGTGGCTGGGGGACGTGGAAGTCAATCGGCGAGAGGTTCCACAGCAGCCAAAGAAC	178	
QY	181	TGGGGCCCCGCTCCGCCCCCTCCAGGGCATTGAGATTCGTGAGTTAACTCCTTGCTCT	240	
Db	179	TGGGGCCCCGCTCCGCCCCCTCCAGGGCATTGAGATTCGTGAGTTAACTCCTTGCTCT	238	
QY	241	GGCAACAAGGGCTTTAGGGGAGAGACAGGATCATAAAGGGTTTCGAGTCAAGCCTCA	300	
Db	239	GGCAACAAGGGCTTTAGGGGAGAGACAGGATCATCAAGGGGTTTCGAGTCAAGCCTCA	298	
QY	301	CTCCCAAGCCTTGGCAGCAGCCTCTTTCGAGAAAGCGGCTACTCTTGGGGCGAGCT	360	
Db	299	CTCCCAAGCCTTGGCAGCAGCCTCTTTCGAGAAAGCGGCTACTCTTGGGGCGAGCT	358	
QY	361	CATCGCCCCAAGATGGCTCCTGAGAGAGACCCACTGCTCAAGCCCGGCTTCAATAGTTCA	420	
Db				

APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLASS, MICHAEL R.


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? COUNTRY: USA
? ZIP: 60064-3500
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/944,483
? FILING DATE:
? CLASSIFICATION: 424
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Becker, Cheryl L.
? REGISTRATION NUMBER: 35,441
? REFERENCE/DOCKET NUMBER: 6183.US.01
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 847/935-1729
? TELEFAX: 847/938-2623
? TELEX:
? INFORMATION FOR SEO ID NO: 7:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1166 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? US-08-944-483-7

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Query Match 81.7%; Score 1063; DB 3; Length 1166;

Best Local Similarity 99.3%; Pred. No. 2,1e-259;

Matches 1096; Conservative 2; Mismatches 3; Indels 3; Gaps 3;

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? 169 ACCAAGGACCTGGGGCCGCTCCCTCCAGGCGATGAGGATTCAGTTAT 228
? 63 AGCCTAGGAACTGGGGCCGCTCCCTCCAGGCGATGAGGATTCAGTTAT 122
? 229 CCTGCTTGTGCGCAACAGGGCTTGTAGGGGAGAGACCAAGATCATCAAGGGTTGA 288
? 123 CTTGCTTGTGCGCAACAGGGCTTGTAGGGGAGAGACCAAGATCATCAAGGGTTGA 182
? 289 GTGCAAGCCTCACTCCAGGCTTGGAGGACGACCTGTTGGAAGAGCGGCTACTCTG 348
? 183 GTGCNAGCCTCACTCCAGGCTTGGAGGACGACCTGTTGGAAGAGCGGCTACTCTG 242
? 349 TGGGGGAGGCTCATCGCCCGCAGATGGCTCTGACAGAGCGCACTGCTCAAGCCCG 408
? 243 TGGGGGAGGCTCATCGCCCGCAGATGGCTCTGACAGAGCGCACTGCTCAAGCCCG 302
? 409 CTACATAGTTCACTGGGGGAGACCAACCTCCAGAGAGAGAGGGCTGTGACAGACCG 468
? 303 CTACATAGTTCACTGGGGGAGACCAACCTCCAGAGAGAGAGGGCTGTGACAGACCG 362
? 469 GACAGCCACTGAGTCTTCCCGACCCCGGCTTCAACAAGACCTCCCAACAAAGACA 528
? 363 GACAGCCACTGAGTCTTCCCGACCCCGGCTTCAACAAGACCTCCCAACAAAGACA 422
? 529 CCGCATATGACATGCTGTGTAAGATGGCATCGCAGTCTGCATCACTGGGGTGTGG 588
? 423 CCGCATATGACATGCTGTGTAAGATGGCATCGCAGTCTGCATCACTGGGGTGTGG 482
? 589 ACCCTCAACCTCTCTCAAGCTGTGTCACTGTGGCAACCACTGCTCATATTTCCGGCTG 648
? 483 ACCCTCAACCTCTCTCAAGCTGTGTCACTGTGGCAACCACTGCTCATATTTCCGGCTG 542
? 649 GGGCAGCAGTCCACCCCAATTTACGCTTGCCTACACCTTGGCATTTGGCCAAATCAC 708
? 543 GGGCAGCAGTCCACCCCAATTTACGCTTGCCTACACCTTGGCATTTGGCCAAATCAC 602
? 709 CATCATTTAGCAGCAGAAATGTGAGACGCGCTACCCCGGCAACATCACAGACCAATG 768
? 603 CATCATTTAGCAGCAGAAATGTGAGACGCGCTACCCCGGCAACATCACAGACCAATG 662

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? 769 GTGTGCCAGCTGCAGAGAGGGGCAAGAGACTCTGCGAGGAGTCCGGGGCCCTCT 828
? 663 GTGTGCCAGCTGCAGAGAGGGGCAAGAGACTCTGCGAGGAGTCCGGGGCCCTCT 722
? 829 GGTCTGTAAACAGTCTCTTCAAGGCAATTAATCTCTGGGGCCAGATCCGTGCGATC 888
? 723 GGTCTGTAAACAGTCTCTTCAAGGCAATTAATCTCTGGGGCCAGATCCGTGCGATC 782
? 889 CCGAAAGCCTGGTGTACAGCAAGTGTGCAATTAATGTGAGTGGATCCAGAGACGAT 948
? 783 CCGAAAGCCTGGTGTACAGCAAGTGTGCAATTAATGTGAGTGGATCCAGAGACGAT 842
? 949 GAAGAACAAATTAGTACGTGAGCCACCCACAGACCCATCACTCCATTTCCACTGGTG 1008
? 843 GAAGAACAAATTAGTACGTGAGCCACCCACAGACCCATCACTCCATTTCCACTGGTG 902
? 1009 TTTGCTCTCTGCTCACTCTGTTAATAAGAACCTTAAGCCAAAGCCCTTACGACATTC 1068
? 903 TTTGCTCTCTGCTCACTCTGTTAATAAGAACCTTAAGCCAAAGCCCTTACGACATTC 962
? 1069 TTTGGGCTCTGCTCACTCTGTTAATAAGAACCTTAATATC-AACCTGGGTTGGA 1127
? 963 TTTGGGCTCTGCTCACTCTGTTAATAAGAACCTTAATATC-AACCTGGGTTGGA 1022
? 1128 TC-AGTAGACCTGATTAATAATTCCTTGAATAATTTGTGACTGTGGAAATGACACA 1186
? 1023 TCNAGTAGACCTGATTAATAATTCCTTGAATAATTTGTGACTGTGGAAATGACACA 1082
? 1187 CCTGTTTCTCTCTGTTAATAAGAACCTTAATATC-AACCTGGGTTGGA 1245
? 1083 CCTGTTTCTCTCTGTTAATAAGAACCTTAATATC-AACCTGGGTTGGA 1142
? 1246 GTTCAATAATTAATTTGCTAATG 1269
? 1143 GTTCAATAATTAATTTGCTAATG 1166

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RESULT 5
US-09-205-258-247
Sequence 247, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
EARLIER FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
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EARLIER APPLICATION NUMBER: 60/048,971
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EARLIER APPLICATION NUMBER: 60/048,964

EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
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EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
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EARLIER APPLICATION NUMBER: 60/048,974
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EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
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EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 247
LENGTH: 1146
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (20)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (35)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (36)
OTHER INFORMATION: n equals a,t,g, or c

FEATURE:
NAME/KEY: SITE
LOCATION: (37)
OTHER INFORMATION: n equals a,t,g, or c
us-09-205-258-247
Query Match 79.1%; Score 1029.2; DB 4; Length 1146;
Best Local Similarity 98.7%; Pred. No. 7.56-251;
Matches 1041; Conservative 4; Mismatches 8; Indels 2; Gaps 1;
OY 237 CTCGCAAGAGGGCTGTAGGGG--AGAGCAAGGATCATCAAGGGGTTCAGTCA 294
DB 87 CTTGGCCACAGGGCTTTAGGGGAGAGACCAGGATCTCAAGGGGTTCAGTCA 146
OY 295 GCGTACTCCAGGCTTGCGAGGAGCCCTTTCAGAAAGCGGCTACTCTGTGGGC 354
DB 147 GCGTACTCCAGGCTTGCGAGGAGCCCTTTCAGAAAGCGGCTACTCTGTGGGC 206
OY 355 GACGCTATCCCGCCAGATGTCTGACAGCAGCCCACTGCTCAAGCCCGCTCAT 414
DB 207 GACGCTATCCCGCCAGATGTCTGACAGCAGCCCACTGCTCAAGCCCGCTCAT 266
OY 415 AGTCACCTGGGGAGGACCACTCCAGAAAGAGAGGGCTGTAGGAGACCGGAGAGC 474
DB 267 AGTCACCTGGGGAGGACCACTCCAGAAAGAGAGGGCTGTAGGAGACCGGAGAGC 326
OY 475 CACTGAGTCTTCCCGCACCCCGGCTTCACACAGCCTCCCAACAAAGACCGCAA 534
DB 327 CACTGAGTCTTCCCGCACCCCGGCTTCACACAGCCTCCCAACAAAGACCGCAA 386
OY 535 TGACATATGTGTGAAGATGGATGCCATGCTTCATCACTGGGCTGTGCACTCT 594
DB 387 TGACATATGTGTGAAGATGGATGCCATGCTTCATCACTGGGCTGTGCACTCT 446
OY 595 CACCCTGCTCAAGCTGTGCTCACTGGGAGGAGGCTGCTTCCGGCTGGGAG 654
DB 447 CACCCTGCTCAAGCTGTGCTCACTGGGAGGAGGCTGCTTCCGGCTGGGAG 506
OY 655 CAGCTCAGCCCCAGTTACGCTGCTCAACCTTCGATGCCCAACATCATCATAT 714
DB 507 CAGCTCAGCCCCAGTTACGCTGCTCAACCTTCGATGCCCAACATCATCATAT 566
OY 715 TGACACCAAGTGTGAAGCCCTACCCGGGCAACATCATCAACACATGTTGTGC 774
DB 567 TGACACCAAGTGTGAAGCCCTACCCGGGCAACATCATCAACACATGTTGTGC 626
OY 775 CAGGTCAGAGAGGGGCAAGGAGCTCTGCGAGGTGATCCGGGGCCCTGCTGCTG 834
DB 627 CAGGTCAGAGAGGGGCAAGGAGCTCTGCGAGGTGATCCGGGGCCCTGCTGCTG 686
OY 835 TAACCAAGTCTTCAAGCATTTATCTCTGGGGCAAGATCCGTGCGATCACCCGAA 894
DB 687 TAACCAAGTCTTCAAGCATTTATCTCTGGGGCAAGATCCGTGCGATCACCCGAA 746
OY 895 GCGTGTGTCTACACGAAAGTCTCAATATGTGATCTGGATCCAGAGACGATGAAGA 954
DB 747 GCGTGTGTCTACACGAAAGTCTCAATATGTGATCTGGATCCAGAGACGATGAAGA 806
OY 955 CAATTAGCTGAGCCACCCACAGCCATCACCTTCATTTCACTGGTGTGGT 1014
DB 807 CAATTAGCTGAGCCACCCACAGCCATCACCTTCATTTCACTGGTGTGGT 866
OY 1015 TCCTGTCTACTGTATATAGAAACCTTAAGCCCAAGCCCTTACGAACTTTTGGG 1074
DB 867 TCCTGTCTACTGTATATAGAAACCTTAAGCCCAAGCCCTTACGAACTTTTGGG 926
OY 1075 CTTCTGAGCTACAGGAGATGCTGTCACTTAATATCAACCTGGGTTCAAAATCACTGA 1134
DB 927 CTTCTGAGCTACAGGAGATGCTGTCACTTAATATCAACCTGGGTTCAAAATCACTGA 986
OY 1135 GACCTGATCAATTTGCTTGAATATTTGATCTGGGATGACACACCTGGTTT 1194
DB 987 GACCTGATCAATTTGCTTGAATATTTGATCTGGGATGACACACCTGGTTT 1046

[illegible]

RESULT 6

US-08-790-137-2
Sequence 2, Application US/08790137
Patent No. 5840871
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: A NOVEL PROSTATE-ASSOCIATED
TITLE OF INVENTION: KALLIKREIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/790,137
FILING DATE: Filed Herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hillings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0195 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 833 base pairs
TYPE: nucleic acid
STANDARDNESS: single
TOPOLOGY: linear
US-08-790-137-2

Query Match	51.7%;	Score 673.2;	DB 2;	Length 833;
Best Local Similarity	95.0%;	Pred. No. 7.1e-161;		
Matches 706; Conservative	0;	Mismatches 28;	Indels 9;	Gaps 1;

QY	264	AGACCAGGATCATCAAGGGGTTCGAGTGCMAACCTCAGTCCAGGCCCTGGCAGGACGCC	323
Db	91	AGTCCCGGATTGTGGAGGCTGGGGTGTTGAGCACATATCCAGCCCTGGCAGGGGGCTC	150
QY	324	TGTTGGAAGAATACGGGCTACTCTGTGTGGGGGAGCGCTCATGCCCCCAATGGCTCCTTA	383
Db	151	TGTACCAAAATACGGGGCTACTCTGTGGGGGAGCACTAATNCCCCTCAATATGGTTCCTTA	210
QY	384	CAGCAGCCCACTGGCTCTCAAGCCCGGCTACATAGTTACACTGGGGGAGCACAACCTCCAGA	443
Db	211	CAGCAGCCCACTGGCTCTCAAGCCCGGCTACATAGTTACACTGGGGGAGCACAACCTCCAGA	270
QY	444	AGGAGGAGGCGCTGTGAGAGCAGAACCCGGACAGCCACTGAATCTCTCCCCACCCCGGCTTCA	503
Db	271	AGGAGGAGGCGCTGTGAGAGCAGAACCCGGACAGCCACTGAATCTCTCCCCACCCCGGCTTCA	330

OY	504	ACAAACAGCCTCCCCCAACAAGACACACCGCAATGACATCATGCTGGTGAAGATGGACTCGC	563
Db	331	ACAAACAGCCTCCCCCAACAAGACACACCGCAATGACATCATGCTGGTGAAGATGGACTCGC	390
OY	564	CAGTCTCATACACCGGGGCTGTGGACGCCCTCAACCCCTCCATCAGCTGTGTACATGCTG	623
Db	331	CAGTCTCATACACCGGGGCTGTGGACGCCCTCAACCCCTCCATCAGCTGTGTACATGCTG	450
OY	624	GCACCAAGCTGCCTCATTTTCCGGCTGGGGGAGCAGCTCCAGCCCCAGTTAACGCTGCCTC	683
Db	451	GCACCAAGCTGCCTCATTTTCCGGCTGGGGGAGCAGCTCCAGCCCCAGTTAACGCTGCCTC	510
OY	684	ACACCTTGCGATGCGCCCAACATCACCATCATTTGAGCACACGAAAGTGTGAAACGCTTACC	743
Db	511	ACACCTTGCGATGCGCCCAACATCACCATCATTTGAGCACACGAAAGTGTGAAACGCTTACC	570
OY	744	CCGGCAACATCACACACACACATGAGTGTGTGCCACGCTGCAGGAAGGGGGCAGAGACTCCT	803
Db	571	CCGGCAACATCACACACACACATGAGTGTGTGCCACGCTGCAGGAAGGGGGCAGAGACTCCT	630
OY	804	GCCAGGATGACATCCGGGGGGCCCTCGTGGTGTAAACAGTCTGTTCAAGGACATTATCTCC	863
Db	631	GCCAGGATGACATCCGGGGGGCCCTCGTGGTGTAAACAGTCTGTTCAAGGACATTATCTCC	690
OY	864	GGGGGACAGATCCGTGTGGATCACCCGAAACCTGGTGTACACAGAAAGTGTGCAAT	923
Db	691	GGGGGACAGATCCGTGTGGATCACCCGAAACCTGGTGTACACAGAAAGTGTGCAAT	750
OY	924	ATGTGACTGTGATCCAGGAGACGATGAAGAACATTGAAGCTGGAC-----CACCC	974
Db	751	ATGTGACTGTGATCCAGGAGACGATGAAGAACATTGAAGCTGGACACCTCCGAAACC	810
OY	975	ACCAACAGCCCATACCTTCATTT	997
Db	811	CCCAACAGCCCATACCTTCATTT	833

RESULT 7

US-09-386-642-10
: Sequence 10, Application US/09386642
: Patent No. 6420157
: GENERAL INFORMATION:
: APPLICANT: Darrow, Andrew
: APPLICANT: Qi, Jensen
: APPLICANT: Andrade-Gordon, Patricia
: TITLE OF INVENTION: Zymogen Activation System
: FILE REFERENCE: ORT-1028
: CURRENT APPLICATION NUMBER: US/09/386,642
: CURRENT FILING DATE: 1999-08-31
: NUMBER OF SEQ ID NOS: 60
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 10
: LENGTH: 1052
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
: OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-10

Query Match	50.98;	Score 662.4;	DB 4;	Length 1052;
Best Local Similarity	98.48;	Pred. No. 4.3e-158;		
Matches 669;	Conservative 0;	Mismatches 11;	Indels 0;	Gaps 0

QY	299	LACHTCCAGCCCTGGCAGGCAAGCCCTGTTTCGAAGACGGGCTACTGTGTGGGGACG	358
	196	CACHTCCAGCCCTGGCAGGCAAGCCCTGTTTCGAAGACGGGCTACTGTGTGGGGACG	255
QY	359	CTCATGCGCCACAGTGGCTCCTGTGACAGAGCCCACTGGCTCAAGCCCGGCTACATAGTT	418
Db	256	CTCATGCGCCACAGTGGCTCCTGTGACAGAGCCCACTGGCTCAAGCCCGGCTACATAGTT	315

OY 419 CACCTGGGGCAGACAACTCTCCAGAAGGAGGGCTGTGACGACACCCGGACAGCCACT 478
DB 316 CACCTGGGGCAGACAACTCTCCAGAAGGAGGGCTGTGACGACACCCGGACAGCCACT 375
OY 479 GAGTCTCTTCCCCCAGCCCGGCTTCAACAACAGCCCTCCCAACAAAGACACCGCAATGAC 538
DB 376 GAGTCTCTTCCCCCAGCCCGGCTTCAACAACAGCCCTCCCAACAAAGACACCGCAATGAC 435
OY 539 ATCATGCTGTGGAAGATGGCATTCGCCATGTCATCACCTGGGCTGTGCGACCCCTCAC 598
DB 436 ATCATGCTGTGGAAGATGGCATTCGCCATGTCATCACCTGGGCTGTGCGACCCCTCAC 495
OY 599 CTCACCTGAGCGTGTGACAGCTGGGACGACGCTGCTCATTTCCGCTGGGGGACGACG 658
DB 496 CTCACCTGAGCGTGTGACAGCTGGGACGACGCTGCTCATTTCCGCTGGGGGACGACG 555
OY 659 TCCAGACCCCAAGTTACGCTGCTCACACCTTGGATGCGCCAAACATCACCATCATTTAG 718
DB 556 TCCAGACCCCAAGTTACGCTGCTCACACCTTGGATGCGCCAAACATCACCATCATTTAG 615
OY 719 CACCAGAAGTGTGAGAACGCTTACCCGCGCAACATCACAGACACCATTGTTGCCAGC 778
DB 616 CACCAGAAGTGTGAGAACGCTTACCCGCGCAACATCACAGACACCATTGTTGCCAGC 675
OY 779 GTGCAGAGAGGGGCAAGGACTCCTGCGAGGGTGAATCCTGGGGGCTCTGCTGTAC 838
DB 676 GTGCAGAGAGGGGCAAGGACTCCTGCGAGGGTGAATCCTGGGGGCTCTGCTGTAC 735
OY 839 CAGTCTCTTCAAGGCATTAATCTCTGCGGCGCAGATCCGTGTGCGATCACCAGAAAGCT 898
DB 736 CAGTCTCTTCAAGGCATTAATCTCTGCGGCGCAGATCCGTGTGCGATCACCAGAAAGCT 795
OY 899 GGTGTCTACAGAAAGTGTGCAATATGTGACGTGATCCAGAGAGAGATGAAGAACAT 958
DB 796 GGTGTCTACAGAAAGTGTGCAATATGTGACGTGATCCAGAGAGAGATGAAGAACAT 855
OY 959 TAGACTGAGCCACCCACCA 978
DB 856 TCTAGACTGACATCACCACCA 875

RESULT 8
US-09-702-705-109
: Sequence 109, Application US/09702705
: Patent No. 6504010
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Lodes, Michael A.
: APPLICANT: Fanger, Gary
: APPLICANT: Vedvick, Tom
: APPLICANT: Carter, Darick
: APPLICANT: Retter, Marc
: APPLICANT: Mannion, Jane
: APPLICANT: Fan, Liqun
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.478C14
: CURRENT APPLICATION NUMBER: US/09/702,705
: CURRENT FILING DATE: 2000-10-30
: NUMBER OF SEQ ID NOS: 1833
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 109
: LENGTH: 662
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-702-705-109

Query Match 42.4%; Score 551.8; DB 4; Length 662;
Best Local Similarity 99.5%; Pred. No. 3,2e-130;
Matches 564; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 672 TAGCCCTGCTCACACCTTGTGATGGCGCAACATCACCATCATTTGAGCACCAGAAAGTGTG 731

DB 14 TAGCCCTGCTCACACCTTGTGATGGCGCAACATCACCATCATTTGAGCACCAGAAAGTGTG 73
OY 732 AGAAGCCTTACCCCGGCAACATCACAGACACCATGATGTGTGCCAGGTGAGAGAGG 791
DB 74 AGAAGCCTTACCCCGGCAACATCACAGACACCATGATGTGTGCCAGGTGAGAGAGG 133
OY 792 GCAAGGACTCTGCCAGGGTACTCTCCGGGGCCCTGTGCTGTAAACAGTCTTTAG 851
DB 134 GCAAGGACTCTGCCAGGGTACTCTCCGGGGCCCTGTGCTGTAAACAGTCTTTAG 193
OY 852 GCATTATCTCTGGGGCCAGGATCCGTGTGATGACCCGGAAGCCGTGTCTACAG 911
DB 194 GCATTATCTCTGGGGCCAGGATCCGTGTGATGACCCGGAAGCCGTGTCTACAG 253
OY 912 AAGTGTCAATATGTGACTGATTCAGAGAGAGATGAAGAACATTTAGACTGAGCCA 971
DB 254 AAGTGTCAATATGTGACTGATTCAGAGAGAGATGAAGAACATTTAGACTGAGCCA 313
OY 972 CCCACACAGCCCATCACCTTCATTTCCACTTGTGTGTGTTCTGTTCTGTTA 1031
DB 314 CCCACACAGCCCATCACCTTCATTTCCACTTGTGTGTGTTCTGTTCTGTTA 373
OY 1032 ATAGAAACCTTAAGCCAAAGACCTCTACGAACATTTCTGGGCTCCTGGACTACAG 1091
DB 374 ATAGAAACCTTAAGCCAAAGACCTCTACGAACATTTCTGGGCTCCTGGACTACAG 433
OY 1092 GATGCTGTACTTAATATCAACCTGGGGTTGAAATCAGTACAGCTGTGAAATTC 1151
DB 434 GATGCTGTACTTAATATCAACCTGGGGTTGAAATCAGTACAGCTGTGAAATTC 493
OY 1152 TGCCCTTGAATATGTGACTCTGGGATGACAAACCTGTTTCTCTGTATGCC 1211
DB 494 TGCCCTTGAATATGTGACTCTGGGATGACAAACCTGTTTCTCTGTATGCC 553
OY 1212 CAGCCCC-AAAGACAGCTCTGGCACT 1237
DB 554 CAGCCCCAAAGACAGCTCTGGCACT 580

RESULT 9
US-09-736-457-109
: Sequence 109, Application US/09736457
: Patent No. 6509448
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Lodes, Michael A.
: APPLICANT: Fanger, Gary
: APPLICANT: Vedvick, Tom
: APPLICANT: Carter, Darick
: APPLICANT: Retter, Marc
: APPLICANT: Mannion, Jane
: APPLICANT: Fan, Liqun
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.478C15
: CURRENT APPLICATION NUMBER: US/09/736,457
: CURRENT FILING DATE: 2000-12-13
: NUMBER OF SEQ ID NOS: 1864
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 109
: LENGTH: 662
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-736-457-109

Query Match 42.4%; Score 551.8; DB 4; Length 662;
Best Local Similarity 99.5%; Pred. No. 3,2e-130;
Matches 564; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 672 TAGCCCTGCTCACACCTTGTGATGGCGCAACATCACCATCATTTGAGCACCAGAAAGTGTG 731

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Db 14 TAGGCTGCTTACACCTTGGCATGCGCCACATCATCATGAGACCCAGAAAGTGG 73
QY 732 AGAAGCCCTACCCCGGCAACATCACAGACACCATGATGTCGCCAGCCGAGGAAAGGG 791
Db 74 AGAAGCCCTACCCCGGCAACATCACAGACACCATGATGTCGCCAGCCGAGGAAAGGG 133
QY 732 GCAAGGACTCTGTCAGAGGTGACTCCGGGGGCCCTGTGTTGTAACAGTCTCTTCAAG 851
Db 134 GCAAGGACTCTGTCAGAGGTGACTCCGGGGGCCCTGTGTTGTAACAGTCTCTTCAAG 193
QY 852 GATATATCTCTGCGGGCCAGAGATCCGTGTGCGATACCCGAAAGCCTGGTGTCTACAGA 911
Db 194 GATATATCTCTGCGGGCCAGAGATCCGTGTGCGATACCCGAAAGCCTGGTGTCTACAGA 253
QY 912 AAGTGTCAATATGTGAGCTGATTCAGAGACAGTGAAGAATTTAGACTGGAGCCA 971
Db 254 AAGTGTCAATATGTGAGCTGATTCAGAGACAGTGAAGAATTTAGACTGGAGCCA 313
QY 972 CCCACACAGCCCATCACCCCTCATTTCCACTTGGTGTGTTGTTCTCTTCACTGTGTA 1031
Db 314 CCCACACAGCCCATCACCCCTCATTTCCACTTGGTGTGTTGTTCTCTTCACTGTGTA 373
QY 1032 ATAAAGAAACCCCTAACGCAAGACCCCTCTACGAACATTTCTTGGGCTCCTGGACTACAGA 1091
Db 374 ATAAAGAAACCCCTAACGCAAGACCCCTCTACGAACATTTCTTGGGCTCCTGGACTACAGA 433
QY 1092 GATGCTGCTACTTAATTAATCAACCTGCGGTTGGAATCAGTGAAGCTGGATTCAAAATTC 1151
Db 434 GATGCTGCTACTTAATTAATCAACCTGCGGTTGGAATCAGTGAAGCTGGATTCAAAATTC 493
QY 1152 TGCCCTGAAATATTTGTGACTCTGGGAATGACAAACCTGGTTGTTCTCTGTGTATCCC 1211
Db 494 TGCCCTGAAATATTTGTGACTCTGGGAATGACAAACCTGGTTGTTCTCTGTGTATCCC 553
QY 1212 CAGCCCC-AAAGACAGCTCTGGCCAT 1237
Db 554 CAGCCCCAAAGACAGCTCTGGACCT 580
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RESULT 10
US-09-280-116-3
; Sequence 3, Application US/09280116A
; Patent No. 631427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: trypsin-like serine proteases
US-09-280-116-3
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Query Match 36.8%; Score 478.8; DB 4; Length 618;
Best Local Similarity 90.8%; Pred. No. 9,1e-112;
Matches 590; Conservative 0; Mismatches 22; Indels 38; Gaps 6;
Db 337 GCGGCTACTGCTGGGGGAGAGCTCATGCCCCAGATGGCTCTGACAGACAGCCACATG 396
1 GCGGCTACTGCTGGGGGAGAC-CTCATG-CTTCAGATGGCTCTGACAGACAGCCACATG 58
QY 397 CCTCAAGCCCGCTCAATAGTTACCTGAGGAGACAACTTCAGAAAGAGAGAGGCTG 456
Db 59 CCTCAAGCCCGCTCAATAGTTACCTGAGGAGACAACTTCAGAAAGAGAGAGGCTG 118
QY 457 TGAGCAGACCCGAGACAGCACTGAGTCTTCCCAACCCCGGCTTCACACACAGCCTCC 516
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Db 119 TGAGCAGACCCCGAGACGCGCATGAGTCTTCCCGCCCGCGGCTTCACACAGCCTCCC 178
QY 517 CAACAAAGACCAACCGAATGACATCATGCTGGGAAGATGGATGCCAGT-CTCATA 575
Db 179 CAACAAAGACCAACCGAATGACATCATGCTGGGAAGATGGATGCCAGTCTCATA 238
QY 576 CCTGGCTGTGGACCCCTCACCCCTCTCCTCAAGCTGTGTCACTGTGTGACACAGCTGCC 635
Db 239 CCTGGCTGTGGACCCCTCACCCCTCTCCTCAAGCTGTGTCACTGTGTGACACAGCTGCC 298
QY 636 TCATTTCCGGCTGGGGCAGACAGTCCAGGCCCCAGTTACGCTGCTCAACCTTGCAT 695
Db 299 TCATTTCCGGCTGGGGCAGACAGTCCAGGCCCCAGTTACGCTGCTCAACCTTGCAT 358
QY 696 GGGCCAACTCAACCATATTGAGACCCAGAAAGTGTGAGAAACCCCTACCCCGGCAATCA 755
Db 359 GGGCCAACTCAACCATATTGAGACCCAGAAAGTGTGAGAAACCCCTACCCCGGCAATCA 418
QY 756 CAGACACCATGGTGTGTGCGCAGCTGACAGAAAGGGGGCAAGGACTCTGCCAGGGTACT 815
Db 419 CAGACACCATGGTGTGTGCGCAGCTGACAGAAAGGGGGCAAGGACTCTGCCAAGTCTTT 478
QY 816 CCGGGGGCCCTCTGTGTGTAACAGTCTCTTCAAGGCATTAATCTCTGGGG--CCAGGA 873
Db 479 C-----AAAGGCATTAATCTCTGGGGCCAGGAC 507
QY 874 TCCGTGTGCGATCACCCGAAAGCCTGCTGTACACAGAAAGTGTGCAATTAATGTGACAG 933
Db 508 TCCGTGTGCGATCACCCGAAAGCCTGCTGTCTACAGAAAGTGTGCAATTAATGTGACAG 567
QY 934 GATCCAGGA--GACGATGAAGAAATTAAGTGTGACGCCACCCACACACAG 981
Db 568 GATCCAGGAAGACGATTAAGAAATTAAGTGTGACGCCACCAACCAACAAAG 617
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RESULT 11
US-09-280-116-136
; Sequence 136, Application US/09280116A
; Patent No. 631427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 136
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: trypsin-like serine proteases
US-09-280-116-136
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Query Match 34.0%; Score 441.8; DB 4; Length 472;
Best Local Similarity 99.1%; Pred. No. 1,8e-102;
Matches 465; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
Db 69 CAACAAAGCTGGAGAGAGA-GGAATCTGCGCTCGGGTTCGCGAGATGCA-GAGGTGAG 126
Db 4 CAACAAAGCTGGAGAGAGAGCAAGAAATCTCGGCTCGGTTCCGCAAGATGCAAGAGTTGAG 63
QY 127 GGGGCTGGGAGCTGAATCATGCGGGGAGAGCTGTCAACAGACAGCAAGAAACCTGGGCT 186
Db 64 GTGGCTGGGAGCTGAATCATGCGGGGAGAGGTTCAACAGACAGCAAGAAACCTGGGCT 123
QY 187 CCGCTCTCCCTCCCTCAAGGACATGAGATTTCTGCAAGTTAATCTGCTGCTGTGGCAAC 246
Db 124 CCGCTCTCCCTCCCTCCAGGACATGAGATTTCTGCAAGTTAATCTGCTGCTGTGGCAAC 183
QY 247 AGGCTTGTAGGGGAGAGACAGATCATCAAGGGGTTGAGTGCACAGCCTCACTCCA 306
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APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESS: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-944-483-6

Query Match      28.3%: Score 368.4: DB 3: Length 406:
Best Local Similarity 99.0%: Pred. No. 6.2e-84:
Matches 402: Conservative 0: Mismatches 1: Indels 3: Gaps 3:

QY 867 GCCAGATCCGTCGATGCAACCCGAAAGCCGTGTCTACAGAAAGTCTCAATATG 926
DB 406 GCCAGATCCGTCGATGCAACCCGAAAGCCGTGTCTACAGAAAGTCTCAATATG 347
QY 927 TGGACTGATCCAGAGCATGAAGAAATTAAGTGGACCCACCCACAGCCCAT 986
DB 346 TGGACTGATCCAGAGCATGAAGAAATTAAGTGGACCCACCCACAGCCCAT 287
QY 987 CACCTCATTTCCCTGCTGTTGTTGTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1046
DB 286 CACCTCATTTCCCTGCTGTTGTTGTTCTCTCTCTCTCTCTCTCTCTCTCTCT 227
QY 1047 CCAAGACCTCTACAGACATTTCTTTGGCTCCCTGAGTACAGAGATGCTCTACTTAA 1106
DB 226 CCAAGACCTCTGCAACATTTCTTTGGCTCCCTGAGTACAGAGATGCTCTACTTAA 167
QY 1107 TAATC-AACTGGGGTGTGAATC-AGTGAAGCTGGAATCAATTTGCTTGAATAT 1164
DB 166 TAATCAGAACTGGGGTGTGAATC-AGTGAAGCTGGAATCAATTTGCTTGAATAT 107
QY 1165 TGTGCTCTGGGAATGACAAACCTGGTTGTCTCTGTGATCCCAAGCCC-AAAGA 1223
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DB 106 TGTGACTGTGGGAATGACAAACCTGGTTGTCTCTCTGTGATCCCAAGCCCGAAGA 47
QY 1224 CAGCTCTGGCCCATATATCAAGTTTCAATTAATTTGCTAAATG 1269
DB 46 CAGCTCTGGCCCATATATCAAGTTTCAATTAATTTGCTAAATG 1
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RESULT 15
US-08-944-483-5
Sequence 5, Application US/08944483
Patent No. 6232456
GENERAL INFORMATION:
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESS: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-944-483-5

Query Match      20.1%: Score 262: DB 3: Length 262:
Best Local Similarity 100.0%: Pred. No. 4.1e-57:
Matches 262: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 734 AACGCTACCCCGGGAACATCAACACACACATGATGTCAGGAGTGAGGAAGGGGC 793
DB 1 AACGCTACCCCGGGAACATCAACACACACATGATGTCAGGAGTGAGGAAGGGGC 60
QY 794 AAGGACTCCTGCGAGGAGTCCGCGGGCCCTGTGCTGTAAACAGTCTCTCAAGC 853
DB 61 AAGGACTCCTGCGAGGAGTCCGCGGGCCCTGTGCTGTAAACAGTCTCTCAAGC 120
QY 854 ATTAATCTCTGGGGCCAGGATCCGTGTGATCACCAGAAACCTGGTGTCTACAGAAA 913
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Db	181	GTCTGCAAAATATGTGACTGTGATCCAGAGAGATGAACAACAATTAGACTGTGACCCACC	240
QY	974	CACGACAGCCGATCACCTTCCA	995
Db	241	CACGACAGCCGATCACCTTCCA	262

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-09-856-320A-1

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 segs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1301	100.0	1301	21	CDNA encoding huma
2	1283.4	98.6	1314	21	CDNA encoding huma
3	1271.4	97.7	1292	22	Human secreted pro
4	1223	94.0	1335	21	Nucleotide sequenc
5	1198	92.1	1304	21	Human PRO1279 (UNQ
6	1198	92.1	1204	22	Human CDNA sequenc
7	1198	92.1	1204	22	DNA encoding prote
8	1198	92.1	1204	24	Human angiotensin

9	1198	92.1	1204	24	ABL88175	Human PRO1279 CDNA
10	1198	92.1	1204	24	ABR33628	CDNA encoding huma
11	1198	92.1	1204	25	ACA03855	CDNA encoding huma
12	1198	92.1	1204	25	ACA04276	Human CDNA encodin
13	1198	92.1	1204	25	ABX89393	DNA encoding novel
14	1183	90.9	1186	24	ABR92131	Prostate cancer-as
15	1183	90.9	1186	25	ABR76468	Lung cancer-associ
16	1150	88.4	1158	20	AAZ26239	CAS12 derived fro
17	1114.4	85.7	1192	22	AAJ14842	Human PS13 gene c
18	1108.8	85.2	1191	22	AAK97777	Extended human sec
19	1106	85.0	1106	20	AAZ2638	CAS12 nucleotide
20	1063	81.7	1166	22	AAJ14841	Human PS13 consen
21	1039.4	79.9	1164	24	ABR51683	DNA encoding huma
22	1029.2	79.1	1146	20	AAV84589	Human secreted pro
23	1029.2	79.1	1146	20	AAV84589	Human secreted pro
24	758.6	58.3	934	21	AAA61765	CDNA encoding huma
25	673.2	51.7	833	19	AAV42925	DNA encoding huma
26	663.4	51.0	1323	21	AAA61764	CDNA encoding huma
27	662.4	50.9	1052	21	AAK87798	Activation constu
28	662.4	50.9	1052	22	AAV52770	Nucleotide sequenc
29	565.6	43.5	762	21	AAH31050	Human colon cancer
30	565.6	43.5	762	21	AAH31051	Human colon cancer
31	551.8	42.4	662	22	AAV68191	Human lung tumour
32	551.8	42.4	662	24	ABR38102	CDNA encoding clon
33	551.8	42.4	662	25	ACA10431	Human lung cancer-
34	551.8	42.4	662	25	ABX93882	Lung cancer therap
35	478.8	36.8	618	24	ABR30233	Human G-protein-co
36	456.2	35.1	502	24	ABL86864	Human ovarian canc
37	441.8	34.0	472	24	ABR30366	Human G-protein-co
38	409	31.4	409	24	ABR39071	Human G-protein-co
39	409	31.4	409	25	ACA11400	Human lung adenoca
40	409	31.4	409	25	ACA02586	Lung cancer therap
41	404.2	31.1	417	24	ABL80919	Human ovarian canc
42	369	28.4	391	24	ABL65887	Lung cancer relat
43	369	28.4	391	24	ABL67873	Ovary cancer relat
44	369	28.4	391	24	ABL69671	Prostate cancer re
45	369	28.4	391	24	ABL80912	Human ovarian canc

ALIGNMENTS

RESULT 1	AAA61763	CDNA: 1301 BP.
ID	AAA61763	standard; CDNA: 1301 BP.
AC	AAA61763;	
XX	23-OCT-2000	(first entry)
DT	23-OCT-2000	(first entry)
DE	CDNA encoding human serine protease BSSP6 (hBSSP6) SEQ ID NO.1.	
XX	BSSP6; serine protease; human; hBSSP6; mouse; mBSSP6; brain;	
KW	diagnostic marker; antibody; transgenic animal; Alzheimer's disease;	
KW	epilepsy; cancer; inflammation; infertility; pancreatitis;	
KW	prostatic hypertrophy; ss.	
OS	Homo sapiens.	
XX		
PN	WO200031257-A1.	
XX		
PD	02-JUN-2000.	
XX		
PF	19-NOV-1999;	99WO-JP06476.
XX		
PR	20-NOV-1998;	98JP-0347802.
XX		
PA	(FUSO) FUSO PHARM IND LTD.	
XX		
PI	Uemura H, Okui A, Komlinami K, Yamaguchi N, Mitsui S;	
XX		
WPI	2000-400067/34.	
DR	P-PSDB; AAB11712.	

XX Serine protease BSSP6, useful in detecting homologs, mutants and
PT polymorphic variants as markers for diagnosis of Alzheimer's disease,
PT epilepsy, cancer, inflammation, infertility and prostate hypertrophy,
PT using blood or other tissues

PS Claim 2; Page 67-69; 94pp; Japanese.

XX The invention relates to novel serine proteases designated BSSP6
XX (AA61712-B11714), and to nucleic acids encoding them (AA61763-AA1765).
CC The invention also relates to vectors and transformants comprising BSSP6
CC nucleic acids; transgenic animals in which the expression level of BSSP6
CC can be varied; and an MBSP6 knockout mouse. The invention additionally
CC encompasses anti-BSSP6 antibodies and methods of production of such
CC antibodies, methods of BSSP6 detection using the antibodies, and the
CC use of BSSP6 proteins or fragments as diagnostic markers for certain
CC medical conditions. Nucleotides encoding BSSP6 were initially
CC isolated in a human brain cDNA library using degenerate PCR primers
CC (AA61795-AA1796) based on conserved regions of serine proteases. The
CC BSSP6 serine proteases and nucleotides encoding them are useful in
CC detecting homologues, mutants and polymorphic variants in biological
CC samples (e.g., blood, urine, brain, prostate gland, placenta, testis
CC and spleen) as diagnostic markers for conditions such as Alzheimer's
CC disease, epilepsy, cancer, inflammation, infertility and prostatic
CC hypertrophy. Sequences AA61763 and AA61765 represent cDNAs encoding
CC human BSSP6 variants (hBSSP6), and sequence AA61764 represents cDNA
CC encoding murine BSSP6 (mBSSP6).

XX Sequence 1301 BP; 332 A; 387 C; 330 G; 252 T; 0 other;

Query Match 100.0%; Score 1301; DB 21; Length 1301;
Best Local Similarity 100.0%; Pred. No. 3e-229;

Matches 1301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTCTCTCACACCTGTGTGAGGAGAGAGGAGAAAGCCAGAGAGGAGACTA 60
DB 1 CTGCTTCTCTCACACCTGTGTGAGGAGAGAGGAGAGAAAGCCAGAGAGGAGACTA 60
QY 61 ACTGAAAAAACAAG 120
DB 61 ACTGAAAAAACAAG 120
QY 121 GTTGAAGGTGGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 121 GTTGAAGGTGGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 181 TGGGGCCCGCTCTCCCTCCCTCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 181 TGGGGCCCGCTCTCCCTCCCTCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 241 GGCACAGAGGCTTGTAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 241 GGCACAGAGGCTTGTAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 301 CTCCAGAGGCTTGTAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 301 CTCCAGAGGCTTGTAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 CATGCCCCCAGATGAGTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 361 CATGCCCCCAGATGAGTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 CTTGGGGAGAGACACTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 421 CTTGGGGAGAGACACTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 481 GTCTTCCCGACCGGCTTCAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 481 GTCTTCCCGACCGGCTTCAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 CATGCTGTGAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 541 CATGCTGTGAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600

QY 601 CTCTCAGAGCTGTGTGACTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 601 CTCTCAGAGCTGTGTGACTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 CAGCCCCAGTTAGAGCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 661 CAGCCCCAGTTAGAGCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 CCAGAGAGTGAAG 780
DB 721 CCAGAGAGTGAAG 780
QY 781 GCAG 840
DB 781 GCAG 840
QY 841 GTCTTCTCAAGAGATTTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 841 GTCTTCTCAAGAGATTTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 901 TGTCTACAG 960
DB 901 TGTCTACAG 960
QY 961 GACTGAG 1020
DB 961 GACTGAG 1020
QY 1021 TCTACTGTTTAAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
DB 1021 TCTACTGTTTAAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1081 GAGCTACAG 1140
DB 1081 GAGCTACAG 1140
QY 1141 GATTCAAAATTTGCTTGAATTAATTAATTAATTAATTAATTAATTAATTA 1200
DB 1141 GATTCAAAATTTGCTTGAATTAATTAATTAATTAATTAATTAATTAATTA 1200
QY 1201 TGTGTATCCCGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
DB 1201 TGTGTATCCCGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
QY 1261 TGTCTAAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1301
DB 1261 TGTCTAAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1301

RESULT 2
AAZ30222
ID AAZ30222 standard; cDNA; 1314 BP.

XX AAZ30222;

DT 11-FEB-2000 (first entry)

DE cDNA encoding a human prostate-associated serum protease (PRASP).

KW Human; prostate-associated serum protease; PRASP; neuropsin; PSA;

KW Inocyte clone 2733646; reproductive disorder; cancer;

KW abnormal prolactin production; infertility; tubal disease;

KW ovulatory defect; endometriosis; polycystic ovary syndrome;

KW autoimmune disorder; ectopic pregnancy; breast cancer;

KW abnormal spermatogenesis; testicular cancer; adenocarcinoma; leukemia;

XX Lymphoma; melanoma; myeloma; sarcoma; teratocarcinoma; ss.

XX Homo sapiens.

XX Key location/Qualifiers
FH 128..976
FT CDS /*tag= a

FT misc-feature /product- "prostate-associated serum protease"
FT 146..181 /tag- b
FT /note- "these nucleotides are separately claimed
FT misc-feature 344..382 under claim 10"
FT /tag- c
FT /note- "these nucleotides are separately claimed
FT misc-feature 551..589 under claim 10"
FT /tag- d
FT /note- "these nucleotides are separately claimed
FT under claim 10"
XX WO941387-A2.
XX 19-AUG-1999.
XX 05-FEB-1999; 99WO-US02571.
XX 17-FEB-1999; 98US-0025059.
XX (INCYTE PHARM INC.
XX Tang YT, Corley NC, Guegler KJ;
XX WPI; 2000-012993/01.
XX P-PSDB; AAY43636.
XX New prostate-associated serum protease and polynucleotides which
XX identify and encode PRASP, useful for treating reproductive disorders
XX and cancer
XX
XX Claim 7: Fig 1A-D; 67pp; English.
XX
XX The present sequence encodes a human prostate-associated serum protease
XX (PRASP). The protein shows homology to neutropin, a brain-specific
XX protease in mice, and PSA, a prostate-specific protease in humans.
XX Nucleic acids encoding PRASP were first identified in Incyte clone
XX 272346 from the lung tumour cDNA library. Pharmaceutical compositions
XX containing PRASP, or antibodies to PRASP, and mimetics, agonists,
XX antagonists or inhibitors of PRASP, are used for treating or preventing
XX a reproductive disorder or cancer. Examples of reproductive disorder
XX include, abnormal prolactin production, infertility, tubal disease,
XX ovulatory defects, endometriosis, polycystic ovary syndrome, autoimmune
XX disorders, ectopic pregnancy, breast cancer, abnormal spermatogenesis
XX and testicular cancer. Examples of cancers which may be treated or
XX prevented include adenocarcinoma, leukemia, lymphoma, melanoma,
XX sarcoma, teratocarcinoma, and cancers of the adrenal gland, bladder,
XX bone, bone marrow, brain, breast, cervix, penis, prostate, salivary
XX glands, skin, spleen, testis, thymus, thyroid and uterus. A vector
XX capable of expressing PRASP or an agonist which modulates the activity of
XX PRASP may be administered to treat or prevent a reproductive disorder or
XX cancer.
XX
XX Sequence 1314 BP; 320 A; 400 C; 337 G; 257 T; 0 other;
XX
XX Query Match 98.6%; Score 1283.4; DB 21; Length 1314;
XX Best Local Similarity 99.9%; Pred. No. 4.9e-226;
XX Matches 1284; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 181 TGGGCGCCGCTCCCTCCCTCCAGGCGCATGAGATTCGTGACGTATATCCGTGCTCT 240
DB 196 TGGGCGCCGCTCCCTCCCTCCAGGCGCATGAGATTCGTGACGTATATCCGTGCTCT 255
QY 241 GGCACAGGGCTTTGAGGGGAGAGACAGGATCATCAAGGGTTGAGTGCAGGCTTA 300
DB 256 GGCACAGGGCTTTGAGGGGAGAGACAGGATCATCAAGGGTTGAGTGCAGGCTTA 315
QY 301 CTCACAGCCCTGAG 360
DB 316 CTCACAGCCCTGAG 375
QY 361 CATCGCCCGCAGATGCTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 376 CATCGCCCGCAGATGCTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 435
QY 421 CCTGGGGGAG 480
DB 436 CCTGGGGGAG 495
QY 481 GTCTTCCCGCAG 540
DB 496 GTCTTCCCGCAG 555
QY 541 CATCTGTGAG 600
DB 556 CATCTGTGAG 615
QY 601 CTCCTCAGCGCTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 616 CTCCTCAGCGCTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 675
QY 661 CAGCCCGCAGTACGCTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 676 CAGCCCGCAGTACGCTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 735
QY 721 CCAGAGAGTGAAG 780
DB 736 CCAGAGAGTGAAG 795
QY 781 GGAGAGAGGGGAG 840
DB 796 GGAGAGAGGGGAG 855
QY 841 GTCTTCAAGCATTTATCTCTGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 856 GTCTTCAAGCATTTATCTCTGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 915
QY 901 TGTCTACAGATTA 960
DB 916 TGTCTACAGATTA 975
QY 961 GAGTGGATTA 1020
DB 976 GAGTGGATTA 1035
QY 1021 TCACTCTGTATTAAG 1080
DB 1036 TCACTCTGTATTAAG 1095
QY 1081 GGAGTACAGATTA 1140
DB 1096 GGAGTACAGATTA 1155
QY 1141 GATTCAGATTA 1200
DB 1156 GATTCAGATTA 1215
QY 1201 TGTGTATCCCGAG 1260
DB 1216 TGTGTATCCCGAG 1275
QY 1261 TGTGTATCCCGAG 1285

Db 1276 TGCTTAATGAAAAAAAAAAAAA 1300

RESULT 3

ABAB3372
ID ABA83372 standard; cDNA; 1292 BP.

AC ABA83372:

DT 07-FEB-2002 (first entry)

DE Human secreted protein gene 179 SEQ ID NO:189.

Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV; dermatological; immunosuppressive; antiinflammatory; immunostimulant; cytosolic; cardiant; vascular; anti-angiogenic; ophthalmological; neuroprotective; nontropic; anticonvulsant; antialzheimers; vulnery; antiparkinsonian; antitubercular; gene therapy; vaccine; immune disorder; multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer; human immunodeficiency virus; hyperproliferative disorder; wound healing; Gaucher's disease; cardiovascular disease; Sclimtar syndrome; Chemotaxis; Chaga's cardiomyopathy; coronary arteriosclerosis; angiogenic disorder; corneal graft neovascularisation; diabetic retinopathy; regeneration; neurological disorder; Huntington's chorea; Alzheimer's disease; Parkinson's disease; infectious disease; ss.

OS Homo sapiens.

PN WO200162891-A2.

PD 30-AUG-2001.

FE 21-FEB-2001; 2001WO-US05614.

PR 24-FEB-2000; 2000US-184836P.

PR 29-MAR-2000; 2000US-193170P.

XX (HUMA-) HUMAN GENOME SCI INC.

PI N1 J, Ebner R, Lafleur DM, Moore PA, Olsen HS, Rosen CA;

PI Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;

PI Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferris AM, Fan P;

PI Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G;

PI Zeng Z, Greene JM;

XX WPI: 2001-625724/72.

DR P-PSDB; ABB50479.

XX Claim 1; Page 1032; 1533pp; English.

CC ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted
CC proteins (I) and polynucleotide (II) sequences. (I) and (II) have various
CC activities based on the tissues and cells the genes are expressed in.
CC Example of these activities include: immunomodulatory; antisclerotic;
CC dermatological; immunosuppressive; antiinflammatory; immunostimulant;
CC anti-HIV; cytosolic; cardiant; anti-angiogenic; ophthalmological;
CC neuroprotective; nontropic; anticonvulsant; antialzheimers; vascular;
CC antiparkinsonian; antitubercular; and vulnery. (I) and (II) can be used
CC in gene therapy and vaccine production. (I) and (II) can be used in the
CC prevention, diagnosis and treatment of immune disorders (e.g. multiple
CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus
CC (HIV) infections), hyperproliferative disorders (e.g. cancers and
CC Gaucher's cardiomyopathy and coronary arteriosclerosis), angiotonic
CC disorders (e.g. corneal graft neovascularisation and diabetic
CC retinopathy), neurological disorders (e.g. Huntington's chorea,
CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or
CC for promoting wound healing, regeneration and/or chemotaxis. ABA83185 to

CC ABA83193 and ABB50300 represent sequences used in the exemplification of
CC the present invention.
XX
SQ Sequence 1292 BP; 319 A; 387 C; 329 G; 253 T; 4 other;

Query Match 97.7%; Score 1271.4; DB 22; Length 1292;
Best Local Similarity 99.5%; Pred. No. 7.8e-224;
Matches 1282; Conservative 4; Mismatches 0; Indels 3; Gaps 1;

1 CTGCTGCTGCTCCACCTGCTCAGGGAGAGGGAGGAAGGCAAGGAGGACCTA 60
2 CTGCTGCTGCTCCACCTGCTCAGGGAGAGAGG---GGAAGGCAAGGAGGACCTA 58
61 ACTGAAACAAACAGCTGGGAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCT 120
59 ACTGAAACAAACAGCTGGGAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 118
121 GTTAGAGTGGTGGGAGCTGGAAGTATCGGGAGAGGCTCTCAGAGCAAGCAAGAAC 180
119 GTTAGAGTGGTGGGAGCTGGAAGTATCGGGAGAGGCTCTCAGAGCAAGCAAGAAC 178
181 TGGGGCCCGCTCTCCCTCCAGGCAATGAGATCTGCAATTAATCTGCTGCTCT 240
179 TGGGGCCCGCTCTCTCCCTCCAGGCAATGAGATCTGCAATTAATCTGCTGCTCT 238
241 GGCAACAGGCTTGTAGGGGAGAGACAGGATCATCAAGGCTTCAGATGCAAGCTCTA 300
239 GGCAACAGGCTTGTAGGGGAGAGACAGGATCATCAAGGCTTCAGATGCAAGCTCTA 298
301 CTCCAGCCCTGCGAG 360
299 CTCCAGCCCTGCGAG 358
361 CATGCCCCAGATGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
359 CATGCCCCAGATGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 418
421 CTTGGGCGAGACAACTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
419 CTTGGGCGAGACAACTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 478
481 GTCTTCCCCACCCCGGCTTCAACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
479 GTCTTCCCCACCCCGGCTTCAACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 538
541 CATGCTGCTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 600
539 CATGCTGCTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 598
601 CTCTCTACGCTGTGTCT 660
599 CTCTCTACGCTGTGTCT 658
661 CAGCCCCAGTTCAGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
659 CAGCCCCAGTTCAGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 718
721 CCAGAAAGTGTAGAAAGCTTACCCCGGCAACATCACAGACCAATGCTGTGTCTGCA 780
719 CCAGAAAGTGTAGAAAGCTTACCCCGGCAACATCACAGACCAATGCTGTGTCTGCA 778
781 GCAGAAAGGCGGCAAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
779 GCAGAAAGGCGGCAAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 838
841 GTCTCTCAAGGATTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
839 GTCTCTCAAGGATTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 898
901 TGCTCTACAGAAAGTGTGCAATATGTGATGATGATGATGATGATGATGATGATGAT 960
899 TGCTCTACAGAAAGTGTGCAATATGTGATGATGATGATGATGATGATGATGATGAT 958

Db 1091 CTGTTCACTCTGTTATTAAGAAACCTTAGCCAAACCTCTACGACATTCTTTGGCC 1150
QY 1077 TCCTGACATACAGAGATGCTGTCACCTATATATCAACCTGGGTTGCAATCAGTGA 1136
Db 1151 TCCTGACATACAGAGATGCTGTCACCTATATATCAACCTGGGTTGCAATCAGTGA 1210
QY 1137 CCTGATTCAAATTCCTGCTTGAATATGTGACTCTGGGATGACACACCTGGTTGT 1196
Db 1211 CCTGATTCAAATTCCTGCTTGAATATGTGACTCTGGGATGACACACCTGGTTGT 1270
QY 1197 TCCTGTTGATFCCCGCCCAAGACAGCTCCTGGCCATATATCAAGTTTCATPAA 1256
Db 1271 TCTCTGTTGATFCCCGCCCAAGACAGCTCCT-GCCATATATCA-GTTTCATPAA 1328
QY 1257 TATTT 1261
Db 1329 TATTT 1333

RESULT 5
AAA37072
ID AAA37072 standard; cDNA; 1204 BP.
XX
AC AAA37072;
XX
DT 08-AUG-2000 (first entry)
XX
DE Human PRO1279 (UNQ649) cDNA sequence SEQ ID NO:169.
XX
KW Human: PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening;
KW ss.
XX
OS Homo sapiens.
XX
PN MO200012708-A2.
XX
PD 09-MAR-2000.
XX
PE 01-SEP-1999; 99WO-US20111.
XX
PR 01-SEP-1998; 98US-0098716.
PR 01-SEP-1998; 98US-0098749.
PR 01-SEP-1998; 98US-0098750.
PR 02-SEP-1998; 98US-0098803.
PR 02-SEP-1998; 98US-0098821.
PR 02-SEP-1998; 98US-0098843.
PR 09-SEP-1998; 98US-0099536.
PR 09-SEP-1998; 98US-0099596.
PR 09-SEP-1998; 98US-0099598.
PR 09-SEP-1998; 98US-0099602.
PR 09-SEP-1998; 98US-0099642.
PR 10-SEP-1998; 98US-0099741.
PR 10-SEP-1998; 98US-0099754.
PR 10-SEP-1998; 98US-0099763.
PR 10-SEP-1998; 98US-0099792.
PR 10-SEP-1998; 98US-0099808.
PR 10-SEP-1998; 98US-0099812.
PR 10-SEP-1998; 98US-0099815.
PR 10-SEP-1998; 98US-0099816.
PR 15-SEP-1998; 98US-0100385.
PR 15-SEP-1998; 98US-0100388.
PR 15-SEP-1998; 98US-0100584.
PR 16-SEP-1998; 98US-0100584.
PR 16-SEP-1998; 98US-0100627.
PR 16-SEP-1998; 98US-0100661.
PR 16-SEP-1998; 98US-0100662.
PR 16-SEP-1998; 98US-0100664.
PR 17-SEP-1998; 98US-0100663.
PR 17-SEP-1998; 98US-0100684.
PR 17-SEP-1998; 98US-0100710.
PR 17-SEP-1998; 98US-0100711.

PR 17-SEP-1998; 98US-0100919.
PR 17-SEP-1998; 98US-0100930.
PR 18-SEP-1998; 98US-0100848.
PR 18-SEP-1998; 98US-0100849.
PR 18-SEP-1998; 98US-0100849.
PR 18-SEP-1998; 98US-0101014.
PR 18-SEP-1998; 98US-0101068.
PR 18-SEP-1998; 98US-0101071.
PR 22-SEP-1998; 98US-0101279.
PR 23-SEP-1998; 98US-0101471.
PR 23-SEP-1998; 98US-0101472.
PR 23-SEP-1998; 98US-0101474.
PR 23-SEP-1998; 98US-0101475.
PR 23-SEP-1998; 98US-0101476.
PR 23-SEP-1998; 98US-0101477.
PR 23-SEP-1998; 98US-0101479.
PR 24-SEP-1998; 98US-0101738.
PR 24-SEP-1998; 98US-0101741.
PR 24-SEP-1998; 98US-0101743.
PR 24-SEP-1998; 98US-0101743.
PR 24-SEP-1998; 98US-0101915.
PR 24-SEP-1998; 98US-0101916.
PR 29-SEP-1998; 98US-0102207.
PR 29-SEP-1998; 98US-0102240.
PR 29-SEP-1998; 98US-0102307.
PR 29-SEP-1998; 98US-0102330.
PR 29-SEP-1998; 98US-0102331.
PR 30-SEP-1998; 98US-0102484.
PR 30-SEP-1998; 98US-0102487.
PR 30-SEP-1998; 98US-0102570.
PR 30-SEP-1998; 98US-0102571.
PR 01-OCT-1998; 98US-0102684.
PR 01-OCT-1998; 98US-0102687.
PR 02-OCT-1998; 98US-0102965.
PR 06-OCT-1998; 98US-0103258.
PR 06-OCT-1998; 98US-0103449.
PR 07-OCT-1998; 98US-0103314.
PR 07-OCT-1998; 98US-0103315.
PR 07-OCT-1998; 98US-0103328.
PR 07-OCT-1998; 98US-0103328.
PR 07-OCT-1998; 98US-0103355.
PR 07-OCT-1998; 98US-0103396.
PR 07-OCT-1998; 98US-0103401.
PR 08-OCT-1998; 98US-0103633.
PR 08-OCT-1998; 98US-0103678.
PR 08-OCT-1998; 98US-0103679.
PR 08-OCT-1998; 98US-0103711.
PR 14-OCT-1998; 98US-0104257.
PR 20-OCT-1998; 98US-0104987.
PR 20-OCT-1998; 98US-0105000.
PR 21-OCT-1998; 98US-0105104.
PR 22-OCT-1998; 98US-0105169.
PR 22-OCT-1998; 98US-0105266.
PR 26-OCT-1998; 98US-0105693.
PR 26-OCT-1998; 98US-0105694.
PR 27-OCT-1998; 98US-0105807.
PR 27-OCT-1998; 98US-0105881.
PR 27-OCT-1998; 98US-0105882.
PR 27-OCT-1998; 98US-0106062.
PR 28-OCT-1998; 98US-0106023.
PR 28-OCT-1998; 98US-0106029.
PR 28-OCT-1998; 98US-0106030.
PR 28-OCT-1998; 98US-0106032.
PR 28-OCT-1998; 98US-0106033.
PR 28-OCT-1998; 98US-0106178.
PR 29-OCT-1998; 98US-0106248.
PR 29-OCT-1998; 98US-0106384.
PR 29-OCT-1998; 98US-0108500.
PR 30-OCT-1998; 98US-0108464.
PR 03-NOV-1998; 98US-0106856.
PR 03-NOV-1998; 98US-0106902.
PR 03-NOV-1998; 98US-0106905.
PR 03-NOV-1998; 98US-0106919.
PR 03-NOV-1998; 98US-0106932.
PR 03-NOV-1998; 98US-0106934.

PR 10-NOV-1998; 98US-0107783.
PR 17-NOV-1998; 98US-0108775.
PR 17-NOV-1998; 98US-0108779.
PR 17-NOV-1998; 98US-0108787.
PR 17-NOV-1998; 98US-0108788.
PR 17-NOV-1998; 98US-0108801.
PR 17-NOV-1998; 98US-0108802.
PR 17-NOV-1998; 98US-0108806.
PR 17-NOV-1998; 98US-0108807.
PR 17-NOV-1998; 98US-0108867.
PR 17-NOV-1998; 98US-0108925.
PR 18-NOV-1998; 98US-0108848.
PR 18-NOV-1998; 98US-0108849.
PR 18-NOV-1998; 98US-0108850.
PR 18-NOV-1998; 98US-0108851.
PR 18-NOV-1998; 98US-0108852.
PR 18-NOV-1998; 98US-0108855.
PR 18-NOV-1998; 98US-0108904.
XX
XX (GENTH) GENENTECH INC.
XX
XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WT;
XX
XX WPI: 2000-237871/20.
XX P-PSDB; AAY99390.
XX
XX New mammalian DNA sequences encoding transmembrane, receptor or
XX secreted PRO polypeptides, useful for screening of potential peptide or
XX small molecule inhibitors of the relevant receptor/ligand interactions
XX
XX Claim 2, Fig 101; 773pp; English.
XX
XX
XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
XX receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
XX transmembrane and receptor PRO proteins can be used for screening of
XX potential peptide or small molecule inhibitors of the relevant
XX receptor/ligand interactions. The polypeptides and nucleotide sequences
XX encoding them have various industrial applications, including uses as
XX pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent
XX PCR primers and hybridisation probes used in the isolation of the PRO
XX polypeptides from the present invention.
XX
XX Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other:
SQ
Query Match . 92.1%; Score 1198; DB 21; Length 1204;
Best Local Similarity 100.0%; Pred. No. 2.1e-210;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 104 GTTCGAGATGCAGAGGTGAGGTGCTGCGGAGCTGGAAGTCAATCGGGAGAGGTCTC 163
DB 1 GTTCGAGATGCAGAGGTGAGGTGCTGCGGAGCTGGAAGTCAATCGGGAGAGGTCTC 60
QY 164 ACAGAGCCAAAGAACTGGGGCCCGCTCCCTCCAGAGCCATGAGATTTGCGAG 223
DB 61 ACAGAGCCAAAGAACTGGGGCCCGCTCCCTCCAGAGCCATGAGATTTGCGAG 120
QY 224 TTAATCTGCTGCTGCTGGCAACAGGGCTTGTAGGGGAGAGACGATCATCAAGGGG 283
DB 121 TTAATCTGCTGCTGCTGGCAACAGGGCTTGTAGGGGAGAGACGATCATCAAGGGG 180
QY 284 TTGCGAGTGAAGCCCTCATCCCAAGCCCTGGCAAGAGCCCTGTTGAGAAAGAGGGGCTA 343
DB 181 TTGCGAGTGAAGCCCTCATCCCAAGCCCTGGCAAGAGCCCTGTTGAGAAAGAGGGGCTA 240
QY 344 CTCTGTGGGGGAGCGCTCATCGCCCGCAGATGAGCTCTGAGACAGCAGCCACATGCGCTCAAG 403
DB 241 CTCTGTGGGGGAGCGCTCATCGCCCGCAGATGAGCTCTGAGACAGCAGCCACATGCGCTCAAG 300
QY 404 CCCCCTACATAGTTACCTGGGGGAGCAGCAAACTCTCCAGAAAGAGAGAGGCTGTGAGCAG 463
DB 301 CCCCCTACATAGTTACCTGGGGGAGCAGCAAACTCTCCAGAAAGAGAGAGGCTGTGAGCAG 360
QY 464 ACCGGAGAGCAGCATGAGTCTTCCCGCAGCCCGGCTTCAACAGCCTCCCAACAAA 523

DB 361 ACCGGAGAGCAGCATGAGTCTTCCCGCAGCCCGGCTTCAACAGCCTCCCAACAAA 420
QY 524 GACCAACCGAATGACATCATGCTGGTGAAGATGAGCATGCGCACTCTCATACCTGGGCT 583
DB 421 GACCAACCGAATGACATCATGCTGGTGAAGATGAGCATGCGCACTCTCATACCTGGGCT 480
QY 584 GTGCGACCCCTCAACCTCTCTCAGCTGTCAGCTGTCAGCTGTCAGCTGTCAGCTGTCAGCT 643
DB 481 GTGCGACCCCTCAACCTCTCTCAGCTGTCAGCTGTCAGCTGTCAGCTGTCAGCTGTCAGCT 540
QY 644 GGCTGGGGAGCAGCAGTCCAGCCCGCAGTTACGCTGCTCTCAGACCTTGGATGGGCAAC 703
DB 541 GGCTGGGGAGCAGCAGTCCAGCCCGCAGTTACGCTGCTCTCAGACCTTGGATGGGCAAC 600
QY 704 ATCACCATCATTTGAGACACCAAGATGTGAGAAAGCTTACCCGGCAACATCAGACACC 763
DB 601 ATCACCATCATTTGAGACACCAAGATGTGAGAAAGCTTACCCGGCAACATCAGACACC 660
QY 764 ATGCTGTGTGCCAGGCTGCGAGAAAGGGGCAAGAGCTCTGCGCAGGCTGCTCGGGGGG 823
DB 661 ATGCTGTGTGCCAGGCTGCGAGAAAGGGGCAAGAGCTCTGCGCAGGCTGCTCGGGGGG 720
QY 824 CCTGTGCTGTGAACCACTCTCTTCAAGGCAATATCTCTGGGGCAGGATCCGTGTGC 883
DB 721 CCTGTGCTGTGAACCACTCTCTTCAAGGCAATATCTCTGGGGCAGGATCCGTGTGC 780
QY 884 ATCACCAGAAAGCTGCTGTCTACACGAAAGCTGCAATATGTGAGCTGTGATCCAGAG 943
DB 781 ATCACCAGAAAGCTGCTGTCTACACGAAAGCTGCAATATGTGAGCTGTGATCCAGAG 840
QY 944 ACAGTGAAGAAACATTTAGACTGAGCCACCCACAGCCATCCCTCATTTCCACT 1003
DB 841 ACAGTGAAGAAACATTTAGACTGAGCCACCCACAGCCATCCCTCATTTCCACT 900
QY 1004 TGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1063
DB 901 TGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 1064 CATTTTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1123
DB 961 CATTTTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1124 GAATACAGTGAAGCTGATTCATTAATTCGCTGAAATATTTGACTCTGGGATGACA 1183
DB 1021 GAATACAGTGAAGCTGATTCATTAATTCGCTGAAATATTTGACTCTGGGATGACA 1080
QY 1184 ACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1243
DB 1081 ACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1244 AGGTTCAATTAATTTGCTTAATGAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1301
DB 1141 AGGTTCAATTAATTTGCTTAATGAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1198
RESULT 6
AAS21496
ID AAS21496 standard; CDNA; 1204 BP.
XX
XX AAS21496;
XX
XX 24-OCT-2001 (first entry)
XX
XX Human cDNA sequence encoding for PRO1279 polypeptide.
XX
XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;
XX breast; prostate; cervical; tumour necrosis factor- α ; TNF- α ; TNF- α ;
XX cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
XX adipocyte; A-peptide; factor VIIa; gene therapy; ss.
XX
XX Homo sapiens.
XX

Db 1081 ACACCTGGTTGTCTCTGTGTATCCCGACCCCAAGACAGCTCCTGGCCATATATCA 1140
QY 1244 AGGTTTCAATTAATATTTGCTAAATGAAAAAAAAAAAAAAAAAAAAAAAAA 1301
Db 1141 AGGTTTCAATTAATATTTGCTAAATGAAAAAAAAAAAAAAAAAAAAAAAAA 1198

RESULT 8
ABL95664
ID ABL95664 standard; cDNA; 1204 BP.
XX
AC ABL95664;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human anglogenesis related cDNA PRO1279 SEQ ID NO: 207.
XX
KW Human; anglogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiac; cytosolic; antiangiogenic; hypotensive; vlnlerary;
KW antiarteriosclerotic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200208284-A2.
XX
PD 31-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US21735.
XX
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220664P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-0643657.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 07-SEP-2000; 2000US-230978P.
PR 15-SEP-2000; 2000US-000000P.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-0709238.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06566.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001US-0866034.
PR 30-MAY-2001; 2001US-0870574.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 28-JUN-2001; 2001WO-US00000.
XX
XX
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.

PA (GODD/) GODDARD A.
PA (GODO/) GORDONSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PRON/) PRONIT N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AU, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephen JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI: 2002-171999/22.
XX P-PSDB: ABB95526.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX infarction), endothelial or angiogenic disorders in a mammal -
XX
XX Claim 1; Fig 207; 567pp; English.
XX
XX The present invention provides the protein and coding sequences of human
XX PRO proteins. These are useful for treating or diagnosing a
XX cardiovascular, endothelial or angiogenic disorder, including cardiac
XX hypertrophy, trauma, cancer, age-related macular degeneration,
XX atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis,
XX angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
XX angiogenesis (such as breast carcinoma and liver carcinoma) and wound
XX healing. The present sequence is a coding sequence of the invention.
SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Query Match 92.1%; Score 1198; DB 24; Length 1204;
Best Local Similarity 100.0%; Pred. No. 2.1e-210;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 GTTCCGAGATGACAGAGTTGAGTGTGCTCGGAGCTGAAAGTCATCGGCGAGAGTCTC 163
Db 1 GTTCCGAGATGACAGAGTTGAGTGTGCTCGGAGCTGAAAGTCATCGGCGAGAGTCTC 60
QY 164 ACAGCAGCCAAAGAACCTGGGGCCCGCTCTCCGCCCTCCAGGCCATGAGATTCAG 223
Db 61 ACAGCAGCCAAAGAACCTGGGGCCCGCTCTCCGCCCTCCAGGCCATGAGATTCAG 120
QY 224 TTATCTGCTGTGCTGTGGCAACAGGCTGTGAGGGGAGAGACAGATCAAGGG 283
Db 121 TTATCTGCTGTGCTGTGGCAACAGGCTGTGAGGGGAGAGACAGATCAAGGGG 180
QY 284 TTCGAGTCAAGGCTCACTCCAGCCCTGGCAGGACGCCCTGTTCGAAGAGCGGGCTA 343
Db 181 TTCGAGTCAAGGCTCACTCCAGCCCTGGCAGGACGCCCTGTTCGAAGAGCGGGCTA 240
QY 344 CTCTGTGGGGCGAGGCTCATGCCCCAGATGCTCTCTGACAGCAGCCCACTGCTCAAG 403
Db 241 CTCTGTGGGGCGAGGCTCATGCCCCAGATGCTCTCTGACAGCAGCCCACTGCTCAAG 300
QY 404 CCCCCGTACATATTTACCTGGGGGACACACCTCCAGAGGAGAGAGGGCTGTGACAG 463
Db 301 CCCCCGTACATATTTACCTGGGGGACACACCTCCAGAGGAGAGAGGGCTGTGACAG 360
QY 464 ACCCGGACAGCCACTGAGTCTTCCCCACCCCGGCTTCAACAAAGCCCTCCCAACAA 523
Db 361 ACCCGGACAGCCACTGAGTCTTCCCCACCCCGGCTTCAACAAAGCCCTCCCAACAA 420
QY 524 GACACACGCAATGACATCATGTGTGAGATGGATCCGACATCCATCACTGGGCT 583
Db 421 GACACACGCAATGACATCATGTGTGAGATGGATCCGACATCCATCACTGGGCT 480
QY 584 GTGCGACCCCTCAACCTCTCTCAGCGTGTGATCATGTGGGACACAGCTGCTCATTTCC 643

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Db      |||||||
481  GTGCAACCCCTCACCCTCTCCACGCTGTGTGCTGAGCCAGCTGCTCATTTCC 540
OY      644  GGCCTGGGAGCAGCAGCTCCAGCCCGCAGTTACGCTGCGCTCACACCTTGATGCCACAC 703
Db      541  GGCCTGGGAGCAGCAGCTCCAGCCCGCAGTTACGCTGCGCTCACACCTTGATGCCACAC 600
OY      704  ATCACCATTGATGAGCAGCAGCAGGAGTGTGAGAAAGCCTTACCCCGGACATCAGACACC 763
Db      601  ATCACCATTGATGAGCAGCAGCAGGAGTGTGAGAAAGCCTTACCCCGGACATCAGACACC 660
OY      764  ATGCTGTGTGCGCAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 823
Db      661  ATGCTGTGTGCGCAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
OY      824  CCGTGTGTGTGTAACGCTGCTTCAAGGATTTCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 883
Db      721  CCGTGTGTGTGTAACGCTGCTTCAAGGATTTCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
OY      884  ATCACCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 943
Db      781  ATCACCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
OY      944  ACGATGAAGAAATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1003
Db      841  ACGATGAAGAAATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
OY      1004  TGGTGTGTGTGTAACGCTGCTTCAAGGATTTCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 1063
Db      901  TGGTGTGTGTGTAACGCTGCTTCAAGGATTTCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
OY      1064  CATTCTTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1123
Db      961  CATTCTTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
OY      1124  GAAATCATGAGAGCTGATTAATTTCTGCTTGAATTTGTGATCTGAGGATGACA 1183
Db      1021  GAAATCATGAGAGCTGATTAATTTCTGCTTGAATTTGTGATCTGAGGATGACA 1080
OY      1244  AGGTTCAATTAATTAATTTGTGTAATGAAAAAATTTGTGTAATGAAAAAATTTGTGTAATG 1301
Db      1141  AGGTTCAATTAATTAATTTGTGTAATGAAAAAATTTGTGTAATGAAAAAATTTGTGTAATG 1198

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PF      20-JUN-2001; 2001WO-US19692.
XX      23-JUN-2000; 2000US-213637P.
PR      20-JUL-2000; 2000US-219556P.
PR      25-JUL-2000; 2000US-220624P.
PR      25-JUL-2000; 2000US-220664P.
PR      28-JUL-2000; 2000WO-US20710.
PR      02-AUG-2000; 2000US-222655P.
PR      17-AUG-2000; 2000US-0643657.
PR      23-AUG-2000; 2000WO-US23522.
PR      24-AUG-2000; 2000WO-US23328.
PR      07-SEP-2000; 2000US-230978P.
PR      18-SEP-2000; 2000US-0664610.
PR      18-SEP-2000; 2000US-0665350.
PR      24-OCT-2000; 2000US-242922P.
PR      08-NOV-2000; 2000US-0709238.
PR      08-NOV-2000; 2000WO-US30952.
PR      10-NOV-2000; 2000WO-US30873.
PR      01-DEC-2000; 2000WO-US32678.
PR      20-DEC-2000; 2000US-0747259.
PR      20-DEC-2000; 2000WO-US34956.
PR      22-JAN-2001; 2001US-0767609.
PR      28-FEB-2001; 2001US-0796498.
PR      28-FEB-2001; 2001WO-US06520.
PR      01-MAR-2001; 2001WO-US06666.
PR      09-MAR-2001; 2001US-0802706.
PR      14-MAR-2001; 2001US-0808689.
PR      22-MAR-2001; 2001US-0816744.
PR      05-APR-2001; 2001US-0828366.
PR      10-MAY-2001; 2001US-0834208.
PR      10-MAY-2001; 2001US-0854280.
PR      25-MAY-2001; 2001US-0866034.
PR      25-MAY-2001; 2001WO-US17092.
PR      30-MAY-2001; 2001US-0870574.
PR      30-MAY-2001; 2001WO-US17443.
PR      01-JUN-2001; 2001WO-US17800.
PA      (GETH ) GENENTECH INC.
PI      Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI      Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI      Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX      WPI; 2002-090516/12.
DR      P-PSDB; ABB84920.
XX      One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX      useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX      infarction), endothelial or angiogenic disorders in a mammal -
XX      Claim 2; Fig 207; 565pp; English.
CC      ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC      ABB85003. The PRO proteins and polynucleotides have cardiant, cytoslatic,
CC      antilangiogenic, hypotensive, vulnery and antiartherosclerotic
CC      activities, and can be used in gene therapy. The PRO polynucleotides,
CC      proteins, agonists and antagonists are useful for treating or diagnosing
CC      a cardiovascular, endothelial or angiogenic disorder in a mammal,
CC      e.g. cardiac hypertrophy, trauma, cancer. Age-related macular
CC      degeneration, atherosclerosis, hypertension, arterial restenosis,
CC      rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
CC      lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
CC      carcinoma) and wound healing. The PRO polynucleotides have applications
CC      in molecular biology, including use as hybridisation probes, and in
CC      chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
CC      probes used in the exemplification of the present invention.
XX      Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

```

Query Match 92.1%; Score 1198; DB 24; Length 1204;
 Best Local Similarity 100.0%; Pred. No. 2.1e-210;
 Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. ABK3356-ABK33657 represent human
CC PRO protein coding sequences of the invention.

XX Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Query Match 92.1%; Score 1198; DB 24; Length 1204;
Best Local Similarity 100.0%; Pred. No. 2,1e-210;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 GTTCGACATGACAGAGTTGAGTGGTGGCGGAGTGAAGTCAATGCGGACAGAGTCTC 163
DB 1 GTTCCGACAGATGACAGAGTTGAGTGGTGGCGGAGTGAAGTCAATGCGGACAGAGTCTC 60
QY 164 ACAGACGCCAAGAACCTGGGCGCGCTCTCCCTCCAGGCCATGAGATTCGACG 223
DB 61 ACAGACGCCAAGAACCTGGGCGCGCTCTCCCTCCAGGCCATGAGATTCGACG 120
QY 224 TTAATCCTGCTGCTGCGCAACAGGCTTGTAGGGGGAGAGACAGATCAATCAAGGGG 283
DB 121 TTAATCCTGCTGCTGCGCAACAGGCTTGTAGGGGGAGAGACAGATCAATCAAGGGG 180
QY 284 TTCGAGTGAAGCCTTACTCCAGCCCTGGCAGGACGCCCTGTGAGAGAGCGGGCTA 343
DB 181 TTCGAGTGAAGCCTTACTCCAGCCCTGGCAGGACGCCCTGTGAGAGAGCGGGCTA 240
QY 344 CTCTGGGGGGGACGCTATCGCCCAATAGTGGCTTCTACAGCAGCCATGCTCTCAAG 403
DB 241 CTCTGGGGGGGACGCTATCGCCCAATAGTGGCTTCTACAGCAGCCATGCTCTCAAG 300
QY 404 CCCCCTACATGATTCACCTGGGGGAGACAACTTCAGAAAGAGAGGCTGTGAGCAG 463
DB 301 CCCCCTACATGATTCACCTGGGGGAGACAACTTCAGAAAGAGAGGCTGTGAGCAG 360
QY 464 ACCCGGACAGCCATGAGTCCCTCCGCCACCCCGGCTTCAACAAAGCTCCCAACAA 523
DB 361 ACCCGGACAGCCATGAGTCCCTCCGCCACCCCGGCTTCAACAAAGCTCCCAACAA 420
QY 524 GACACCGCAATGACATGCTGTGGTGAAGATGGATGCCAGTCCATCACTCGGGCT 583
DB 421 GACACCGCAATGACATGCTGTGGTGAAGATGGATGCCAGTCCATCACTCGGGCT 480
QY 584 GTGCGACCCCTCACCCTCTCTCAGCGTGTGTCACTGTGGGACAGCTGCTCATTTTC 643
DB 481 GTGCGACCCCTCACCCTCTCTCAGCGTGTGTCACTGTGGGACAGCTGCTCATTTTC 540
QY 644 GGCTGGGGGACAGCTCCAGCCCCAGTTACGCTGCTCAGACCTTGCGATGCCCAAC 703
DB 541 GGCTGGGGGACAGCTCCAGCCCCAGTTACGCTGCTCAGACCTTGCGATGCCCAAC 600
QY 704 ATCACCATCATGAGACACAGAGTGTGAAGCGCTACCCCGGCAACATCAACACACC 763
DB 601 ATCACCATCATGAGACACAGAGTGTGAAGCGCTACCCCGGCAACATCAACACACC 660
QY 764 ATGCTGTGTGCGAGCGTGAAGAGAGGGGCAAGAGACTCCGACAGGTTGACTCGGGGCG 823
DB 661 ATGCTGTGTGCGAGCGTGAAGAGAGGGGCAAGAGACTCCGACAGGTTGACTCGGGGCG 720
QY 824 CCTCTGTGTGTAAACAGTCTCTTAAAGGCAATATCTCTCTGGGGCGAGATCGTGTGG 883
DB 721 CCTCTGTGTGTAAACAGTCTCTTAAAGGCAATATCTCTCTGGGGCGAGATCGTGTGG 780
QY 884 ATCACCAGCAAGCGTGTGTACAGGAAAGTCTCAATATGTGAGCTGATCCAGAG 943

DB 781 ATCACCAGCAAGCGTGTGTACAGGAAAGTCTGCAAAATATGTGAGCTGATCCAGAG 840
QY 944 ACAGTGAAGAACATTTAGACTGGAGCCACACACAGCCCATACCTCATTTCCACT 1003
DB 841 ACAGTGAAGAACATTTAGACTGGAGCCACACACAGCCCATACCTCATTTCCACT 900
QY 1004 TGGTGTGGTTCCTGCTGCTGCTGTTAATTAAGAAACCTAAGCCAAAGACCTTACGAA 1063
DB 901 TGGTGTGGTTCCTGCTGCTGCTGTTAATTAAGAAACCTAAGCCAAAGACCTTACGAA 960
QY 1064 CATCTTGTGGGCTCTCTGAGCTACAGAGATGCTGCTATATATCAACCTGGGGTTC 1123
DB 961 CATCTTGTGGGCTCTCTGAGCTACAGAGATGCTGCTATATATCAACCTGGGGTTC 1020
QY 1124 GAAATCAGTGAACCTGATTCGAATTCGCTTGAATATGTGACTGGGAATGACA 1183
DB 1021 GAAATCAGTGAACCTGATTCGAATTCGCTTGAATATGTGACTGGGAATGACA 1080
QY 1184 ACACCTGTTTGTCTCTGTTGTATCCAGGCCCAAGACAGCTTCGGCCATATATCA 1243
DB 1081 ACACCTGTTTGTCTCTGTTGTATCCAGGCCCAAGACAGCTTCGGCCATATATCA 1140
QY 1244 AGCTTTCATTAATATTTCTTAATGAAAAAATTTTAAAAAATTTTAAAAAATTTT 1301
DB 1141 AGCTTTCATTAATATTTCTTAATGAAAAAATTTTAAAAAATTTTAAAAAATTTT 1198

RESULT 11
ACAO3855
ID ACAA03855 standard; cDNA; 1204 BP.
XX
ACAO3855;
XX
23-MAY-2003 (first entry)
XX
DE cDNA encoding human PRO polypeptide #253.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003036180-A1.
PD 20-FEB-2003.
XX
PE 09-MAY-2002; 2002US-0143114.
XX
PR 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1998; 98WO-US12456.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.

PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 22-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00227.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 10-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0862636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.

PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX
XX
PA (GETH) GENENTECH INC.
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,
PI Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI: 2003-332040/31.
DR P-PSDB; AB068822.
XX
XX New secreted and transmembrane PRO nucleic acids, useful for gene
PT therapy, in chromosome and gene mapping, as chromosome markers, in
PT tissue typing, and in chromosome identification -
XX
XX Claim 2; Fig 505; 660pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for
CC linking bioactive molecules to cells expressing PRO polypeptides,
CC for modulating biological activities of cells expressing PRO
CC polypeptides, and for identifying agonists or antagonists.
CC The PRO polypeptides are useful for stimulating the release of
CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating the
CC proliferation or differentiation of chondrocytes, and detecting the
CC presence of tumours. The polynucleotide sequences encoding PRO
CC polypeptides are useful as hybridisation probes, in chromosome and
CC gene mapping, in the generation of antisense RNA and DNA, in the
CC preparation of PRO polypeptides, for generating transgenic animals or
CC knockout animals, for the genetic analysis of individuals with genetic
CC disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs
CC encoding the human PRO polypeptides of the invention.
CC Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at
CC seqdata.uspto.gov/psipdidentity.html.
CC
XX
SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;
Query Match 92.1%; Score 1198; DB 25; Length 1204;
Best Local Similarity 100.0%; Pred. No. 2,1e-210;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 104 GTTCGCGAGATGCGAGGTGAGGTGCTGCGGAGCTGTAAGTCATCGGCGAGAGCTC 163
DB 1 GTTCGCGAGATGCGAGGTGAGGTGCTGCGGAGCTGTAAGTCATCGGCGAGAGCTC 60
QY 164 ACAGCAGCCAGAGAACTGGGGCCCGCTCTCCCGCTCCAGGCGCATGAGATTCTGCAG 223
DB 61 ACAGCAGCCAGAGAACTGGGGCCCGCTCTCCCGCTCCAGGCGCATGAGATTCTGCAG 120
QY 224 TTATCTCTGCTGTGCTGCGAAGAGGCTGTGAGGGGAGAGACAGATCATCAAGGG 283
DB 121 TTATCTCTGCTGTGCTGCGAAGAGGCTGTGAGGGGAGAGACAGATCATCAAGGG 180
QY 284 TTCGAGTCAAGCTCTCACTCCAGCCCTGGCAGGACAGCCCTGTTCGAGAGAGCGGCTA 343
DB 181 TTGAGAGTCAAGCTCTCACTCCAGCCCTGGCAGGACAGCCCTGTTCGAGAGAGCGGCTA 240
QY 344 CTCTGTGGGGCGAGCGTCAATCGCCCGCAGATGGCTCTGACAGACGACCACTCTCTACG 403
DB 241 CTCTGTGGGGCGAGCGTCAATCGCCCGCAGATGGCTCTGACAGACGACCACTCTCTACG 300
QY 404 CCGCGCTACATAGTTCACCTTGGGGCAGACAACTCTCAGAGAGAGAGGCTGTGACAG 463
DB 301 CCGCGCTACATAGTTCACCTTGGGGCAGACAACTCTCAGAGAGAGAGGCTGTGACAG 360
QY 464 ACCCGGACAGCACTGATGCTCTCCCGCAGCCCGGCTTCAACAAAGCCCTCCCAACAA 523
DB 361 ACCCGGACAGCACTGATGCTCTCCCGCAGCCCGGCTTCAACAAAGCCCTCCCAACAA 420

QY 524 GACACCGCATATGATCATGCTGTGAAGATGGCATCCGACGTCCATTCACCTGGGCT 583
 DB 421 GACACCGCATATGATCATGCTGTGAAGATGGCATCCGACGTCCATTCACCTGGGCT 480
 QY 584 GTGGCAGCCCTCAGCCCTCTCAGCCTGTGTACAGTGGGACGACGCGCCCATTTCC 643
 DB 481 GTGGCAGCCCTCAGCCCTCTCAGCCTGTGTACAGTGGGACGACGCGCCCATTTCC 540
 QY 644 GGCCTGGGGAGCAGCTGCAGCCGCCAGTTACGCTGCTCCACACCTTGGGATGGCCAAC 703
 DB 541 GGCCTGGGGAGCAGCTGCAGCCGCCAGTTACGCTGCTCCACACCTTGGGATGGCCAAC 600
 QY 704 ATCACCATTATGAGCAGCAGAAAGTGTGAAGGCTTACCCGGGCAACATCACAGACCC 763
 DB 601 ATCACCATTATGAGCAGCAGAAAGTGTGAAGGCTTACCCGGGCAACATCACAGACCC 660
 QY 764 ATGGTGTGTGCGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 823
 DB 661 ATGGTGTGTGCGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
 QY 824 CCTGTGTGTGTACAGCTCTCTCAAGCATTTATCTCTGGGGCCAGGATCCGTGTGC 883
 DB 721 CCTGTGTGTGTACAGCTCTCTCAAGCATTTATCTCTGGGGCCAGGATCCGTGTGC 780
 QY 884 ATCACCAGCAGCAGCTGTGTGTACAGGAAAGTGTGCAATATGTGAGCTGATCCAGAG 943
 DB 781 ATCACCAGCAGCAGCTGTGTGTACAGGAAAGTGTGCAATATGTGAGCTGATCCAGAG 840
 QY 944 ACAGTGAAGACAAATTAAGACTGGACCCACCCACCCAGCCATCCCTCCATTCACCT 1003
 DB 841 ACAGTGAAGACAAATTAAGACTGGACCCACCCACCCAGCCATCCCTCCATTCACCT 900
 QY 1004 TGGTGTGTGTGTCTGT 1063
 DB 901 TGGTGTGTGTGTCTGT 960
 QY 1064 CATTTCTTTGGGCTCTGT 1123
 DB 961 CATTTCTTTGGGCTCTGT 1020
 QY 1124 GAAATCAGTGAAGACCTGT 1183
 DB 1021 GAAATCAGTGAAGACCTGT 1080
 QY 1184 ACACCTGT 1243
 DB 1081 ACACCTGT 1140
 QY 1244 AGCTTCAATTAATTTGTCTAAATGAAAAAATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1301
 DB 1141 AGCTTCAATTAATTTGTCTAAATGAAAAAATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1198

RESULT 12
 ID ACA04276 standard; cDNA; 1204 BP.
 AC ACA04276;
 DT 27-MAY-2003 (first entry)
 DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 505.
 KW Human; ss; gene; secreted protein; transmembrane protein; PRO;
 KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
 KW infertility; birth defects; premature aging; AIDS; biosensor;
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;
 KW biofactor; tumour.
 OS Homo sapiens.
 XX US2003032155-A1.
 PN

XX 13-FEB-2003.
 PD 13-FEB-2003.
 XX 03-MAY-2002; 2002US-0137865.
 XX 31-MAR-1997; 97WO-US05230.
 PR 12-JUN-1998; 98WO-US12456.
 PR 14-JUL-1998; 98WO-US14552.
 PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.
 PR 16-SEP-1998; 98WO-US19177.
 PR 17-SEP-1998; 98WO-US19330.
 PR 07-OCT-1998; 98WO-US21141.
 PR 29-OCT-1998; 98WO-US22991.
 PR 29-OCT-1998; 98WO-US22992.
 PR 20-NOV-1998; 98WO-US24855.
 PR 01-DEC-1998; 98WO-US25108.
 PR 05-JAN-1999; 99WO-US00106.
 PR 08-MAR-1999; 99WO-US05028.
 PR 10-MAR-1999; 99WO-US05190.
 PR 20-APR-1999; 99WO-US08615.
 PR 14-MAY-1999; 99WO-US10733.
 PR 02-JUN-1999; 99WO-US12252.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21947.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 02-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 16-DEC-1999; 99WO-US28565.
 PR 20-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 22-DEC-1999; 99WO-US30720.
 PR 30-DEC-1999; 99WO-US31243.
 PR 05-JAN-2000; 99WO-US31274.
 PR 06-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 11-FEB-2000; 2000WO-US00376.
 PR 18-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04342.
 PR 24-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06684.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.

PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0806889.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 18-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 01-JUN-2001; 2001US-0866034.
 PR 05-JUN-2001; 2001US-0872035.
 PR 14-JUN-2001; 2001US-0874503.
 PR 19-JUN-2001; 2001US-0882636.
 PR 21-JUN-2001; 2001US-0886342.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Geritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;
 XX
 DR WPI: 2003-331925/31.
 DR P-PSDB: AB067098.
 XX
 PT New secreted and transmembrane nucleic acids and polypeptides,
 PT designated as PRO, useful for treating inflammation, organ failure,
 PT atherosclerosis, cardiac injury, infertility, birth defects, premature
 PT aging, AIDS, or cancer -
 XX
 XX Claim 2; Fig 505; 659pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising, or which is
 CC at least 80% identical to, or the full-length coding sequence of, any of
 CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid
 CC further comprises the full-length coding sequence of the DNA deposited
 CC under American Type Culture Collection (ATCC) accession number in a list
 CC given in the specification. Also included are vectors and host
 CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO
 CC antibodies, PRO extracellular domains and mature sequences, methods
 CC of detecting PRO proteins, methods for stimulating the release of
 CC TNF-alpha (tumour necrosis factor alpha) from human blood,
 CC and the proliferation of differentiation of chondrocyte cells, the
 CC proliferation of, or gene expression in pericyte cells, the release or
 CC proteoglycans from cartilage, proliferation of inner ear utricular
 CC supporting cells, the proliferation of T-lymphocyte cells, the release
 CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the
 CC proliferation of endothelial cells), a method for modulating the uptake
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
 CC a method for inhibiting the binding of A-peptide to factor VIIa,
 CC or the differentiation of adipocyte cells, a method for detecting the
 CC presence of a tumour in a mammal and an oligonucleotide probe derived
 CC from any of the nucleotide sequences cited above. The nucleic acids and
 CC polypeptides are useful for treating inflammatory diseases, organ
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or

CC diabetic complications. The nucleic acids are useful as hybridisation
 CC probes, in chromosome and gene mapping, and in generating antisense RNA
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
 CC biosensors or bioreactors. Both are useful in tissue typing.
 CC The present sequence encodes a PRO protein of the invention.
 XX
 SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;
 Query Match 92.1%; Score 1198; DB 25; Length 1204;
 Best Local Similarity 100.0%; Pred. No. 2.1e-210;
 Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 104 GTTCCGAGATGACAGAGTTAGGTGGTGGGAGCTGGAAGTATCGGAGAGTCTC 163
 DB 1 GTTCCGAGATGACAGAGTTAGGTGGTGGGAGCTGGAAGTATCGGAGAGTCTC 60
 OY 164 ACAGAGCCAGAGAACTGGGGCCGCTCCGCCCTCCAGGGCCATGAGATTCCTCAG 223
 DB 61 ACAGAGCCAGAGAACTGGGGCCGCTCCGCCCTCCAGGGCCATGAGATTCCTCAG 120
 OY 224 TTAATCCTGCTTGTGGCAACAGGGCTTGAAGGGAGAGACAGGATCATCAAGGG 283
 DB 121 TTAATCCTGCTTGTGGCAACAGGGCTTGAAGGGAGAGACAGGATCATCAAGGG 180
 OY 284 TTGAGATGCAAGCTTCACTCCAGCCTTGGCAGCAGCCTGTTGAGAGACGGCCTA 343
 DB 181 TTGAGATGCAAGCTTCACTCCAGCCTTGGCAGCAGCCTGTTGAGAGACGGCCTA 240
 OY 344 CTGTGGGGGGAGCGCATGCGCCCAAGATGGTCTCGAGAGAGCCATGCTCTCAG 403
 DB 241 CTGTGGGGGGAGCGCATGCGCCCAAGATGGTCTCGAGAGAGCCATGCTCTCAG 300
 OY 404 CCCCCTACATATGTTCACTGGGGCAGACACAACTCCAGAAAGAGAGAGGCTGAGCAG 463
 DB 301 CCCCCTACATATGTTCACTGGGGCAGACACAACTCCAGAAAGAGAGAGGCTGAGCAG 360
 OY 464 ACCCGAGAGCAGCATGAGTCTTCCCAACCCCGGCTTCAACAACAGCCTCCCAACAA 523
 DB 361 ACCCGAGAGCAGCATGAGTCTTCCCAACCCCGGCTTCAACAACAGCCTCCCAACAA 420
 OY 524 GACCACCGCAATGACATCATCTGCTGTAAGATGGATCGGCAATCTCATCACTGGGCT 583
 DB 421 GACCACCGCAATGACATCATCTGCTGTAAGATGGATCGGCAATCTCATCACTGGGCT 480
 OY 584 GTGGACCCCTGACCCCTCTCTCAAGCTGTGTCACTGCTGGACACAGCTGCTTATTC 643
 DB 481 GTGGACCCCTGACCCCTCTCTCAAGCTGTGTCACTGCTGGACACAGCTGCTTATTC 540
 OY 644 GCGTGGGGCAGACAGTGTCAAGCCCACTTACGCTGCTCAACACTTGGATGGCCAC 703
 DB 541 GCGTGGGGCAGACAGTGTCAAGCCCACTTACGCTGCTCAACACTTGGATGGCCAC 600
 OY 704 ATCACATCATTTGAGCAGCAAGAGTGTGAGAACGCTTACCCGGCAATCATCAGACAC 763
 DB 601 ATCACATCATTTGAGCAGCAAGAGTGTGAGAACGCTTACCCGGCAATCATCAGACAC 660
 OY 764 ATGGTGTGTCCAGCGTGTGAGAGAAAGGGGCAAGAGACTCTGCCAGGGTGAATCCGGGG 823
 DB 661 ATGGTGTGTCCAGCGTGTGAGAGAAAGGGGCAAGAGACTCTGCCAGGGTGAATCCGGGG 720
 OY 824 CTTCTGGTGTGTACCAAGTCTCTTCAAGGCAATATCTCTGGGGCCAGATTCCTGTGCG 883
 DB 721 CTTCTGGTGTGTACCAAGTCTCTTCAAGGCAATATCTCTGGGGCCAGATTCCTGTGCG 780
 OY 884 ATCACCGGAAGGCTGTGTCTCTACAGAAAGTGTGCAAAATATGTGGATGGATCCAGGAG 943
 DB 781 ATCACCGGAAGGCTGTGTCTCTCTACAGAAAGTGTGCAAAATATGTGGATGGATCCAGGAG 840
 OY 944 ACGATGAAGAACATTTAGATGTGAGACCCACACAGCCATACCTTCATTTCTCACT 1003
 DB 841 ACGATGAAGAACATTTAGATGTGAGACCCACACAGCCATACCTTCATTTCTCACT 900
 OY 1004 TGGTGTGTGTCTCTGTCTCACTCTGTATTAAGAAACCTTAAGCAAGACCTCTTACGAA 1063

PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
PA (GENTH) GEMENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart JA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI: 2003-148238/14.
DR P-PSDB: ABUS9903.
XX
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments
XX
PS
XX
XX Claim 2; Fig 505; 659pp; English.
XX
CC The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth and PRO536,
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and
CC are thus useful for treating sports injuries, and arthritis. This
CC sequence encodes a novel human PRO protein.
XX
XX
SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;
Query Match 92.1%; Score 1198; DB 25; Length 1204;
Best Local Similarity 100.0%; Pred. No. 2.1e-110;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 104 GTTCCGAGATGACAGAGTGTGAGTGTGCTGCGAGTGAAGTCAATGCGGACAGAGTCTC 163
DB 1 GTTCCGAGATGACAGAGTGTGAGTGTGCTGCGAGTGAAGTCAATGCGGACAGAGTCTC 60
QY 164 ACAGCAGCCCAAGAACCTGGGGCCGCTCTCCCTCCAGGCGCATGAGATTCTGCAG 223
DB 61 ACAGCAGCCCAAGAACCTGGGGCCGCTCTCCCTCCAGGCGCATGAGATTCTGCAG 120
QY 224 TTAATCTGCTTCTGCTGCGACACAGGGCTTGTAGGGGGAGAGACACAGATCATCAAGGG 283
DB 121 TTAATCTGCTTCTGCTGCGACACAGGGCTTGTAGGGGGAGAGACACAGATCATCAAGGG 180
QY 284 TTGGAGTGAAGCTCACTCCACGCTTGGCAGGACACCTGTTCGAGAGAGCGGCTA 343
DB 181 TTGGAGTGAAGCTCACTCCACGCTTGGCAGGACACCTGTTCGAGAGAGCGGCTA 240
QY 344 CTCTGTGGGGGAGAGCTCATGCGCCACAGATGGCTCTGACAGACAGCCACTGCTCAAG 403
XX

DB 241 CTCTGTGGGGGAGAGCTCATGCGCCACAGATGGCTCTGTACAGACAGCCCACTGCTCAAG 300
QY 404 CCCCCTACATAGTTACCTGGGGCAGACACAACCTCCAGAGAGAGAGGGCTGTGACAG 463
DB 301 CCCCCTACATAGTTACCTGGGGCAGACACAACCTCCAGAGAGAGAGGGCTGTGACAG 360
QY 464 ACCCGAGACGCACTGAGTCTTCCCGACCCCGGCTTCAACAACAGCCTCCCAACAAA 523
DB 361 ACCCGAGACGCACTGAGTCTTCCCGACCCCGGCTTCAACAACAGCCTCCCAACAAA 420
QY 524 GACACCGCAATGACATCATCTGTTGTAAGATGGCATATCCAGTCTCATCTGGGCT 583
DB 421 GACACCGCAATGACATCATCTGTTGTAAGATGGCATATCCAGTCTCATCTGGGCT 480
QY 584 GTGGACCCCTCACCTCTCTCTACAGGTGTGTCTGCTGTGACACAGCTGCTCATTTCC 643
DB 481 GTGGACCCCTCACCTCTCTCTACAGGTGTGTCTGCTGTGACACAGCTGCTCATTTCC 540
QY 644 GCGTGGGGAGACAGTCTCAGCCCGCCAGTTACGCTGCTCTACACCTTGCATGCGGCAAC 703
DB 541 GCGTGGGGAGACAGTCTCAGCCCGCCAGTTACGCTGCTCTACACCTTGCATGCGGCAAC 600
QY 704 ATCAGCATATTGAGACACAGAAAGTGTGAGAAAGCCCTACCCCGGCAATCATACAGAAC 763
DB 601 ATCAGCATATTGAGACACAGAAAGTGTGAGAAAGCCCTACCCCGGCAATCATACAGAAC 660
QY 764 ATGCTGTGTGACAGCTGTGACAGAAAGGGGCAAGGACTCTGCGAGGGTGAATCCGGGGG 823
DB 661 ATGCTGTGTGACAGCTGTGACAGAAAGGGGCAAGGACTCTGCGAGGGTGAATCCGGGGG 720
QY 824 CCTGTGTGTGTACCAAGTCTCTTCAAGGCAATATCTCTGCGGCGCAGATCCGTGTGCG 883
DB 721 CCTGTGTGTGTACCAAGTCTCTTCAAGGCAATATCTCTGCGGCGCAGATCCGTGTGCG 780
QY 884 ATCAGCGAAAGCTGTGTGTACAGAAAGTGTGCAAAATATGTGATGATGATCCAGAG 943
DB 781 ATCAGCGAAAGCTGTGTGTGTACAGAAAGTGTGCAAAATATGTGATGATGATCCAGAG 840
QY 944 AGCATGAAGAACATTAATGACTGACCCACACAGCCATCCATCCATTTCCACT 1003
DB 841 AGCATGAAGAACATTAATGACTGACCCACACAGCCATCCATCCATTTCCACT 900
QY 1004 TGGGTGTGTGTCTCTGTCTACCTGTCTTAATGAAGAAACCTTAAGCAAGACCTCTACGA 1063
DB 901 TGGGTGTGTGTCTCTGTCTACCTGTCTTAATGAAGAAACCTTAAGCAAGACCTCTACGA 960
QY 1064 CATCTTTGGGCTCTCTGACTACAGAGATGCTGCTTAATTAATCAACTGGGGTTC 1123
DB 961 CATCTTTGGGCTCTCTGACTACAGAGATGCTGCTTAATTAATCAACTGGGGTTC 1020
QY 1124 GAAATCAATTAATTAATTTGCTTAATGAAGAAAGGGGGGGGGGGGGGGGGGGGGGG 1183
DB 1021 GAAATCAATTAATTAATTTGCTTAATGAAGAAAGGGGGGGGGGGGGGGGGGGGGGG 1080
QY 1184 ACACCTGCTTGTCTCTGTGTATCCCGACCCCAAGGACCTCTCTGCGCATATATCA 1243
DB 1081 ACACCTGCTTGTCTCTGTGTATCCCGACCCCAAGGACCTCTCTGCGCATATATCA 1140
QY 1244 AGGTTCAATTAATTAATTTGCTTAATGAAGAAAGGGGGGGGGGGGGGGGGGGGGGG 1301
DB 1141 AGGTTCAATTAATTAATTTGCTTAATGAAGAAAGGGGGGGGGGGGGGGGGGGGGGG 1198
XX
RESULT 14
ABR92131
ID ABR92131 standard; DNA: 1186 BP.
XX
AC ABR92131;
XX
DT 15-AUG-2002 (first entry)
XX
DE Prostate cancer-associated DNA sequence #17.
XX

XX 02-APR-2003 (first entry)
 XX Lung cancer-associated polynucleotide #332.
 DE
 XX
 KW Lung cancer-associated polynucleotide; gene: ds; cytosolic; emphysema;
 KW antiinflammatory; antileukemic; non-small cell lung cancer; atelectasis;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 XX
 OS Unidentified.
 XX
 PN W0200286443-A2.
 PD 31-OCT-2002.
 XX
 PF 18-APR-2002; 2002MO-US12476.
 XX
 PR 18-APR-2001; 2001US-284770P.
 PR 10-MAY-2001; 2001US-290492P.
 PR 09-NOV-2001; 2001US-339245P.
 PR 13-NOV-2001; 2001US-350666P.
 PR 29-NOV-2001; 2001US-334370P.
 PR 12-APR-2002; 2002US-372246P.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 PI Aziz N, Murray R;
 XX WPI: 2003-093161/08.
 DR P-PSDB; ABUS6739.
 DR
 XX
 PT Detecting a lung cancer-associated transcript in a cell from a patient
 PT for treating lung cancer, by contacting a biological sample from the
 PT patient with a polynucleotide that exhibits increased or decreased
 PT expression in lung cancer -
 PS
 PS Claim 22; Page 443; 453pp; English.
 XX
 CC The invention relates to a method for detecting a lung cancer-associated
 CC transcript in a cell from a patient, comprising contacting a biological
 CC sample from the patient with a polynucleotide that selectively hybridises
 CC to a sequence that is at least 80 % identical to a gene that exhibits
 CC increased or decreased expression in lung cancer samples. Lung
 CC cancer-associated polynucleotides and polypeptides are used for
 CC identifying a compound that modulates a lung cancer-associated
 CC polypeptide, for inhibiting proliferation of a lung cancer-associated
 CC cell to treat lung cancer in a patient and for treating a mammal having
 CC lung cancer by administering a modulatory compound identified. The
 CC methods are useful for treating lung cancer, such as small cell lung
 CC cancer, non-small cell lung cancer or other benign or precancerous
 CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
 CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
 CC and polypeptides are useful for diagnostic purposes and as targets for
 CC screening for therapeutic compounds that modulate lung cancer, such as
 CC antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated
 CC polynucleotides of the invention.
 CC
 CC
 SO Sequence 1186 BP; 272 A; 368 C; 302 G; 244 T; 0 other;
 Query Match 90.9%; Score 1183; DB 25; Length 1186;
 Best Local Similarity 100.0%; Pred. No. 1.2e-207;
 Matches 1183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 88 AGGAATCTGGCTCGGTTCCGAGATGCGAGGTGAGTGGCTGGGAGCTGGAATC 147
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Thu Oct 16 09:48:33 2003

us-09-856-320a-1.rmg

Page 21

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OM nucleic - nucleic search, using sw model

Run on: October 15, 2003, 11:00:23 ; Search time 6360.37 Seconds

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Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1301	100.0	1301	6	AB041036 Homo sapi
3	1283.4	98.6	1314	6	AR098430 Sequence
4	1283.4	98.6	1314	6	BD130920 Serline pr
5	1198	92.1	1204	6	AX358932 Sequence
6	1198	92.1	1204	6	AX362425 Sequence
7	1198	92.1	1204	6	AX454622 Sequence
8	1198	92.1	1204	6	AX464372 Sequence
9	1198	92.1	1204	6	AX491100 Sequence
10	1198	92.1	1204	6	AX697101 Sequence
11	1181.4	90.8	1186	6	AB012917 Homo sapi
12	1150	88.4	1158	6	AX016289 Sequence
13	1150	88.4	1158	6	BD137020 Human CAS
14	1114.4	85.7	1192	6	AR152174 Sequence
15	1111.2	85.4	1213	6	BC022068 Homo sapi
16	1108.8	85.2	1191	6	BD139483 Extended
17	1106	85.0	1106	6	AX016287 Sequence
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ALIGNMENTS

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DEFINITION Novel serine protease BSSP.
ACCESSION BD091587
VERSION BD091587.1 GI:22637198
KEYWORDS WO 0031257-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1301)
AUTHORS Uemura,H., Okui,A., Komianai,K., Yamaguchi,N. and Mitsui,S.
TITLE Novel serine protease BSSP
JOURNAL Patent: WO 0031257-A 1 02-JUN-2000;

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BASE COUNT 332 a 387 c 330 g 252 t

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Matches 1301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 781 GCAGGAAGGGGAGAGAGATCTGCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840

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DEFINITION Sequence 2 from patent US 6075136.
ACCESSION AR098430
VERSION AR098430.1 GI:12807687
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1314)
AUTHORS Tang, Y. Tom., Corley, N.C. and Guegler, K.J.
TITLE Prostate-associated serine protease
JOURNAL Patent: US 6075136-A 2 13-JUN-2000;
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BASE COUNT 320 a 400 c 337 g 257 t
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AUTHORS
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JOURNAL
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PN JP 2002503471-A/1
PD 05-FEB-2002
PF 05-FEB-1999 JP 2000531568
PR 17-FEB-1998 US 09/025059
PI TOM Y TANG, NEIL C CORLEY, KARL J GUEGLER
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Best local Similarity 99.9% Pred. No. 2.7e-297;
Matches 1284; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 361 CATGCGCCCGCATGAGTCTCTGACAGCAGCGCTCAAGCGCCGCTCATATGATTCA 420
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QY 421 CTTGGGGGAGACACTCCAGAAAGAGAGGCTGTGAGAGACCGGAGACCGCATGA 480

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QY 481 GTCTCTTCCCAACCCCGGCTTCAACACAGCCTCCCAACAAAGACACCGCATGACAT 540
Db 496 GTCTCTTCCCAACCCCGGCTTCAACACAGCCTCCCAACAAAGACACCGCATGACAT 555
QY 541 CATGCTGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
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RESULT 5
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LOCUS AX358932
DEFINITION Sequence 185 from Patent WO0193983.
ACCESSION AX358932
VERSION AX358932.1 GI:18675367
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homilidae; Homo.
REFERENCE
AUTHORS Baker,K.P., Desnoyers,L., Gerlitsen,M.E., Goddard,A.,

Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
Watanabe,C.K. and Wood,W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
Patent: WO 0193983-A 185 13-DEC-2001;
Genentech Inc. (US)
FEATURES
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/mol_type="genomic DNA"
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BASE COUNT 306 a 364 c 294 g 240 t
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Query Match 92.1%; Score 1198; DB 6; Length 1204;
Best Local Similarity 100.0%; Pred. No. 8.9e-277; Mismatches 0; Indels 0; Gaps 0;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 644 GGCTGGGGGAGCAGCTGACGCCCCAGTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 703
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LOCUS Sequence 185 from Patent WO0208288.
DEFINITION AX362425
ACCESSION AX362425
VERSION AX362425.1 GI:18694670
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Geddes, J.P., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K., and Wood, W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
Patent: WO 0208288-A 185 31-JAN-2002;
JOURNAL Genentech, Inc. (US)
FEATURES
Source Location/Qualifiers
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BASE COUNT 306 a 364 c 294 g 240 t
ORIGIN

Query Match 92.1%; Score 1198; DB 6; Length 1204;
Best Local Similarity 100.0%; Pred. No. 8.9e-277;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 104 GTTCCGCAATGCAAGAGTTGAGTGGCTCGGGAGCTGGAAGTATCGGGCAGAGTCTC 163
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QY 284 TTGAGATGCAAGCTCTACTCCAGCCCTGGCAGGACAGCTTGTTCGAAAGAGCGGCTA 343
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LOCUS Sequence 207 from Patent WO0208284.
DEFINITION AX454622
ACCESSION AX454622
VERSION AX454622.1 GI:21713935
KEYWORDS Homo sapiens (human)
SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
Baker, R.P., Ferrara, N., Gerber, H., Gerlitsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.

TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
Patent: WO 0208284-A 207 31-JAN-2002;

JOURNAL Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerlitsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scott A. (US) ; Pan, James (US)
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)

FEATURES
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BASE COUNT 306 a 364 c 294 g 240 t

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Best Local Similarity 100.0%; Pred. No. 8.9e-277;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8
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LOCUS Sequence 505 from Patent WO0140466.
DEFINITION AX464372
ACCESSION AX464372.1 GI:21899202
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
Baker, R.P., Beresini, M., DeForge, L., Desnoyers, L., Filvaroff, E.,
Gao, W.O., Gerlitsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,
Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Wood, W.I. and Zhang, Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
same
Patent: WO 0140466-A 505 07-JUN-2001;

TITLE JOURNAL
Genentech Inc. (US)

FEATURES
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BASE COUNT 306 a 364 c 294 g 240 t

ORIGIN

Query Match 92.1%; Score 1198; DB 6; Length 1204;
Best Local Similarity 100.0%; Pred. No. 8.9e-277;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

104 GTTCCGAGATGACAGAGTTGAGTGGCTGCGGAGCTGAGATCATCGGGCAGAGTCTC 163
1 GTTCCGAGATGACAGAGTTGAGTGGCTGCGGAGCTGAGATCATCGGGCAGAGTCTC 60

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RESULT 9
AX491100 1204 bp DNA linear PAT 16-AUG-2002
LOCUS Sequence 207 from Patent WO0200690.
DEFINITION AX491100
ACCESSION AX491100
VERSION AX491100.1 GI:22323887
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1
Baker, K.P., Ferrara, N., Gerber, H., Gertlisen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Pohl, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
Patent: WO 0200690-A 207 03-JAN-2002;
Genentech, Inc. (US)
Location/Qualifiers
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/organism="Homo sapiens"
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BASE COUNT 306 a 364 c 294 g 240 t
ORIGIN

Query Match 92.1%; Score 1198; DB 6; Length 1204;
Best Local Similarity 100.0%; Pred. No. 8 9e-277;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

104 GTTCCGAGATGACAGAGTTGAGGTGAGTGGCTGGGAGTGAAGTCAATGCGGAGAGTCTC 163
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DEFINITION Sequence 169 from Patent W00078961.
ACCESSION AX697101
VERSION AX697101.1 GI:29498066
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1
Ferrara, N., Stewart, T.A., Williams, P.M., Baker, K.P., Desnoyers, L.,
Eaton, D.L., Gao, W.Q., Pan, J., Botstein, D., Fong, S., Goddard, A.,
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Patent: WO 0078961-A 169 28-DEC-2000;
JOURNAL Genentech Inc. (US)
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ACCESSION AB012917			
VERSION AB012917.1 GI:3649790			
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ORGANISM Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
REFERENCE			
AUTHORS Yoshida,S., Taniguchi,M., Suemoto,T., Oka,T., He,X. and Shiosaka,S.			
TITLE cDNA cloning and expression of a novel serine protease, TLSP			
JOURNAL Biochim. Biophys. Acta 1399 (2-3), 225-228 (1998)			
MEDLINE 98438738			
PubMed 9765601			
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AUTHORS Yoshida,S.			
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BASE COUNT 274 a 359 c 306 g 219 t

ORIGIN

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ORIGIN


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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

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(without alignments)
2468.773 Million cells updates/sec

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1355	57.2	250	12	US-10-015-387A-170	Sequence 170, App
3	1355	57.2	250	12	US-10-137-870-506	Sequence 506, App
4	1355	57.2	250	12	US-10-140-018-506	Sequence 506, App
5	1355	57.2	250	12	US-10-140-021-506	Sequence 506, App
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7	1355	57.2	250	12	US-10-140-471-506	Sequence 506, App
8	1355	57.2	250	12	US-10-140-807-506	Sequence 506, App
9	1355	57.2	250	12	US-10-140-922-506	Sequence 506, App
10	1355	57.2	250	12	US-10-140-924-506	Sequence 506, App
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13	1355	57.2	250	12	US-10-141-702-506	Sequence 506, App
14	1355	57.2	250	12	US-10-141-704-506	Sequence 506, App
15	1355	57.2	250	12	US-10-142-421-506	Sequence 506, App
16	1355	57.2	250	12	US-10-142-432-506	Sequence 506, App
17	1355	57.2	250	12	US-10-142-433-506	Sequence 506, App
18	1355	57.2	250	12	US-10-143-033-506	Sequence 506, App
19	1355	57.2	250	12	US-10-144-994-506	Sequence 506, App
20	1355	57.2	250	12	US-10-145-628-506	Sequence 506, App
21	1355	57.2	250	12	US-10-145-631-506	Sequence 506, App
22	1355	57.2	250	12	US-10-145-633-506	Sequence 506, App
23	1355	57.2	250	12	US-10-145-746-506	Sequence 506, App
24	1355	57.2	250	12	US-10-145-748-506	Sequence 506, App
25	1355	57.2	250	12	US-10-145-823-506	Sequence 506, App
26	1355	57.2	250	12	US-10-145-826-506	Sequence 506, App
27	1355	57.2	250	12	US-10-145-870-506	Sequence 506, App
28	1355	57.2	250	12	US-10-145-876-506	Sequence 506, App
29	1355	57.2	250	12	US-10-145-959-506	Sequence 506, App
30	1355	57.2	250	12	US-10-146-724-506	Sequence 506, App
31	1355	57.2	250	12	US-10-146-725-506	Sequence 506, App
32	1355	57.2	250	12	US-10-146-793-506	Sequence 506, App
33	1355	57.2	250	12	US-10-147-495-506	Sequence 506, App
34	1355	57.2	250	12	US-10-147-501-506	Sequence 506, App
35	1355	57.2	250	12	US-10-147-504-506	Sequence 506, App
36	1355	57.2	250	12	US-10-147-508-506	Sequence 506, App
37	1355	57.2	250	12	US-10-147-509-506	Sequence 506, App
38	1355	57.2	250	12	US-10-147-510-506	Sequence 506, App
39	1355	57.2	250	12	US-10-147-511-506	Sequence 506, App
40	1355	57.2	250	12	US-10-147-529-506	Sequence 506, App
41	1355	57.2	250	12	US-10-153-397-506	Sequence 506, App
42	1355	57.2	250	12	US-10-153-586-506	Sequence 506, App
43	1355	57.2	250	12	US-10-158-783-506	Sequence 506, App
44	1355	57.2	250	12	US-10-158-786-506	Sequence 506, App
45	1355	57.2	250	12	US-10-006-130A-170	Sequence 170, App

ALIGNMENTS

RESULT 1
US-09-946-374-170
; Sequence 170, Application US/09946374
; Publication No. US20030073129A1
GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillen, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumata, Daniel
; APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830PIC1
CURRENT APPLICATION NUMBER: US/09/946,374
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
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PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098803
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098821
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098843
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/099336
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099596
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099602
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099642
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099741
PRIOR FILING DATE: 1998-09-10
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PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099808
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PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099815
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099816
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100385
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100388
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100390
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100584
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100627
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PRIOR APPLICATION NUMBER: 60/100661
PRIOR FILING DATE: 1998-09-16
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PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100664
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100683
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100684
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100710
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100711
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100848
PRIOR FILING DATE: 1998-09-18

PRIOR APPLICATION NUMBER: 60/100849
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100919
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100930
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101014
PRIOR FILING DATE: 1998-09-18
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PRIOR FILING DATE: 1998-09-18
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PRIOR FILING DATE: 1998-09-18
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PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102487
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PRIOR APPLICATION NUMBER: 60/102570
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102684
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/102687
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/102965
PRIOR FILING DATE: 1998-10-02
PRIOR APPLICATION NUMBER: 60/103258
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PRIOR APPLICATION NUMBER: 60/103314
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PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103328
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PRIOR APPLICATION NUMBER: 60/103395
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103396


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? PRIOR FILING DATE: 1998-10-07
? PRIOR APPLICATION NUMBER: 60/103401
? PRIOR FILING DATE: 1998-10-07
? PRIOR APPLICATION NUMBER: 60/103449
? PRIOR FILING DATE: 1998-10-06
? PRIOR APPLICATION NUMBER: 60/103633
? PRIOR FILING DATE: 1998-10-08
? PRIOR APPLICATION NUMBER: 60/103678
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? PRIOR APPLICATION NUMBER: 60/103679
? PRIOR FILING DATE: 1998-10-08
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? PRIOR FILING DATE: 1998-10-08
? PRIOR APPLICATION NUMBER: 60/104257
? PRIOR FILING DATE: 1998-10-14
? PRIOR APPLICATION NUMBER: 60/104987
? PRIOR FILING DATE: 1998-10-20
? PRIOR APPLICATION NUMBER: 60/105000
? PRIOR FILING DATE: 1998-10-20
? PRIOR APPLICATION NUMBER: 60/105002
? PRIOR FILING DATE: 1998-10-20
? PRIOR APPLICATION NUMBER: 60/105104
? PRIOR FILING DATE: 1998-10-21
? PRIOR APPLICATION NUMBER: 60/105169
? PRIOR FILING DATE: 1998-10-22
? PRIOR APPLICATION NUMBER: 60/105286
? PRIOR FILING DATE: 1998-10-22
? PRIOR APPLICATION NUMBER: 60/105693
? PRIOR FILING DATE: 1998-10-26
? PRIOR APPLICATION NUMBER: 60/105694
? PRIOR FILING DATE: 1998-10-26
? PRIOR APPLICATION NUMBER: 60/105807

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Alignment Scores:

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Pred. No.: 1.85e-87 Length: 250
Score: 1355.00 Matches: 250
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.17% Indels: 0
DB: 11 Gaps: 0

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US-09-856-320a-1 (1-1301) x US-09-946-374-170 (1-250)

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QY 209 ATGAGGATTCGTCAGTTAATCTGCTGCTGGCAACAGGGCTGTAGGGAGAGACC 268
DB 1 MetArgileLeuGlnleuileuLeuAlaLeuAlaThrGlyLeuValGlyGlyIuThr 20
QY 269 AGGATCATCAAGGGGTTCGAGTGCAGCCTCACTCCAGCCGTCGGAGGACGCCCTTC 328
DB 21 ArgIleIleuGlyPheGlyIuGlySylsProHISerGlnProIleAlaLeuPhe 40
QY 329 GAGAAAGCGGGCTACTCTGTGGGGGAGCTATCGCCCGAGATGGCTCTGCAGACA 388
DB 41 GluIuThrArgLeuLeuGlySylsGlyAlaThrIleuAlaProArgIleuLeuThrAla 60
QY 389 GCGCCACTGCTCAGAGCCCGCTACATAGTTCACCTGGGGCAGACAACTCCAGAGAG 448
DB 61 AlaHIScysLeuIlyProArgIyIleValHISLeuGlyGlnHISasnLeuGlnIySylu 80
QY 449 GAGGGCTGTAGCAGACCCGAGCAGCAGCTGAGTCTCCGCCACCCCGGCTTCAACAC 508
DB 81 GluIyGlySylGlnIuThrArgIleuThrAlaThrGluSerPheProHISProGlyPheAsn 100
QY 509 AGCTCCCCCAACAAAGACCCAGCAGATGATCATGCTGGTGAAGATGGCATCGCAGTC 568
DB 101 SerIeuProAsnIlyAspHISArgAsnAspIleMetLeuValIlyMetAlaSerProVal 120
QY 569 TCCATCAGCTGGGTGTGGCAGCCCTCAGCTCTCTCCTCAGCTGTGTCACTGCTGGCACC 628
DB 121 SerIleThrIleAlaValArgProLeuThrIleuSerSerArgCysValThrAlaGlyThr 140
QY 629 ACCTGCTCATTTCCGGCTGGGGGAGACAGCTCAGCCCGCCAGATTCAGCTGCTCAGACC 688

```

```

DB 141 SerCysLeuIleSerGlyTyrPlySerThrSerSerProGlnLeuArgLeuProHISrThr 160
QY 689 TTGCGATGGCCCAACATCACCATCATTTGAGCACCAGAGTGTGAGAGCGCTACCCGGC 748
DB 161 LeuArgCysAlaAsnIleThrIleIleGlnHISGlnIlyCysGlnAsnAlaTyrProGly 180
QY 749 AACATCAGACACACATGTTGTGTCAGCGTCAGAGAGGGGGCAGAGACTCTCCAG 808
DB 181 AsnIleThrAspThrMetValCysAlaSerValGlnGlnIyGlyIlyAspSerCysGln 200
QY 809 GGTGATCCGGGGGGCCCTGTGCTGTATACCATCTCTTCAAGCATTTATCTCTGGGC 868
DB 201 GlyAspSerGlyIyProLeuValCysAsnGlnSerLeuGlnIyIleIleSerPly 220
QY 869 CAGGATCCGTGTGTCATCACCCAGAACCTGTGTGTACAGCAAGTGTGCAATATGTG 928
DB 221 GlnAspProCysAlaIleThrArgIySylProGlyValTyrThrIlyValCysIySylVal 240
QY 929 GACTGATCCAGAGACATGAAGAACAT 958
DB 241 AspTyrIleGlnIuThrMetIlySAsnAsn 250

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RESULT 2

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US-10-015-387A-170
? Sequence 170, Application US/10015387A
? Publication No. US20030135034A1
? GENERAL INFORMATION:

```

```

? APPLICANT: Baker, Kevin P.
? APPLICANT: Botsteijn, David
? APPLICANT: Desnoyers, Luc
? APPLICANT: Eaton, Dan I.
? APPLICANT: Ferrara, Napoleone
? APPLICANT: Fong, Sherman
? APPLICANT: Gao, Wei-Qiang
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Grimaldi, Christopher J.
? APPLICANT: Gurney, Austin L.
? APPLICANT: Hillan, Kenneth J.
? APPLICANT: Pan, James
? APPLICANT: Paoli, Nicholas F.
? TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
? FILE OF INVENTION: Acids Encoding the Same
? FILE REFERENCE: P2830PIC54
? CURRENT APPLICATION NUMBER: US/10/015,387A
? CURRENT FILING DATE: 2001-12-12
? Prior Application removed - See File Wrapper or Palm
? NUMBER OF SEQ ID NOS: 477
? SEQ ID NO 170
? LENGTH: 250
? TYPE: PRT
? ORGANISM: Homo sapiens
US-10-015-387A-170

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Alignment Scores:

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Pred. No.: 1.85e-87 Length: 250
Score: 1355.00 Matches: 250
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.17% Indels: 0
DB: 12 Gaps: 0

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US-09-856-320a-1 (1-1301) x US-10-015-387A-170 (1-250)

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QY 209 ATGAGGATTCGTCAGTTAATCTGCTGCTGGCAACAGGGCTGTAGGGAGAGACC 268
DB 1 MetArgileLeuGlnleuileuLeuAlaLeuAlaThrGlyLeuValGlyGlyIuThr 20
QY 269 AGGATCATCAAGGGGTTCGAGTGCAGCCTCACTCCAGCCGTCGGAGGACGCCCTTC 328
DB 21 ArgIleIleuGlyPheGlyIuGlySylsProHISerGlnProIleAlaLeuPhe 40
QY 329 GAGAAAGCGGGCTACTCTGTGGGGGAGACAGCTCAGCCCGCCAGATTCAGCTGCTCAGACA 388

```

```
Db 41 GlnuylstrArgrLeuLeuCysGlyAlaThrLeuIleAlaProArgrTrpLeuLeuThrAla 60
OY 389 GCCCACTGCTCAAGCCCCGCTACATAGTCACTGGGGAGACACCTCCAGAAAGAG 448
Db 61 AlaHtScySleuLysProArgrTrpIleValHtSleuGlyGlnHtSAsnLeuGlnLysGlu 80
OY 449 GAGGGCTGTGAGCAGACCCGGAGACAGCCAGTCCCTTCCCGACCCGGCTTCAACAC 508
Db 81 GluGlyCysGluGlnThrArgThrAlaThrGlnSerPheProHtSProGlyPheAsnAsn 100
OY 509 AGCTCCCAACAAGACCCAGCAATGACATGCTGCGTGAAGATGGCATCGCCATC 568
Db 101 SerLeuProAsnLysAsPhtSArgAsnAspIleMetLeuValLysMetAlaSerProVal 120
OY 569 TCCATCACTGGGCTGTGCGACCCCTCACCTTCCTCAGCTGCTGCTGCTGCGAC 628
Db 121 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 140
OY 629 AGCTGCTCATTTCCGGCTGGGGAGACAGCTCCAGCCCCAGTTACGCTTCCACAC 688
Db 141 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHtSThr 160
OY 689 TTGGCATGCGCAACATCACCATCATTCATGAGCAGCAGAAAGTGAAGAGCGCTACCCGCGC 748
Db 161 LeuArgCysAlaAsnIleThrIleIleGlnHtSglnLysCysGlnAsnAlaTrpProGly 180
OY 749 AACATCAGACAGACCCATGCTGTGCGACGCTGAGAAAGGGGGAGAGCATCTGCGAC 808
Db 181 AsnIleThrAspThrMetValCysAlaSerValGlnGlnLysGlyLysAspSerCysGln 200
OY 809 GGTGACTCCGGGGGCGCTGCTGTGTACCAAGTCTCTCAAGCATTAATCTCGGGGCG 868
Db 201 GlnAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 220
OY 869 CAGATCCGCTGTGGATCACCAGCCGGAAGCGCTGCTCAGCAAGTCTGCAAAATATGTC 928
Db 221 GlnAspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTrpVal 240
OY 929 GACTGATCCAGAGACGATGAAGACAAT 958
Db 241 AspTrpIleGlnGlnThrMetLysAsnAsn 250

RESULT 3
; Sequence 506, Application US/10137870
; Publication No. US20030138883A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P333081C15
; CURRENT APPLICATION NUMBER: US/10/137,870
; PRIOR APPLICATION REMOVED - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
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; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-870-506

Alignment Scores:
Pred. No.: 1,85e-87
Score: 1355.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 57.17%
Db: 12 Gaps: 0

US-09-856-320a-1 (1-1301) x US-10-137-870-506 (1-250)

OY 209 ATGAGGATTCGTGACGTTAATCTGCTGCTGTCACACAGGGGCTTGAAGGGGAGAGAC 268
Db 1 MetArgIleLeuGlnLeuIleLeuLeuAlaLeuAlaThrGlyLeuValGlyGlyThr 20
OY 269 AGGATCATCAAGGGGTTTCGAGTGCAGAGCTTCACCCAGCCCTGCGAGCGAGCCCTGTC 328
Db 21 ArgIleIleLysGlyPheGlnCysLysLysProHtSserGlnProTrpGlnAlaLeuPhe 40
OY 329 GAGAAGACGGGCTACCTGTGGGGGCGACGCTATCCGCCCAATGGCTTCTTACAGCA 388
Db 41 GlnuylstrArgrLeuLeuCysGlyAlaThrLeuIleAlaProArgrTrpLeuLeuThrAla 60
OY 389 GCCCACTGCTCAAGCCCCGCTACATAGTCACTGGGGAGACACCTCCAGAAAGAG 448
Db 61 AlaHtScySleuLysProArgrTrpIleValHtSleuGlyGlnHtSAsnLeuGlnLysGlu 80
OY 449 GAGGGCTGTGAGCAGACCCGGAGACAGCCAGTCCCTTCCCGACCCGGCTTCAACAC 508
Db 81 GluGlyCysGluGlnThrArgThrAlaThrGlnSerPheProHtSProGlyPheAsnAsn 100
OY 509 AGCTCCCAACAAGACCCAGCAATGACATGCTGCGTGAAGATGGCATCGCCATC 568
Db 101 SerLeuProAsnLysAsPhtSArgAsnAspIleMetLeuValLysMetAlaSerProVal 120
OY 569 TCCATCACTGGGCTGTGCGACCCCTCACCTTCCTCAGCTGCTGCTGCTGCGAC 628
Db 121 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 140
OY 629 AGCTGCTCATTTCCGGCTGGGGAGACAGCTCCAGCCCCAGTTACGCTTCCACAC 688
Db 141 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHtSThr 160
OY 689 TTGGCATGCGCAACATCACCATCATTCATGAGCAGCAGAAAGTGAAGAGCGCTACCCGCGC 748
Db 161 LeuArgCysAlaAsnIleThrIleIleGlnHtSglnLysCysGlnAsnAlaTrpProGly 180
OY 749 AACATCAGACAGACCCATGCTGTGCGACGCTGAGAAAGGGGGAGAGCATCTGCGAC 808
Db 181 AsnIleThrAspThrMetValCysAlaSerValGlnGlnLysGlyLysAspSerCysGln 200
OY 809 GGTGACTCCGGGGGCGCTGCTGTGTACCAAGTCTCTCAAGCATTAATCTCGGGGCG 868
Db 201 GlnAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 220
OY 869 CAGATCCGCTGTGGATCACCAGCCGGAAGCGCTGCTCAGCAAGTCTGCAAAATATGTC 928
Db 221 GlnAspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTrpVal 240
OY 929 GACTGATCCAGAGACGATGAAGACAAT 958
Db 241 AspTrpIleGlnGlnThrMetLysAsnAsn 250

RESULT 4
; Sequence 506, Application US/10140018
; Publication No. US20030138885A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
```

```

; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C158
; CURRENT APPLICATION NUMBER: US/10/140,018
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION REMOVED - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRP
; ORGANISM: Homo Sapien
US-10-140-018-506

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Alignment Scores:
Pred. No.: 1,85e-87 Length: 250
Score: 1355.00 Matches: 250
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.17% Indels: 0
DB: 12 Gaps: 0

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US-09-856-320a-1 (1-1301) x US-10-140-018-506 (1-250)

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QY 209 ATGAGGATTCCTGACATTAATCTGCTGCTGCGCAACAGGGCTTTAGGGGAGAGACC 268
DB 1 MetArgIleLeuGlnLeuIleuLeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThr 20
QY 269 AGGATCATCAAGGGGTTCAGTGCAGACCTCACTCCAGCCCTGGCAGGACCCCTGTTC 328
DB 21 ArgIleIleuGlyPheGlnCysLysProHisSerGlnProThrGlnAlaIleuPhe 40
QY 329 GAGAGAGCGGGCTACTCTGTGGGGGAGGCTCATCGCCCGGAGATGGCTCTGACAGCA 388
DB 41 GlnLysThrArgLeuLeuLeuGlyGlyAlaThrLeuIleAlaProLysGlyLeuThrAla 60
QY 389 GCGCCACTGCTCAAGCCCGGCTACATAGTTCACTGGGGGAGCAGACCTCCAGAGAGAG 448
DB 61 AlaHisCysLeuLeuProLysGlyThrLeuValHisLeuGlyGlnHisAsnLeuGlnLysGln 80
QY 449 GAGGCTGTGACAGACCCGGAGACGACCTAGTCTCCCGCCAGCCCGGCTTCAACAC 508
DB 81 GlnGlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsn 100
QY 509 AGCCTCCCAACAAGACGACCCGCAATGACATCATGCTGGTAAATGGCATGGCCAGTC 568
DB 101 SerLeuProAlaHisAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 120
QY 569 TCCATACACCTGGGCTGTGCGAGCCCTCACTCTGCTCAAGCTGTGTCACCTCTGGACAC 628
DB 121 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaIleThr 140
QY 629 AGCTCCCTCATTTCCGGCTGGGGGAGACAGCTCCAGCCCGCAATGACGCTGTGCTACAC 688
DB 141 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 160
QY 689 TTGGCATGGCCAAATCATCATCATGTGAGCACCAGAGTGTGAAGAAGCCCTACCCCGGC 748

```

```

DB 161 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTrpProGly 180
QY 749 AACATCAGACACACATGGTGTGTGTCACAGCTGCAGAGGGGCAAGGACTCTGCAG 808
DB 181 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGln 200
QY 809 GGTGACTCCGGGGGCGCTGTGTGTAAACAGCTCTTCAGCAATTAATCTCTGGGGC 868
DB 201 GlyAspSerGlyCylProLeuValCysAsnGlnSerLeuGlnIleIleSerTrpGly 220
QY 869 CAGGATCCGTCGCCATTCACCCGGAAGCCTGGTGTGTACACGAAATTCGCAATTTGTC 928
DB 221 GlnAspProCysAlaIleThrArgLysProGlyValTrpThrLysValCysLysTrpVal 240
QY 929 GACTGATCCAGAGACGATGAAGACAT 958
DB 241 AspTrpIleGlnGlnThrMetLysAsnAsn 250

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RESULT 5
US-10-140-021-506
Sequence 506, Application US/10140021
Publication No. US2003013886A1

GENERAL INFORMATION:

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; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C167
; CURRENT APPLICATION NUMBER: US/10/140,021
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION REMOVED - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRP
; ORGANISM: Homo Sapien
US-10-140-021-506

```

```

Alignment Scores:
Pred. No.: 1,85e-87 Length: 250
Score: 1355.00 Matches: 250
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.17% Indels: 0
DB: 12 Gaps: 0

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US-09-856-320a-1 (1-1301) x US-10-140-021-506 (1-250)

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QY 209 ATGAGGATTCCTGACATTAATCTGCTGCTGCGCAACAGGGCTTTAGGGGAGAGACC 268
DB 1 MetArgIleLeuGlnLeuIleuLeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThr 20
QY 269 AGGATCATCAAGGGGTTCAGTGCAGACCTCACTCCAGCCCTGGCAGGACCCCTGTTC 328
DB 21 ArgIleIleuGlyPheGlnCysLysProHisSerGlnProThrGlnAlaIleuPhe 40
QY 329 GAGAGAGCGGGCTACTCTGTGGGGGAGGCTCATCGCCCGGAGATGGCTCTGACAGCA 388

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Db 41 GlnlysthrArgLeuLeuLeuGlyAlaIlethrLeuIleAlaProAlaGlyTrpLeuLeuThrAla 60
QY 389 GCCCATGCTCTCAAGCCCGCTACATAGTTCACCTGGGGGAGCACAACCTCCAGAAAGAG 448
Db 61 AlaHisCysLeuLysProAlaGlyTrIleValHisIleuGlyGlnHisAsnLeuGlnLysGln 80
QY 449 GAGGGCTGTGAGCAGACCCGAGCAGCCTAGTCCCTTCCCCCAGCCCGGCTTCACACAC 508
Db 81 GlnIlyCysGlnGlnThrArgThrAlaIleThrGlnSerPheProHisProGlyPheAsnAsn 100
QY 509 AGCCTCCCAACAAGACACCCGCAATGACATCATGCTGGAGATGGCATGCGCACTC 568
Db 101 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 120
QY 569 TCCATCATCTGGGTGTGGCAGCCCTCAGCCCTCTCCTCAGCTGTGCTGCTGCGCAC 628
Db 121 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 140
QY 629 AGCTGCTCATTTCCGGCTGGGGGAGCAGCCTCCAGCCCGGTTACGCTGCTCCACAC 688
Db 141 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 160
QY 689 TTGGGATGCGCCCAATCACCATCATGAGCAGCAGAAAGTGTGAAGCGCTTACCGCGC 748
Db 161 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaIleTrpGly 180
QY 749 AACATCAGACAGACCCATGCTGTGTGCCAGCGTCAGAGAGGGGGCAAGACTCTGCCAG 808
Db 181 AsnIleThrAspTrpIleMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 200
QY 809 GGTGATCTCGGGGGGCGCTGTGCTGTAAACAGTCTCTCAAGCATTAATCTCTGGGCG 868
Db 201 GlnAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 220
QY 869 CAGGATCCGTGGGATCACCAGCAAGCCTGTGTCTACAGAAAGTCTGCAAAATATGTG 928
Db 221 GlnAspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTyVal 240
QY 929 GACTGGATCCAGAGAGAGATGAAGAACAAT 958
Db 241 AspTrpIleGlnGlnIleThrMetLysAsnAsn 250

RESULT 6
US-10-140-274-506
; Sequence 506, Application US/10140274
; Publication No. US20030143674A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria A.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P333081C161
; CURRENT APPLICATION NUMBER: US/10/140,274
; PCT FILING DATE: 2002-05-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
```

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; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-140-274-506

Alignment Scores:
Pred. No.: 1,856-87
Score: 1355.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 57.17%
DB: 12 Gaps: 0

US-09-856-320a-1 (1-1301) x US-10-140-274-506 (1-250)

QY 209 ATGAGGATTTGCAAGTTAATCTGCTGCTGCAACAGGGCTTGTAGGGGAGAGACC 268
Db 1 MetArgIleLeuGlnLeuIleLeuLeuAlaLeuAlaThrGlyLeuValGlyGlyIleThr 20
QY 269 AGGATCATCAAGGGGGTGGAGTGCAGAGCTTCTCCAGCCCTGGCAGGAGCCCTGTTC 328
Db 21 ArgIleIleLysGlyPheGlnCysLysProHisSerGlnProTrpGlnAlaIleLeuPhe 40
QY 329 GAGAAGAGCGGCTACTGTGGGGGAGCGCTCATGCCGCCCGCCAGATGGCTCTGCACGCA 388
Db 41 GlnlysthrArgLeuLeuCysGlyAlaIleThrLeuIleAlaProAlaGlyTrpLeuThrAla 60
QY 389 GCCCATGCTCTCAAGCCCGCTACATAGTTCACCTGGGGGAGCACAACCTCCAGAAAGAG 448
Db 61 AlaHisCysLeuLysProAlaGlyTrIleValHisIleuGlyGlnHisAsnLeuGlnLysGln 80
QY 449 GAGGGCTGTGAGCAGACCCGAGCAGCCTAGTCCCTTCCCCCAGCCCGGCTTCACACAC 508
Db 81 GlnIlyCysGlnGlnThrArgThrAlaIleThrGlnSerPheProHisProGlyPheAsnAsn 100
QY 509 AGCCTCCCAACAAGACACCCGCAATGACATCATGCTGGAGATGGCATGCGCACTC 568
Db 101 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 120
QY 101 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 120
QY 569 TCCATCATCTGGGTGTGGCAGCCCTCAGCCCTCTCCTCAGCTGTGCTGCTGCGCAC 628
Db 121 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 140
QY 629 AGCTGCTCATTTCCGGCTGGGGGAGCAGCCTCCAGCCCGGTTACGCTGCTCCACAC 688
Db 141 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 160
QY 689 TTGGGATGCGCCCAATCACCATCATGAGCAGCAGAAAGTGTGAAGCGCTTACCGCGC 748
Db 161 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaIleTrpGly 180
QY 749 AACATCAGACAGACCCATGCTGTGTGCCAGCGTCAGAGAGGGGGCAAGACTCTGCCAG 808
Db 181 AsnIleThrAspTrpIleMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 200
QY 809 GGTGATCTCGGGGGGCGCTGTGCTGTAAACAGTCTCTCAAGCATTAATCTCTGGGCG 868
Db 201 GlnAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 220
QY 869 CAGGATCCGTGGGATCACCAGCAAGCCTGTGTCTACAGAAAGTCTGCAAAATATGTG 928
Db 221 GlnAspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTyVal 240
QY 929 GACTGGATCCAGAGAGATGAAGAACAAT 958
Db 241 AspTrpIleGlnGlnIleThrMetLysAsnAsn 250

RESULT 7
US-10-140-471-506
; Sequence 506, Application US/10140471
; Publication No. US20030138887A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
```

```

; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P330R1C163
; CURRENT APPLICATION NUMBER: US/10/140,471
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PR1
; ORGANISM: Homo Saplen
US-10-140-471-506

```

Alignment Scores:

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Pred. No.: 1,85e-87 Length: 250
Score: 1355.00 Matches: 250
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.17% Indels: 0
DB: 12 Gaps: 0

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US-09-856-320A-1 (1-1301) x US-10-140-471-506 (1-250)

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QY 209 ATGAGAGATTCTGACGTTAATCTGCTGCTGGCAACAGGGCTTTAGGGGAGAGACC 268
DB 1 Metatgilleuenglneuleuleuleuallathhclyleuvalcilyglutrr 20
QY 269 AGATATCATAGAGGGTTGAGTGCAGAGCTCACTCCAGCCCTGGCAGGACCCCTGTTT 328
DB 21 Argillelletygllypneglucylsyrpnhlserrglnprctrglnalalaieuphe 40
QY 329 GAGAGAGCCGGCTACTGCTGGGGAGGCTCAATCGCCCAAGTGGCTCTGACAGCA 388
DB 41 Gltlysthrargleuencysglyalathrleullealaproargtrpleuuthrala 60
QY 389 GCCCACTGCTCAAGCCCGCTACATAGTTCACTGGGGCAGACAACTCCAGAGAG 448
DB 61 Alahiscysleuleuylproargtrylevalnhlsleuglylnhlsasnleuclnlysglu 80
QY 449 GAGGGCTGTGACACACCCGGACAGGCACTGAGTCTTCCCAACCCGGCTTCAACAC 508
DB 81 Gltgltcysgluglntthrargthraltgtrglnserpneprohlsiprogllypheasn 100
QY 509 AGCCTCCCAACAAAGACACCCGCAATGACATGATCTGTTGAAGATGGCATCCGCAATC 568
DB 101 Serleuproasnlyalsprlsaragsnspillemelevallysmetrlaserproval 120
QY 569 TCCATCACTGGGCTGTGGACCCCTCACTGCTCACTGCTGTCACCTGCTGGACAC 628
DB 121 SerillethrtpralvalargproleuthrleuuserSerargcysvalthraltgltthr 140
QY 629 AGCTGCTCATTTCCGGCTGGGAGACAGCTCCAGCCCAAGTACAGCTGCTGCACAC 688
DB 141 SercysleuillesercllytrpelyserthrSerSerProglInleuargleuProhlsThr 160
QY 689 TTGGCATGGCCCAACATCAACATCAATGAGCAACGAATGTGAGAAACCCCTACCCGGC 748
DB 161 leuargcysalasnlierthrllelleglnhlsnglnlyscysgluasnlatytrprogly 180

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QY 749 AACATCAAGACACCATGTGTGTGCCACGTGCAGAGAGGGGCAAGGACTCTCCAG 808
DB 181 Asnillethrasprrhmetvalcysalaservalglncluglylyyspsercysgln 200
QY 809 GGTGACTCCGGGGCCCTGTGTGTAAACAGTCTTTCAGGCAATATCTCTGGGGC 868
DB 201 GlyaspserglylypProleuvalcysAasnglnserleuglncllylletlesertrgly 220
QY 869 CAGATCCGCTGGCCATCAACCCGAAGCCTGGTGTATACCGAAATCTGCAATATGTC 928
DB 221 Glnaspprocysalaliethrarglysproglyvaltyrthlyvalcysystyval 240
QY 929 GACTGATCCAGAGACGATGAACAAAT 958
DB 241 Asprrpilleglnclnthrmetlysnasn 250

```

RESULT 8

```

US-10-140-807-506
; Sequence 506, Application US/10140807
; Publication No. US20030134354A1
; GENERAL INFORMATION:

```

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; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P330R1C174
; CURRENT APPLICATION NUMBER: US/10/140,807
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PR1
; ORGANISM: Homo Saplen
US-10-140-807-506

```

Alignment Scores:

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Pred. No.: 1,85e-87 Length: 250
Score: 1355.00 Matches: 250
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.17% Indels: 0
DB: 12 Gaps: 0

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US-09-856-320A-1 (1-1301) x US-10-140-807-506 (1-250)

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QY 209 ATGAGAGATTCTGACGTTAATCTGCTGCTGGCAACAGGGCTTTAGGGGAGAGACC 268
DB 1 Metatgilleuenglneuleuleuleuallathhclyleuvalcilyglutrr 20
QY 269 AGATATCATAGAGGGTTGAGTGCAGAGCTCACTCCAGCCCTGGCAGGACCCCTGTTT 328
DB 21 Argillelletygllypneglucylsyrpnhlserrglnprctrglnalalaieuphe 40
QY 329 GAGAGAGCCGGCTACTGCTGGGGAGGCTCAATCGCCCAAGTGGCTCTGACAGCA 388
DB 41 Gltlysthrargleuencysglyalathrleullealaproargtrpleuuthrala 60

```

```

QY 389 GCCCACTGCTCAAGCCCCGCTACATGACTCCTGGGGCAGCAGCACTCCAGAGGAG 448
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    |
Db 61 AAlahsCysLeuLysProArgTyrIleValHisLeuGlnHisAsnLeuGlnLysGlu 80
QY 449 GAGGGCTGTGAGCAGCCGGAGCCGACCTGAGTCCCTCCCGCCCGGCTTCAGAACAC 508
    |
    |
    |
Db 81 GlnGlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsn 100
QY 509 AGCCTCCCAACAAAGACCCAGCCGCAATGACATCATGCTGTGAAGATGGCATCCGACATC 568
    |
    |
    |
Db 101 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 120
QY 569 TCATCACTGCTGGGCTGTGAGCAGCCCTCCTCCTCCTGCTGTGCTGTGCTGAGCAGC 628
    |
    |
    |
Db 121 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 140
QY 629 AGCTGCTCATTTCCGGCTGGGGCAGCAGCTCCAGCCCGGATTAAGCTGCTCCACAGC 688
    |
    |
    |
Db 141 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 160
QY 689 TTGGGATGCGCCCAACATCACCATCATGATGAGCAGCAGAGTGTGAAGCCCTACCCGCGC 748
    |
    |
    |
Db 161 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaIleTrpProGly 180
QY 749 AACATCACAGACACCATGTGTGTGCGCAGCCTGCAAGAGGGGGCAGAGACTCCTGCCAG 808
    |
    |
    |
Db 181 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 200
QY 809 GGTGACTCGGGGGGCGCTGTGCTGTAAACAGTCTCTTCAAGGATATATCTCTGGGGGC 868
    |
    |
    |
Db 201 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 220
QY 869 CAGGATCGGTGTGGATCACCCGGAAGCCTGTGTACAGAAAGTCTGCAAAATATGTG 928
    |
    |
    |
Db 221 GlnAspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTyrVal 240
QY 929 GACTGATCCAGGAGAGCATGAAGAACAT 958
    |
    |
    |
Db 241 AspTrpIleGlnGlnThrMetLysAsn 250

RESULT 9
US-10-140-922-506
; Sequence 506, Application US/10140922
; Publication No. US2003013889A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaeroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P33081C179
; CURRENT APPLICATION NUMBER: US/10/140,922
; PRIOR APPLICATION REMOVED - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PR

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; ORGANISM: Homo Sapien
US-10-140-922-506
Alignment Scores:
Pred. No.: 1,85e-87
Score: 1355.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 57.17%
DB: 12
Gaps: 0

US-09-856-320a-1 (1-1301) x US-10-140-922-506 (1-250)

QY 209 ATGAGGATTTGCAAGTTAATCTGCTGCTGCGCAACAGGCGTTGAGGGGAGAGACC 268
    |
    |
    |
Db 1 MetArgIleLeuGlnLeuIleLeuLeuAlaLeuAlaThrGlyLeuValGlyGlyThr 20
QY 269 AGGATTCATCAAGGGGTTGAGTGTGAGAGCCTGACCTCCAGCCCTGGCAGCAGCCCTTCC 328
    |
    |
    |
Db 21 ArgIleIleLysGlyPheGlnCysLysProHisSerGlnProTrpGlnAlaAlaLeuPhe 40
QY 329 GAGAGAGAGCGGCTACTCTGTGGGGCAGCAGCTCATGCGCCCGCAGATGAGTCTTGACAGCA 388
    |
    |
    |
Db 41 GlnLysThrArgLeuLeuCysGlyAlaThrIleuIleAlaProArgTrpLeuThrAla 60
QY 389 GCCCACTGCTCAAGCCCCGCTACATGATGTTACCTGGGGCAGCAGCACTCCAGAGGAG 448
    |
    |
    |
Db 61 AAlahsCysLeuLysProArgTyrIleValHisLeuGlnHisAsnLeuGlnLysGlu 80
QY 449 GAGGGCTGTGAGCAGCCGGAGCCGACCTGAGTCCCTCCCGCCCGGCTTCAGAACAC 508
    |
    |
    |
Db 81 GlnGlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsn 100
QY 509 AGCCTCCCAACAAAGACCCAGCCGCAATGACATCATGCTGTGAAGATGGCATCCGACATC 568
    |
    |
    |
Db 101 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 120
QY 569 TCATCACTGCTGGGCTGTGAGCAGCCCTCCTCCTCCTGCTGTGCTGTGCTGAGCAGC 628
    |
    |
    |
Db 121 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 140
QY 629 AGCTGCTCATTTCCGGCTGGGGCAGCAGCTCCAGCCCGGATTAAGCTGCTCCACAGC 688
    |
    |
    |
Db 141 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 160
QY 689 TTGGGATGCGCCCAACATCACCATCATGATGAGCAGCAGAGTGTGAAGAGCCTCCGCGC 748
    |
    |
    |
Db 161 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaIleTrpProGly 180
QY 749 AACATCACAGACACCATGTGTGTGCGCAGCCTGCAAGAGGGGGCAGAGACTCCTGCCAG 808
    |
    |
    |
Db 181 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 200
QY 809 GGTGACTCGGGGGGCGCTGTGCTGTAAACAGTCTCTTCAAGGATATATCTCTGGGGGC 868
    |
    |
    |
Db 201 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 220
QY 869 CAGGATCGGTGTGGATCACCCGGAAGCCTGTGTACAGAAAGTCTGCAAAATATGTG 928
    |
    |
    |
Db 221 GlnAspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTyrVal 240
QY 929 GACTGATCCAGGAGAGCATGAAGAACAT 958
    |
    |
    |
Db 241 AspTrpIleGlnGlnThrMetLysAsn 250

RESULT 10
US-10-140-924-506
; Sequence 506, Application US/10140924
; Publication No. US20030134355A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura

```

```

? APPLICANT: Desnoyers, Luc
? APPLICANT: Filvaroff, Ellen
? APPLICANT: Gao, Wei-Qiang
? APPLICANT: Gerlitsen, Mary E.
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Gurney, Austin L.
? APPLICANT: Sherwood, Steven
? APPLICANT: Smith, Victoria
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Tamas, Daniel
? APPLICANT: Tamas, Colin K
? APPLICANT: Wood, William
? APPLICANT: Zhang, Zemin
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
? FILE OF INVENTION: ACIDS ENCODING THE SAME
? FILE REFERENCE: P330R1C177
? CURRENT APPLICATION NUMBER: US/10/140,924
? CURRENT FILING DATE: 2002-05-07
? Prior Application removed - See File Wrapper or Palm
? NUMBER OF SEQ ID NOS: 550
? SEQ ID NO 506
? LENGTH: 250
? TYPE: PRT
? ORGANISM: Homo Sapien
US-10-140-924-506

```

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Alignment Scores:
Pred. No.: 1,85e-87 Length: 250
Score: 1355.00 Matches: 250
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.17% Indels: 0
Gaps: 12

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US-09-856-320a-1 (1-1301) x US-10-140-924-506 (1-250)

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? 209 ATGAGAGATTCTGCACTTAATCTGCTGCTGGCAACAGGGCTTGTAGGGGAGAGACC 268
? 1 MetArgIleLeuGlnLeuIleLeuAlaLeuAlaThrGlyLeuValGlyGlyIthr 20
? 269 AGGATCATCAAGGGGTGAGTGAAGCAAGCTCACTCCAGCCCTGGGAGGACCCGCTTC 328
? 21 ArgIleIleGlyGlyPheGlnCysIysProHisSerGlnProTrpGlnAlaLeuPhe 40
? 329 GAGAAGACGGGCTACTGTGTGGGGGAGCTCATCGCCCGAGATGGCTCTGCAGACA 388
? 41 GluIysThrArgLeuLeuCysGlyAlaThrIleAlaProArgTrpLeuIthrAla 60
? 388 GCGCACTGCTCAAGCCCGCTACATAGTTCACCTGGGGAGACACAACTCCAGAAAGAG 448
? 61 AlaHisCysLeuIysProArgTrpGlyIleValHisLeuGlyGlnHisAsnLeuGlnIysGln 80
? 449 GAGGGCTGAGACAGCCCGGAGACGACATGATGCTCCGCCACCCCGGCTTCAACAC 508
? 81 GluGlyCysGlnGlnThrArgThrAlaTrpGlnPheProHisProGlyPheAsnAsn 100
? 509 AGCCTCCCAACAAAGACACCGCAATGATCATCTGGTGAAGATGGCATCGCAGTTC 568
? 101 SerLeuProAsnIlyAspHisArgAsnAspIleMetLeuValIlyMetAlaSerProVal 120
? 569 TCCATACACCTGGGCTGTGGACCCCTCACCTCTCCACGCTGTGTCACTGTGGACCC 628
? 121 SerIleThrTrpAlaValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 140
? 629 ACCTGCTCATTTGCGGGTGGGGGAGACAGCTCAGCCCGCATTCAGCGCTGCTCAGAC 688
? 141 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 160
? 689 TTGCGATGGCCCAACATCATCATCTATGAGCAGCAGAAAGTGTGAGAAAGCCTTACCCGGC 748
? 161 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnIlyCysGlnAsnAlaIlyTrpGly 180

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? 749 AACATCAGACACCATGTGTGTGCCAGCTGCAGAAAGGGGCAAGGACTCTGCCAG 808
? 181 AsnIleThrAspThrMetValCysAlaSerValGlnGlyIlyAspSerCysGln 200
? 809 GGTGATCCGGGGGGCCCTGTGCTGTAAACATCTCTTCAAGGCAATATCTCTGGGC 868
? 201 GlyAspSerGlyCylProLeuValCysAsnGlnSerLeuGlnIlyIleIleSerTrpGly 220
? 869 CAGATCCGTGTGCGATCACCCGAAAGCCTGTGTACACGAAAGTCTGCAATATGTC 928
? 221 GlnAspProCysAlaIleThrArgIysProGlyValIlyThrIysValCysIysTrpVal 240
? 929 GACTGATCCAGAGACATGAAGAACAAT 958
? 241 AspTrpIleGlnGlnIthrMetIlyAsnAsn 250

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RESULT 11

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US-10-140-926-506
? Sequence 506, Application US/10140926
? Publication No. US20030134356A1
? GENERAL INFORMATION:
? APPLICANT: Baker, Kevin P.
? APPLICANT: Beresini, Maureen
? APPLICANT: Deforge, Laura
? APPLICANT: Desnoyers, Luc
? APPLICANT: Filvaroff, Ellen
? APPLICANT: Gao, Wei-Qiang
? APPLICANT: Gerlitsen, Mary E.
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Gurney, Austin L.
? APPLICANT: Sherwood, Steven
? APPLICANT: Smith, Victoria
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Tamas, Daniel
? APPLICANT: Tamas, Colin K
? APPLICANT: Wood, William

```

```

? APPLICANT: Zhang, Zemin
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
? FILE OF INVENTION: ACIDS ENCODING THE SAME
? FILE REFERENCE: P330R1C187
? CURRENT APPLICATION NUMBER: US/10/140,926
? CURRENT FILING DATE: 2002-05-07
? Prior Application removed - See File Wrapper or Palm
? NUMBER OF SEQ ID NOS: 550
? SEQ ID NO 506
? LENGTH: 250
? TYPE: PRT
? ORGANISM: Homo Sapien
US-10-140-926-506

```

```

Alignment Scores:
Pred. No.: 1,85e-87 Length: 250
Score: 1355.00 Matches: 250
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.17% Indels: 0
Gaps: 12

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US-09-856-320a-1 (1-1301) x US-10-140-926-506 (1-250)

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? 209 ATGAGAGATTCTGCACTTAATCTGCTGCTGGCAACAGGGCTTGTAGGGGAGAGACC 268
? 1 MetArgIleLeuGlnLeuIleLeuAlaLeuAlaThrGlyLeuValGlyGlyIthr 20
? 269 AGGATCATCAAGGGGTGAGTGAAGCAAGCTCACTCCAGCCCTGGGAGGACCCGCTTC 328
? 21 ArgIleIleGlyGlyPheGlnCysIysProHisSerGlnProTrpGlnAlaLeuPhe 40
? 329 GAGAAGACGGGCTACTGTGTGGGGGAGCTCATCGCCCGAGATGGCTCTGCAGACA 388
? 41 GluIysThrArgLeuLeuCysGlyAlaThrIleAlaProArgTrpLeuIthrAla 60

```

389 GCCCAGCTGCTCAAGCCCCGCTACATAGTTCACCTGGGGGACAGACACCTTCAGAGAG 448
|||||
Db 61 Alaniscysleuvsproargtrytllevalhisleuglyglnhisasnlenglnlysglu 80
449 GAGGCGCTTGAGCAGACCCGGACAGCCACTGAGTCTTCCCCACCCCGGCTTCAACAC 508
|||||
Db 81 Gluglycysgluglnthralargthralthrghuserpherohisprogllyphenasmn 100
509 AGCCTCCCAACAAAGACCCAGCCAGATGATCATGCTGGTGAAGATGGCATGGCCAGTC 568
101 Serleuproasnlysasphiasargasmnasprilemelleuvallysmetalasertproval 120
569 TCCATCACCTGGGCTGGGAGCCCTCACCCCTCTCTCCAGTGTGTCATGCTGGCCAC 628
|||||
Db 121 SerleuthrtrpalaalargproleuthrleuserSerArgcysvalthrAlaGlythr 140
629 AGCTGCTCATTTCCGCTGGGGGACAGCAGTCCAGCCCCAGTTCAGCCTGCTGACACC 688
|||||
Db 141 SercysleuilieserGlyTrrpGlySerthrSerSerProglInleuArgleuProhlsThr 160
689 TTGGGATGCGCCAAACATGACATCATGTCAGACAGAAAGTGTGAGAACGCTTACCCGGC 748
161 LeuArgcysAlaasnIlethrIleleGlnhisGlnlyscysgluasnAlaTyrrProGly 180
749 AACATCACAGACACCATGCTGTGTGCCAGCGTGAAGAGGGGGCAAGACTCCTGCCAG 808
181 AsnIlethrAsprThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 200
809 GGTGACTCCGGGGCCCTGTGCTGTACACAGTCTTTCAGAGCATTAATTCCTGGGGC 868
201 GlyAspSerGlyGlyProleuValCysasnGlnSerleuGlnGlyIleIleSerTrpGly 220
869 CAGATCCGCTGGGATGATCCCGGAAAGCCTGTGCTACAGAAAGTGTGCAATATGTG 928
221 GlnAspProCysAlaIleThrArgLysProGlyValThrLysValCysLysTyVal 240
929 GACTGATCCAGAGAGCATGATGAAGAACT 958
241 AsprThrIleGlnGlnThrMetLysAsn 250

RESULT 12
US-10-141-698-506
; Sequence 506, Application US/10141698
; Publication No. US20030134357A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C206
; CURRENT APPLICATION NUMBER: US/10/141,698
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien

US-10-141-698-506
Alignment Scores:
Pred. No.: 1,856-87 Length: 250
Score: 1355.00 Matches: 250
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.17% Indels: 0
DB: 12 Gaps: 0

US-09-856-320a-1 (1-1301) x US-10-141-698-506 (1-250)

209 ATGAGAGATTCCTGCACTTAATCTCTGCTTCTGGACACAGGGCTTGAAGGGAGAGACC 268
|||||
Db 1 MetArgIleleuGlnleuIleleuValleuAlaThrGlyleuValGlyGlythr 20
269 AGGATCATCAAGGGGTTGAGTGAAGCTCACTCCAGCCCTGGAGGCGCCCTGTGTC 328
|||||
Db 21 ArgIleIleLysGlyPheGlnCysLysProhlsSerGlnProThrGlnAlaAlaLeuphe 40
329 GAGAAGACGCGCTACTCTGTGGGGGACAGCCTCATCCGCCCCAGATGGCTCTGACAGCA 388
41 GluysThrArgleuLeuCysGlyAlaThrleuIleAlaProArgTrpLeuThrAla 60
389 GCCCAGCTGCTCAAGCCCCGCTACATAGTTCACCTGGGGGACAGACAACTCCAGAGAG 448
61 Alaniscysleuvsproargtrytllevalhisleuglyglnhisasnlenglnlysglu 80
449 GAGGCGCTTGAGCAGACCCGGACAGCCACTGAGTCTTCCCCACCCCGGCTTCAACAC 508
81 GluglycysgluglnthralargthralthrghuserPherohisprogllyphenasmn 100
509 AGCCTCCCAACAAAGACCCAGCCAGATGATCATGCTGGTGAAGATGGCATGGCCAGTC 568
101 Serleuproasnlysasphiasargasmnasprilemelleuvallysmetalasertproval 120
569 TCCATCACCTGGGCTGGGAGCCCTCACCCCTCTCTCCAGCTGTGTCATGCTGGCCAC 628
121 SerleuthrtrpalaalargproleuthrleuserSerArgcysvalthrAlaGlythr 140
629 AGCTGCTCATTTCCGCTGGGGGACAGCAGTCCAGCCCCAGTTCAGCCTGCTGACACC 688
141 SercysleuilieserGlyTrrpGlySerthrSerSerProglInleuArgleuProhlsThr 160
689 TTGGGATGCGCCAAACATGACATCATGTCAGACAGAAAGTGTGAGAACGCTTACCCGGC 748
161 LeuArgcysAlaasnIlethrIleleGlnhisGlnlyscysgluasnAlaTyrrProGly 180
749 AACATCACAGACACCATGCTGTGTGCCAGCGTGAAGAGGGGGCAAGACTCCTGCCAG 808
181 AsnIlethrAsprThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 200
809 GGTGACTCCGGGGCCCTGTGCTGTACACAGTCTTTCAGAGCATTAATTCCTGGGGC 868
201 GlyAspSerGlyGlyProleuValCysasnGlnSerleuGlnGlyIleIleSerTrpGly 220
869 CAGATCCGCTGGGATGATCCCGGAAAGCCTGTGCTACAGAAAGTGTGCAATATGTG 928
221 GlnAspProCysAlaIleThrArgLysProGlyValThrLysValCysLysTyVal 240
929 GACTGATCCAGAGAGCATGATGAAGAACT 958
241 AsprThrIleGlnGlnThrMetLysAsn 250

RESULT 13
US-10-141-702-506
; Sequence 506, Application US/10141702
; Publication No. US20030134358A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc


```

; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C208
; CURRENT APPLICATION NUMBER: US/10/141,702
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: prt
; ORGANISM: Homo Saplen
US-10-141-702-506

```

Alignment Scores:

```

Pred. No.: 1,85e-87      Length: 250
Score: 1355.00           Matches: 250
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 57.17%      Indels: 0
DB: 12      Gaps: 0

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US-09-856-320A-1 (1-1301) x US-10-141-702-506 (1-250)

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QY 209 ATGAGAGATTCTGACGTAATTAATCTGCTGCTGCGCAACAGGCGCTGTAGGGGAGAGACC 268
DB 1 MetatgileuGlnleuileuileuualaleuAlathGlyleuValGlyGluThr 20
QY 269 AGCATCATCAAGGGGTGAGTGCAGTCAAGCGCTCACTCCGACCGCTGGAGGACCGCTGTC 328
DB 21 AtgilelleuGlyPheGlnCysGlySProHISserGlnProTrrpInlaIaleuPhe 40
QY 329 GAGAAGACGCGGCTACTGTGTGGGGGAGCGACTATCGCCCCAGATGGCTCCGTGACAGCA 388
DB 41 GluYsthrArgleuIeuCysGlyAlathrleuileAlaProArgTrrleuIeuThrAla 60
QY 389 GCCCACTGCTCAAGCCCCGCTACATAGTTCACCTGGGGGACACAACTCCAGAAAGAG 448
DB 61 AlathCysleuIeuYProArgTrrleuValHISleuGlyGlnHISAsnleuGlnIuysGlu 80
QY 449 GAGGGCTGTGAGACACCCGAGACGCACTGAGCTTCCGCCACCGCGCTTCAACAGC 508
DB 81 GluGlyCysGlnGlnThrArgThrAlathrGlnSerPheProHISProGlyPheAsn 100
QY 509 AGCCTCCCAACAAAGACACCCGCAATGACATCATGCTGTGTAGATGGCATCGCCAGTC 568
DB 101 SerleuProAsnIuYAspHISArgAsnAspIleMetleuValIlyMetAlaSerProVal 120
QY 569 TCCATCACTGGGCTGTGCGACCCCTCACCTCTCTCTCAAGCTGTGTCTACCTGGACCC 628
DB 121 SerIleThrPAlaValAlaArgProleuThrleuSerSerArgCysValThrAlaGlyThr 140
QY 629 AGCTGCTCATTTCCGGCTGGGGGAGCAGTGCAGGCCCCCAATTAAGCCTGGCTCACACC 688
DB 141 SerCysleuIleSerIleYtrpGlySerThrSerSerProGlnleuArgleuProHISThr 160
QY 689 TTGCGATGCGCCCAACATCAACATCATTTGAGCAGCAGAAAGTGTAGAAACGCTTACCCGGC 748
DB 161 leuArgCysAlaAsnIleThrIleleuGlnHISGlnIuYCysGlnAsnAlaYtrProGly 180
QY 749 AACATTCACAGACACCATGGTGTGTGTGCGACGCTGCAAGAAAGGGGGCAAGGATCTCTGCAG 808

```

```

DB 181 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyIleYAspSerCysGln 200
QY 809 GGTGACTCCGGGGGCCCTGTGCTGTATACCAAGTCTCTCAAGGCAATTAATTCGCGGGC 868
DB 201 GlysAspSerGlyGlyProleuValCysAsnGlnSerleuGlnGlyIleSertrpGly 220
QY 869 CAGATCCGTGTGCGATCAACCCGAAAGCCTGTGTCTACAGCAAAAGTCTGCAAAATATGTG 928
DB 221 GlnAspProCysAlaIleThrArgIuYsProGlyValIlyThrIlyValCysIuYstrYVal 240
QY 929 GACTGATCCAGAGACGATGAAGAACAAT 958
DB 241 AspTrrpIleGlnGluThrMetIlySAsn 250

```

RESULT 14

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US-10-141-704-506
; Sequence 506, Application US/10141704
; Publication No. US20030134359A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C209
; CURRENT APPLICATION NUMBER: US/10/141,704
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: prt
; ORGANISM: Homo Saplen
US-10-141-704-506

```

Alignment Scores:

```

Pred. No.: 1,85e-87      Length: 250
Score: 1355.00           Matches: 250
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 57.17%      Indels: 0
DB: 12      Gaps: 0

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US-09-856-320A-1 (1-1301) x US-10-141-704-506 (1-250)

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QY 209 ATGAGAGATTCTGACGTAATTAATCTGCTGCTGCGCAACAGGCGCTGTAGGGGAGAGACC 268
DB 1 MetatgileuGlnleuileuileuualaleuAlathGlyleuValGlyGluThr 20
QY 269 AGCATCATCAAGGGGTGAGTGCAGTCAAGCGCTCACTCCGACCGCTGGAGGACCGCTGTC 328
DB 21 AtgilelleuGlyPheGlnCysGlySProHISserGlnProTrrpInlaIaleuPhe 40
QY 329 GAGAAGACGCGGCTACTGTGTGGGGGAGCGACTATCGCCCCAGATGGCTCCGTGACAGCA 388
DB 41 GluYsthrArgleuIeuCysGlyAlathrleuileAlaProArgTrrleuIeuThrAla 60
QY 389 GCCCACTGCTCAAGCCCCGCTACATAGTTCACCTGGGGGACACAACTCCAGAAAGAG 448

```

```

Db      61  Alahiscysleuylsproargtryllevalhisleuglyglnhisasnleuglnlysglu 80
QY      449  GAGGGCTGTGAGACAGACCCGGAGACGACACTAGTCTTCCCGACCCGGCTTCAACAC 508
Db      81  Gluglycysgluglnthrargthralathrgluserpheprohnsproglypheasnsn 100
QY      509  AGCTCCCCAACAAGACACCCGCAATGACATCATGTGGTGAGATGGCATGGCCAGTC 568
Db      101  Serleuproanlysaasphlsargasnaspillemeulleuvallysmetlaserproval 120
QY      569  TCCATCAGCTGGGCTGTGCGACCCCTCACCTCTCTCAGCTGTGTACAGCTGGCGACC 628
Db      121  SerlethrtrpalaivalargProleuthrleuSerSerargCysvalthrAlaelythr 140
QY      629  AGTGGCTCATTTCCGGCTGGGGGAGACAGTCACAGCCCGCAATTACGCTGCTCACACC 688
Db      141  SerCysleuilleserGlytrpGlyserthrSerSerProglInleuArgleuProhlsThr 160
QY      689  TTGGGATGCGCCACATACCATCATCTTGTAGCACAGAAAGTGAGAACGCTTACCCGGGC 748
Db      161  LeuArgCysAlaAsnIlethrIlellegluhlsGlnlyscysgluAsnAlaIatyrProgly 180
QY      749  AACATCAGACAGACCATGATGTGTGTCCAGCGTGAGAGAAAGGGGCAAGGACTCCGGCCAG 808
Db      181  AsnIlethrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGln 200
QY      809  GGTGACTCGGGGGCCCTGTGTGTGTACAGTCTCTTCAAGGCAATTATCTCTGGGGC 868
Db      201  GlyAspSerGlyGlyProleuValCysAsnGlnSerleuGlnGlyIleIleSerTrpGly 220
QY      869  CAGATCCGTGTGGGATACCCCGAAAGCCTGTGTCTACAGAAAGTGTGCAATATATGTG 928
Db      221  GlnAspProCysAlaIlethrArgLysProglyValIlyThrLysValCysLysIlyVal 240
QY      929  GACTGCATCCAGAGACGATGAGAACAAT 958
Db      241  AspTrpIleGlnGlnThrMetLysAsnAsn 250

RESULT 15
US-10-142-421-506
; Sequence 506, Application US/10142421
; Publication No. US20030134360A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C218
; CURRENT APPLICATION NUMBER: US/10/142,421
; PRIORITY FILING DATE: 2002-05-09
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-421-506

```

```

Alignment Scores:
Pred. No.: 1,856-87 Length: 250
Score: 1355.00 Matches: 250
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.17% Indels: 0
DB: 12 Gaps: 0

US-09-856-320A-1 (1-1301) x US-10-142-421-506 (1-250)

QY      209  ATGAGGATTCGAGCTTAATCTCTCTCTGTGGCAACAGGCTTTGTAGGGGAGAGACC 268
Db      1  MetArgIleleuGlnleuIleleuLeuAlaLeuAlaThrIleValGlyGlyLuthr 20
QY      269  AGGATCATCAAGGGTTTGAGTGCAGGCTCACTCCAGCCCTGGAGAGGAGCCCTGTGTC 328
Db      21  ArgIleIleLysGlyPheGlnCysLysProhlsSerGlnProtrpGlnAlaIaleuphe 40
QY      329  GAGAAGACGCGCTACTCTGTGGGGGAGCGCTCATCGCCCGCAGATGGCTCTGACAGCA 388
Db      41  GluLysThrArgleuLeuCysGlyAlaThrIleuIleAlaProLargTrpLeuThrAla 60
QY      389  GCCCAGCTGCTCAAGCCCGCTTACATAGTTACCTGGGGGAGCAAACTTCCAAAGAGAG 448
Db      61  Alahiscysleuylsproargtryllevalhisleuglyglnhisasnleuglnlysglu 80
QY      449  GAGGGCTGTGAGACAGACCCGGAGACGACACTAGTCTTCCCGACCCGGCTTCAACAC 508
Db      81  Gluglycysgluglnthrargthralathrgluserpheprohnsproglypheasnsn 100
QY      509  AGCTCCCCAACAAGACACCCGCAATGACATCATGTGGTGAGATGGCATGGCCAGTC 568
Db      101  Serleuproanlysaasphlsargasnaspillemeulleuvallysmetlaserproval 120
QY      569  TCCATCAGCTGGGCTGTGCGACCCCTCACCTCTCTCAGCTGTGTACAGCTGGCGACC 628
Db      121  SerlethrtrpalaivalargProleuthrleuSerSerargCysvalthrAlaelythr 140
QY      629  AGTGGCTCATTTCCGGCTGGGGGAGACAGTCACAGCCCGCAATTACGCTGCTCACACC 688
Db      141  SerCysleuilleserGlytrpGlyserthrSerSerProglInleuArgleuProhlsThr 160
QY      689  TTGGGATGCGCCACATACCATCATCTTGTAGCACAGAAAGTGAGAACGCTTACCCGGGC 748
Db      161  LeuArgCysAlaAsnIlethrIlellegluhlsGlnlyscysgluAsnAlaIatyrProgly 180
QY      749  AACATCAGACAGACCATGATGTGTGTCCAGCGTGAGAGAAAGGGGCAAGGACTCCGGCCAG 808
Db      181  AsnIlethrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGln 200
QY      809  GGTGACTCGGGGGCCCTGTGTGTGTACAGTCTCTTCAAGGCAATTATCTCTGGGGC 868
Db      201  GlyAspSerGlyGlyProleuValCysAsnGlnSerleuGlnGlyIleIleSerTrpGly 220
QY      869  CAGATCCGTGTGGGATACCCCGAAAGCCTGTGTGTACAGAAAGTGTGCAATATATGTG 928
Db      221  GlnAspProCysAlaIlethrArgLysProglyValIlyThrLysValCysLysIlyVal 240
QY      929  GACTGCATCCAGAGACGATGAGAACAAT 958
Db      241  AspTrpIleGlnGlnThrMetLysAsnAsn 250

```

Search completed: October 15, 2003, 20:55:02
 Job time : 174.824 secs

XX 17-MAR-1999; 99WO-EP01894.
 XX 20-MAR-1998; 98GB-0006095.
 XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX Bruck CEM, Cassart J, Coche T, Vinals-bassols C;
 DR WPI; 1999-580450/49.
 DR N-PSDB; AA22638.
 PT New human serine protease CASB12, for treatment, prevention and
 PT diagnosis of cancer and autoimmune diseases
 XX
 PS Claim 3; Page 48; 58pp; English.

CC This is the amino acid sequence of the CASB12 protein. The nucleotide
 CC sequence of AA22638 shows homology with neuropsin and the encoded
 CC protein AAV42439 is structurally related to other proteins of the
 CC serine protease family, having homology and/or structural similarity
 CC with neuropsin. It is expected that as well as similar structure, these
 CC proteins will also share similar biological functions and properties.
 CC The CASB12 polypeptides and polynucleotides can be used to develop
 CC methods for identifying agonists and antagonists/inhibitors of these
 CC molecules, and thereby treating conditions associated with CASB12
 CC polypeptide imbalance. The invention also provides for diagnostic assays
 CC for detecting diseases associated with inappropriate CASB12 polypeptide
 CC activity or levels.
 CC Since CASB12 is either specifically expressed or highly over-expressed
 CC in tumors compared to normal cells, the polypeptides and polynucleotides
 CC of the invention are believed to be important immunogens for specific
 CC prophylactic or therapeutic immunization against tumors. The
 CC polypeptides and polynucleotides can therefore be targeted by antigen
 CC specific immune reactions (which result in the destruction of the tumor
 CC cell) or they can be used to diagnose the occurrence of tumor cells
 XX
 SO Sequence 282 AA:

Alignment Scores:
 Pred. No.: 2,24e-110 Length: 282
 Score: 1523.00 Matches: 282
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 64.26% Indels: 0
 DB: 20 Gaps: 0

US-09-856-320A-1 (1-1301) x AAV42439 (1-282)

OY 113 ATGCAGAGGTTGAGGTGGCTGGGAGTGCATGATCGGGCAGAGTCTCAGACGACC 172
 DB 1 MetGlnArgLeuAlaGlyTrpLeuAlaGlyAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
 OY 173 AAGGACCTGGGGCGGCTCTCTCCCTCCAGGCGCATGAGATTGCGAGTTATCTCTG 232
 DB 21 LysGlnProGlyAlaArgSerProLeuGlnAlaMetAlaGlyLeuGlnLeuLeu 40
 OY 233 CTTCCTGTGGCAGACGGCTTGTAGGGGAGAGACGACGATCATCAAGGGCTGTGAGTGC 292
 DB 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLurThrArgIleIleLysGlyPheGlnLys 60
 OY 293 AAGCCTCACTCCAGCCCTGGCAGGACGCTGTTCGAGAAAGCGGCTACTGTGGG 352
 DB 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysTrpArgLeuLeuGlyGly 80
 OY 353 GCGACGCTCAGTCCGCCCAAGTGGCTCTGACAGCAGCCCATGCTCAACCCCGCTAC 412
 DB 81 AlaThrLeuIleAlaProAlaGlyTrpLeuThrAlaAlaHisCysLeuLysProArgTyr 100
 OY 413 ATAGTTCACCTGGGGCAGACACCTCCAGAAAGAGAGAGGGCTGTGAGCAGACCGGACA 472
 DB 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlnLysGlnLysGlnLysGlnLys 120

OY 473 GCCACTGAGTCTTCCCGCCAGCCGGCTTCACACACAGCTCCCAACAAAGACACCGC 532
 DB 121 AlaThrGlnSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
 OY 533 AATGACATCATGCTGGTGAAGATGTCATCGGCATGCTCCTCAGTGGGCTGTGCGACC 592
 DB 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
 OY 593 CTCACCCCTCTCCTCAGCGCTGTGTGCTGCTGACAGCAGCTGCTCATTTCCGGCTGGGC 652
 DB 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrPhe 180
 OY 653 AGCAGCTCCAGCCCGCCAGTACGCTGCTCAGACCTTGCGATGCGCCACATCAGCATC 712
 DB 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
 OY 713 ATTAGACACCAAGTGTGAGAGAGCCATCCCGCCCAACATCAGACACCATGCTGTGT 772
 DB 201 IleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
 OY 773 GCCAGCGTCAGAAAGGGGCGCAGAGACTCTGCGCAGGCTGACCTCGGGGCGCTGTGTC 832
 DB 221 AlaSerValGlnGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyLysProLeuVal 240
 OY 833 TGTAACACGTCTCTTCAAGGCATTATCTCTGGGGCCAGATCCGCTGCGATACCCGA 892
 DB 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
 OY 893 AAGCCTGTCTCTACAGCAAGTCTGCAATATGATGAGTGCATGACAGACGATGATG 952
 DB 261 LysProGlyValIlyrThrLysValCysLysTyrValAspTrpIleGlnLysThrMetLys 280
 OY 953 AACCAAT 958
 DB 281 AsnAsn 282

RESULT 2

AB11712
 ID AB11712 standard; Protein: 282 AA.

AC AB11712;

DT 23-OCT-2000 (first entry)

DE Human serine protease BSSP6 (hBSSP6) SEQ ID NO:2.

DE BSSP6: serine protease; human; hBSSP6; mouse; MBSSP6; brain;

KW diagnostic marker; antibody; transgenic animal; Alzheimer's disease;

KW epilepsy; cancer; inflammation; infertility; pancreatitis;

OS prostatic hypertrophy.

OS Homo sapiens.

PN WO200031257-A1.

PD 02-JUN-2000.

PF 19-NOV-1999; 99WO-JP06476.

PR 20-NOV-1998; 98JP-0347802.

PA (FUSO) FUSO PHARM IND LTD.

PI Uemura H, Okui A, Komlami K, Yamaguchi N, Mitsui S;

DR WPI: 2000-400067/34.

DR N-PSDB; AAA61763.

PT Serine protease BSSP6, useful in detecting homologs, mutants and
 PT polymorphic variants as markers for diagnosis of Alzheimer's disease,
 PT epilepsy, cancer, inflammation, infertility and prostate hypertrophy,
 PT using blood or other tissues

PS Claim 1; Page 69-70; 94pp; Japanese.

CC The invention relates to novel serine proteases designated BSSP6
CC (AA611712-B11714) and to nucleic acids encoding them (AA61763-661765).
CC (AA611712-B11714) and to nucleic acids encoding them (AA61763-661765).
CC The invention also relates to vectors and transformants comprising BSSP6
CC nucleic acids; transgenic animals in which the expression level of BSSP6
CC can be varied; and an mBSSP6 knockout mouse. The invention additionally
CC encompasses anti-BSSP6 antibodies and methods of production of such
CC antibodies, methods of BSSP6 detection using the antibodies, and the
CC use of BSSP6 proteins or fragments as diagnostic markers for certain
CC medical conditions. Nucleotides encoding BSSP6 were initially
CC isolated in a human brain cDNA library using degenerate PCR primers
CC (AA61793-A61796) based on conserved regions of serine proteases. The
CC BSSP6 serine proteases and nucleotides encoding them are useful in
CC detecting homologous, mutants and polymorphic variants in biological
CC samples (e.g., blood, urine, brain, prostate gland, placenta, testis
CC and spleen) as diagnostic markers for conditions such as Alzheimer's
CC disease, epilepsy, cancer, inflammation, infertility and prostatic
CC hypertrophy. Sequences AA61172 and AA61174 represent human BSSP6
CC variants (mBSSP6), and sequence AA61173 represents murine BSSP6
CC (mBSSP6).

Alignment Scores:	
Pred. No.:	2, 24e-110
Score:	1523.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	64, 26%
DB:	21
	Gaps:
	0
	Length:
	282
	Matches:
	282
	Conservative:
	0
	Mismatch:
	0
	Indels:
	0
	Gaps:
	0

FT	/note=	"this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
FT	192	
FT	/note=	"potential protein kinase C phosphorylation site"
FT	195	
FT	/note=	"this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
FT	197	
FT	/note=	"potential N-glycosylation site"
FT	199	
FT	/note=	"potential casein kinase II phosphorylation site"
FT	206	
FT	/note=	"this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
FT	213	
FT	/note=	"potential N-glycosylation site"
FT	220	
FT	/note=	"this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
FT	222	
FT	/note=	"potential casein kinase II phosphorylation site"
FT	229..240	
FT	/note=	"serine protease trypsin family active site motif"
FT	229	
FT	/note=	"the corresponding residue (together with Ser235, Gly252 and Gly263) in neuropsin forms a oxyanion hole"
FT	231	
FT	/note=	"this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
FT	235	
FT	/note=	"the corresponding residue (together with Asp229, Gly252 and Gly263) in neuropsin forms a oxyanion hole"
FT	235	
FT	/note=	"this forms the active site catalytic triad with His94 and Asp142"
FT	241	
FT	/note=	"this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
FT	242	
FT	/note=	"potential N-glycosylation site"
FT	252	
FT	/note=	"the corresponding residue (together with Asp229, Ser235 and Gly263) in neuropsin forms a oxyanion hole"
FT	256	
FT	/note=	"this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
FT	259	
FT	/note=	"potential protein kinase C phosphorylation site"
FT	263	
FT	/note=	"the corresponding residue (together with Asp229, Ser235 and Gly263) in neuropsin forms a oxyanion hole"
FT	278	
FT	/note=	"potential protein kinase C phosphorylation site"
XX	MO99A41387-A2.	
XX	PD	
XX	19-AUG-1999.	
XX	05-FEB-1999;	99MO-USO2571.
XX	17-FEB-1998;	98US-0025059.
XX		

Accession	Sequence	Length	Matches	Conservative	Mismatches	Indels	Gaps
PA (INCYTE PHARM INC.							
XX							
PI Tang YT, Corley NC, Guejler KJ;							
XX							
DR WP1; 2000-012993/01.							
XX							
DR N-PSDB: AA230222.							
XX							
PT New prostate-associated serum protease and polynucleotides which							
PT identify and encode PRASP, useful for treating reproductive disorders							
PI and cancer							
PS							
XX							
XX	Claim 1; Fig 1A-D; 67pp; English.						
CC							
CC	The present sequence represents human prostate-associated serum protease						
CC	(PRASP). The protein shows homology to neuropilin, a brain-specific						
CC	protease in mice, and PSA, a prostate-specific protease in humans.						
CC	Nucleic acids encoding PRASP were first identified in Incyte clone						
CC	273666 from the lung tumour cDNA library. Pharmaceutical compositions						
CC	containing PRASP, or antibodies to PRASP, and mimetics, agonists,						
CC	antagonists or inhibitors of PRASP, are used for treating or preventing						
CC	a reproductive disorder or cancer. Examples of reproductive disorder						
CC	include, abnormal prolactin production, infertility, tubal disease,						
CC	ovulatory defects, endometriosis, polycystic ovary syndrome, autoimmune						
CC	disorders, ectopic pregnancy, breast cancer, abnormal spermatogenesis						
CC	and testicular cancer. Examples of cancers which may be treated or						
CC	prevented include adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma,						
CC	sarcoma, teratocarcinoma, and cancers of the adrenal gland, bladder,						
CC	bone, bone marrow, brain, breast, cervix, penis, prostate, salivary						
CC	glands, skin, spleen, testis, thymus, thyroid and uterus. A vector						
CC	capable of expressing PRASP or an agonist which modulates the activity of						
CC	PRASP may be administered to treat or prevent a reproductive disorder or						
CC	cancer.						
XX							
XX	Sequence 282 AA;						
S0							
Alignment Scores:							
Pred. NO.:	2,24e-110	Length:	282				
Score:	1523.00	Matches:	282				
Percent Similarity:	100.00%	Conservative:	0				
Best Local Similarity:	100.00%	Mismatches:	0				
Query Match:	64.26%	Indels:	0				
DB:	21	Gaps:	0				
US-09-856-320A-1 (1-1301) x AAY43636 (1-282)							
OY	113 ATGCAGAGGTTGAGGGTGGCTGGGGAGACTGGAAGTATGCGGACAGGTCTACAGACAGCC						
DB	1 MetcGlnArGleuNArGtrPrleuNArGsArPrIlySerSerGlyArGgLYleuThrAlaLa						
OY	173 AAGGAACCTGGGGCCGGCTCCGCCGCCGCCCGGACATGAGAGATTCGCACTTAATCTG						
DB	21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArGgLYleuGlnLeuLeu						
OY	233 CTTCGCTCTGGCAACAGGGCTTGAAGGGGAGAGACAGGATCATCMAAGGGTGTGAGTGC						
DB	41 LeuAlaLeuNArHrGlyLeuValGlyGlyGluThrArgIleIleIleYsgLYphGluCys						
OY	293 AAGCTCATCTCCACAGCCCTGGGACGAGCCCTGTTCGAAAGACGGCTACTGTGGGG						
DB	61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluIlyThrArgLeuLeuGlyGly						
OY	353 GGCAGCGTATGCGCCCGAGATGGGCTCCGACAGAGCCCATCGCTCAAGCCCGGCTAC						
DB	81 AlaThrLeuLeuLeuProArGtrPrleuLeuThrAlaAlaHisCysLYleuYsProAlGlyr						
OY	413 ATATGTTACACTGGGAGGACACAACCTCCAGAAGAGAGAGGCTGTGAGACAGCCGAGCA						
DB	101 IleValHisLeuGlyIlyHisHisLeuGlnIlyGlyGluGlyGlyGluGlnIlyThrArgThr						
OY	473 GCCACTGAGTCTTCCCGCCAGCCCGGCTTCAACAACAGCCCTCCCAACAAAGACACCGC						
DB	121 AlaThrGlySerThrProHisProGlyPrleuHisHisSerLeuProAlnLYAspHISArg						


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Db      221  AAserValGIngluGlyLysaspSerCysgInglYaspSerGlyProleuVal 240
QY      833  TGIACCAAGTCCTCAAGGATATATCTCGGGCCAGGATCCGTGGCCATCCGCCA 892
Db      241  CysangInSerleuGInGlyIleIleSerTrpGlyInaspProCysAlaIleThrArg 260
QY      893  AAGCCTGTGTCTACACCAAGTCGCAATATGTGACGTGATCCAGAGACGATGAAG 952
Db      261  LysProGlyValIYrThrLysValCysLysTyValAspTrpIleGIngluThrMetLys 280
QY      953  AAC 955
Db      281  Asn 281

RESULT 5
AAB21325
ID  AAB21325 standard; Protein; 250 AA.
XX
AC  AAB21325;
XX
DT  02-FEB-2001 (first entry)
XX
DE  Human TLSP.
XX
KM  Human; KIK-L1; KIK-L2; KIK-L3; KIK-L4; KIK-L5; KIK-L6; TLSP;
KW  trypsin-like serine protease; kallikrein-like protein; serine protease;
KM  cytosolic; cancer; prostate cancer.
XX
OS  Homo sapiens.
XX
PN  WO200053776-A2.
PD  14-SEP-2000.
XX
PF  09-MAR-2000; 2000WO-CA00258.
XX
PR  11-MAR-1999; 99US-0124260.
PR  01-APR-1999; 99US-0127386.
PR  21-JUL-1999; 99US-0144919.
XX
PA  (MOON ) MOUNT SINAI HOSPITAL.
XX
PI  Yousef GM, Diamandis EP;
XX
DR  WPI; 2000-587440/55.
XX
PT  New kallikrein-like (KIK-L) proteins for diagnosing and treating KIK-L
PT  protein mediated disorders, especially cancer.
XX
PS  Example 5; Fig 27; 184pp; English.
XX
CC  The present sequence is human trypsin-like serine protease (TLSP), a
CC  member of the serine protease family. Kallikreins and
CC  kallikrein-like proteins are a subgroup of the serine protease enzyme
CC  family. They catalyze the selective cleavage of specific polypeptide
CC  precursors to release peptides with potent biological activity. Nucleic
CC  acids encoding kallikrein-like proteins KIK-L1, KIK-L2, KIK-L3, KIK-L4,
CC  KIK-L5 and KIK-L6 have been isolated. The proteins are useful in the
CC  treatment, monitoring and diagnosis of cancers, especially prostate
CC  cancer. They can also be used to identify a substance that can associate
CC  with or mediate the biological activity of the proteins. Antibodies can
CC  be used to treat conditions mediated by the kallikrein-like proteins.
XX
SQ  Sequence 250 AA;

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US-09-856-320A-1 (1-1301) x AAB21325 (1-250)
QY      209  ATGAGGATTCGCGAGTTAATCTGCTGCTGGCAACAGGGCTTGAAGGGGAGAGACC 268
Db      1  MetArgIleLeuGInleuIleLeuLeuAlaLeuAlaThrGlyLeuValGlyGlyIuThr 20
QY      269  AGATATCATCAAGGGGTTCTGACTGCAAGCCCTCACTCCAGCCCTGGCAGGAGCCCTGTC 328
Db      21  ArgIleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaIleLeuPhe 40
QY      329  GAGAAAGACGGCGCTACTGTGTGGGCGACGCTCATCGCCCGCCAGATGGCTCTGACAGCA 388
Db      41  GluLysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThrAla 60
QY      389  GCCCAGCTGCTCAAGCCCCGCTACATAGTTACCTGGGGGAGCAGCAACCTCCAGAGAG 448
Db      61  AlaHisCysLeuLysProArgTrpIleValHisLeuGlnHisAsnLeuGlnLysGlu 80
QY      449  GAGGCGTGTGAGACAGCCCGGACAGCCAGCTGAGTCCTTCCCGCCAGCCGCTTCACAGAC 508
Db      81  GluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsn 100
QY      509  AGCCTCCCGCCACAAGACCCAGCCAGATGACATCATGCTGGTGAAGATGGCATCCCGCAGTC 568
Db      101  SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 120
QY      569  TCCATCACTGAGGTGTGTCGACCCCTCAGCTCCTCAGCTGTCAGTGTGTCGAGCAGC 628
Db      121  SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 140
QY      629  AGCTGCTCATTTCCGGCTGGGCGACAGCAGTCACGCCCGCCAGTTACGCTGCTCAGACC 688
Db      141  SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 160
QY      689  TTGGGAGCGCCACATCATCATGAGACAGACAGAGTGTGAACCGCTTACCCGGCC 748
Db      161  LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaLysProGly 180
QY      749  AACATCAAGACACCATGCTGTGTCGACGCTGAGAGAGGGGCGCAAGAGATCTGCGCAG 808
Db      181  AsnIleThrAspTrpMetValCysAlaSerValGlnGluGlyLysAspSerCysGln 200
QY      809  GGTGACTCCGGGGGCGCTGTGCTGTATACCATGCTCTTCAAGGCAATATCTCTGGGGC 868
Db      201  GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 220
QY      869  CAGATCCGTTGGGATCACCCGAAAGCTGCTGTACAGCAAGTGTGAATATAGTG 928
Db      221  GlnAspProCysAlaIleThrArgLysProGlyValIYrThrLysValCysLysTyVal 240
QY      929  GACTGATCCAGAGAGCATGAGACAAAT 958
Db      241  AspTrpIleGlnGluThrMetLysAsnAsn 250

RESULT 6
AAY99390
ID  AAY99390 standard; Protein; 250 AA.
XX
AC  AAY99390;
XX
DT  08-AUG-2000 (first entry)
XX
DE  Human PRO1279 (UNQ649) amino acid sequence SEQ ID NO:170.
XX
KM  Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW  transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
XX
OS  Homo sapiens.
XX
PN  WO200012708-A2.
XX
DB: 09-MAR-2000.

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XX	01-SEP-1999;	99WO-US2011.	PR	07-OCT-1998;	98US-0103401.
XX	01-SEP-1998;	98US-0098716.	PR	08-OCT-1998;	98US-0103633.
PR	01-SEP-1998;	98US-0098749.	PR	08-OCT-1998;	98US-0103678.
PR	01-SEP-1998;	98US-0098803.	PR	08-OCT-1998;	98US-0103679.
PR	02-SEP-1998;	98US-0098803.	PR	08-OCT-1998;	98US-0103711.
PR	02-SEP-1998;	98US-0098821.	PR	14-OCT-1998;	98US-0104257.
PR	02-SEP-1998;	98US-0098843.	PR	20-OCT-1998;	98US-0104987.
PR	02-SEP-1998;	98US-0099536.	PR	20-OCT-1998;	98US-0105000.
PR	09-SEP-1998;	98US-0099596.	PR	21-OCT-1998;	98US-0105104.
PR	09-SEP-1998;	98US-0099599.	PR	22-OCT-1998;	98US-0105169.
PR	09-SEP-1998;	98US-0099602.	PR	22-OCT-1998;	98US-0105266.
PR	09-SEP-1998;	98US-0099642.	PR	26-OCT-1998;	98US-0105693.
PR	10-SEP-1998;	98US-0099741.	PR	26-OCT-1998;	98US-0105694.
PR	10-SEP-1998;	98US-0099754.	PR	27-OCT-1998;	98US-0105807.
PR	10-SEP-1998;	98US-0099763.	PR	27-OCT-1998;	98US-0105881.
PR	10-SEP-1998;	98US-0099792.	PR	27-OCT-1998;	98US-0105882.
PR	10-SEP-1998;	98US-0099808.	PR	27-OCT-1998;	98US-0106062.
PR	10-SEP-1998;	98US-0099812.	PR	28-OCT-1998;	98US-0106023.
PR	10-SEP-1998;	98US-0099815.	PR	28-OCT-1998;	98US-0106029.
PR	15-SEP-1998;	98US-0100385.	PR	28-OCT-1998;	98US-0106030.
PR	15-SEP-1998;	98US-0100388.	PR	28-OCT-1998;	98US-0106032.
PR	15-SEP-1998;	98US-0100390.	PR	28-OCT-1998;	98US-0106033.
PR	16-SEP-1998;	98US-0100584.	PR	29-OCT-1998;	98US-0106178.
PR	16-SEP-1998;	98US-0100627.	PR	29-OCT-1998;	98US-0106248.
PR	16-SEP-1998;	98US-0100661.	PR	29-OCT-1998;	98US-0106384.
PR	16-SEP-1998;	98US-0100662.	PR	29-OCT-1998;	98US-0108500.
PR	16-SEP-1998;	98US-0100664.	PR	30-OCT-1998;	98US-0106454.
PR	17-SEP-1998;	98US-0100663.	PR	03-NOV-1998;	98US-0106856.
PR	17-SEP-1998;	98US-0100684.	PR	03-NOV-1998;	98US-0106902.
PR	17-SEP-1998;	98US-0100710.	PR	03-NOV-1998;	98US-0106905.
PR	17-SEP-1998;	98US-0100711.	PR	03-NOV-1998;	98US-0106919.
PR	17-SEP-1998;	98US-0100919.	PR	03-NOV-1998;	98US-0106932.
PR	17-SEP-1998;	98US-0100930.	PR	10-NOV-1998;	98US-0107783.
PR	16-SEP-1998;	98US-0100848.	PR	17-NOV-1998;	98US-0108775.
PR	18-SEP-1998;	98US-0100849.	PR	17-NOV-1998;	98US-0108779.
PR	18-SEP-1998;	98US-0101014.	PR	17-NOV-1998;	98US-0108787.
PR	18-SEP-1998;	98US-0101068.	PR	17-NOV-1998;	98US-0108788.
PR	22-SEP-1998;	98US-0101071.	PR	17-NOV-1998;	98US-0108801.
PR	22-SEP-1998;	98US-0101279.	PR	17-NOV-1998;	98US-0108802.
PR	23-SEP-1998;	98US-0101471.	PR	17-NOV-1998;	98US-0108806.
PR	23-SEP-1998;	98US-0101472.	PR	17-NOV-1998;	98US-0108807.
PR	23-SEP-1998;	98US-0101474.	PR	17-NOV-1998;	98US-0108867.
PR	23-SEP-1998;	98US-0101475.	PR	17-NOV-1998;	98US-0108925.
PR	23-SEP-1998;	98US-0101476.	PR	16-NOV-1998;	98US-0108848.
PR	23-SEP-1998;	98US-0101477.	PR	18-NOV-1998;	98US-0108849.
PR	24-SEP-1998;	98US-0101738.	PR	18-NOV-1998;	98US-0108850.
PR	24-SEP-1998;	98US-0101741.	PR	18-NOV-1998;	98US-0108851.
PR	24-SEP-1998;	98US-0101743.	PR	18-NOV-1998;	98US-0108852.
PR	24-SEP-1998;	98US-0101915.	PR	18-NOV-1998;	98US-0108858.
PR	24-SEP-1998;	98US-0101916.	PR	18-NOV-1998;	98US-0108904.
PR	29-SEP-1998;	98US-0102207.	XX	(GETH) GENENTECH INC.	
PR	29-SEP-1998;	98US-0102240.	XX		
PR	29-SEP-1998;	98US-0102307.	PI	Baker K,	

CC PCR primers and hybridisation probes used in the isolation of the PRO
CC polypeptides from the present invention.

XX Sequence 250 AA:

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score: 2.68e-97	250	250	0	0	0	0
Percent Similarity: 100.00%						
Best Local Similarity: 100.00%						
Query Match: 57.17%						
DB: 21						

US-09-856-320a-1 (1-1301) x AAY93930 (1-250)

```

OY 209 ATGAGGATTCGACGATTATTCCTGCTGGCAGACAGGGCTGTGAGGGGAGAGACC 268
DB 1 MetArgLeuGlnLeuIleLeuLeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThr 20
OY 269 AGGATCATCAAGGGGTTGAGTGCAGAGCTTCACCTCCAGCCCTGGCAGGACGCTGTTC 328
DB 21 ArgIleIleGlyGlyPheGlyCysLeuProHisSerGlnProTyrGlnAlaAlaLeuPhe 40
OY 329 GAGAGAGAGGGGCTACTGTCGAGGGGCGACGTCATCGCCCGACATGGCTCTGTGACAGCA 388
DB 41 GlnGlyThrArgLeuLeuGlyGlyAlaThrLeuIleAlaProArgTyrPheLeuValAla 60
OY 389 GCCCACTGCTCAAGCCCCGCTACATAGTTCACCTGGGGGAGCAGCAACCTCCAGAGAG 448
DB 61 AlaHisCysLeuGlyProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLeuGlu 80
OY 449 GAGGGCTGTGAGCAGACCCGAGCAGCCAGCTGCTCCGCCACCCGCTTCAACAC 508
DB 81 GlnGlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsn 100
OY 509 AGCTCCCAACAAAGACACCGCATATGATGATGCGTGGAGATGGATGGATGGATGTC 568
DB 101 SerLeuProAsnGlyAspHisArgAsnAspIleMetLeuValGlyMetAlaSerProVal 120
OY 569 TCCATACCTGGGCTGTGAGACCCCTCACCCTCTCAGCTGTGTCTGTCAGCACC 628
DB 121 SerIleThrThrAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 140
OY 629 AGTGGCCGATTCGCGGCTGGGGGAGCAGCTCCAGCCCGGATACCGCTCCCTCACACC 688
DB 141 SerCysLeuIleSerGlyTyrPglySerThrSerSerProGlnLeuArgLeuProHisThr 160
OY 689 TTGGGATGCGCCACATCACCATCATTTGAGCAGCAGAAAGTGTGAGAAAGCCTACCCGAG 748
DB 161 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnGlyGlyGlyGlyGlyGlyGlyGly 180
OY 749 AACATCAGACAGACCATGCTGTGTCGACGCTGAGAGAGGGGGCAGAGGACTCTGCCAG 808
DB 181 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyGlyGlyGlyGlyGly 200
OY 809 GGTGATCCGGGGGCGCCCTGCTGTGTAACAGCTCTTCAAGCATATATCTCTGGAGGC 868
DB 201 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrPgly 220
OY 869 CAGATCGATGCTGATCAGTACCCGAAAGCCTGCTGTACAGCAAGTGTGCAAAATATGTCG 928
DB 221 GlnAspProCysAlaIleThrArgGlyProGlyValIleThrIleValCysGlyTyrVal 240
OY 929 GACTGATCCGAGAGCAGATGAGAACAAAT 958
DB 241 AspTyrIleGlnGlnIleThrMetGlyAsnAsn 250

```

RESULT 7

ABBS0479 standard: Protein: 250 AA.

XX ABB50479;
AC ABB50479;
XX

DT 07-FEB-2002 (first entry)
XX
DE Human secreted protein encoded by gene 179 SEQ ID NO:427.
XX

Human: secreted protein; immunomodulatory; antisclerotic; anti-HIV; dermatological; immunosuppressive; antiinflammatory; immunostimulant; cytoskeletal; cardiac; anti-angiogenic; ophthalmological; neuroprotective; nootropic; anticonvulsant; antialzheimers; vulnery; antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder; multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer; human immunodeficiency virus; hyperproliferative disorder; wound healing; Gaucher's disease; cardiovascular disease; Schmittar syndrome; chemotaxis; Chaga's cardiomyopathy; coronary arteriosclerosis; angiogenic disorder; corneal graft neovascularisation; diabetic retinopathy; regeneration; neurological disorder; Huntington's chorea; Alzheimer's disease; Parkinson's disease; infectious disease.

OS Homo sapiens.

PN WO200162891-A2.

PD 30-AUG-2001.

PE 21-FEB-2001; 2001WO-US05614.

PR 24-FEB-2000; 2000US-184836P.

PR 29-MAR-2000; 2000US-193170P.

PA (HMA-) HUMAN GENOME SCI INC.

PI Nt J, Edner R, Lafleur DW, Moore PA, Olsen HS, Rosen CA;
PI Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;
PI Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferrle AM, Fan P;
PI Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G;
PI Zeng Z, Greene JM;

DR WPI: 2001-625724/72.
DR N-PSDB: ABA83372.

XX Nucleic acids encoding 207 human secreted polypeptides, useful for
PT preventing, diagnosing and/or treating, e.g. cancers, Parkinson's
PT disease and diabetic retinopathy -
XX

XX Claim 11; Page 1181-1182; 153pp; English.

XX ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted
CC proteins (I) and polynucleotide (II) sequences. (I) and (II) have various
CC activities based on the tissues and cells the genes are expressed in.
CC Example of these activities include: immunomodulatory; antisclerotic;
CC dermatological; immunosuppressive; antiinflammatory; immunostimulant;
CC anti-HIV; cytoskeletal; cardiac; anti-angiogenic; ophthalmological;
CC neuroprotective; nootropic; anticonvulsant; antialzheimers; vascular;
CC antiparkinsonian; antimicrobial; and vulnery. (I) and (II) can be used
CC in gene therapy and vaccine production. (I) and (II) can be used in the
CC prevention, diagnosis and treatment of immune disorders (e.g. multiple
CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus
CC (HIV) infections), hyperproliferative disorders (e.g. cancers and
CC Gaucher's disease), cardiovascular diseases (e.g. Schmittar syndrome,
CC Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic
CC disorders (e.g. corneal graft neovascularisation and diabetic
CC retinopathy), neurological disorders (e.g. Huntington's chorea,
CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or
CC for promoting wound healing, regeneration and/or chemotaxis. ABA83185 to
CC ABA83193 and ABB50300 represent sequences used in the exemplification of
CC the present invention.
XX

XX Sequence 250 AA;

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:
Score: 2.68e-97	250	250	0	0
Percent Similarity: 100.00%				
Best Local Similarity: 100.00%				

Query Match: 57.17% Indels: 0
 DB: 22 Gaps: 0
 US-09-856-320A-1 (1-1301) x ABB50479 (1-250)

QY 209 ATGAGGATCTCGACTTAATCTGCTGTGCTGGACACAGGGCTGTAGGGGAGAGACC 268
 DB 1 MetArgIleLeuGlnLeuIleLeuLeuAlaLeuAlaThrGlyLeuValGlyGlyIuThr 20
 QY 269 AGCATCATCAAGGGGTTCGATGCAAGCCTCACTCCAGCCTGGAGGACGCCGTTC 328
 DB 21 ArgIleIleLysGlyPheGlnLysLysProHisSerGlnProTyrPheIleAlaLeuPhe 40
 QY 339 GAGAAGACGGGCTACTGTGTGGGAGACGCTATCGCCCCAGATGGCTCTCTGACAGA 388
 DB 41 GlyLysThrArgLeuLeuLysGlyAlaThrLeuIleAlaProArgTyrLeuThrAla 60
 QY 389 GCGCCACTGCTCAACCCCGCTACATAGTCACTGGGGGACACAACTCCAGAAAGAG 448
 DB 61 AlaHisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisLeuGlnLysGln 80
 QY 449 GAGGCTGTGAGCACACCCGACGACGCACTGAGTCTTCCCGCCGCGCTTCAACAG 508
 DB 81 GluGlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsn 100
 QY 509 AGCTTCCCAACAAAGACACCGCAATGACATCATGCTGTGAGATGGCATCGCCAGTC 568
 DB 101 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 120
 QY 569 TCATCATCACTGGGCTGTGCGACCCCTCACTCTCTCAAGCTGTGTCACTGCTGGACC 628
 DB 121 SerIleThrIlePheAlaValAlaArgProLeuThrLeuSerSerArgCysValThrIleGlyThr 140
 QY 629 AGCTGCTCATTTCCGGCTGGGGGACGACGCTCACGCCCCCAATGACGCTGCTCAAC 688
 DB 141 SerCysIleIleIleSerGlyTyrPheLysThrSerThrSerProGlnIleuArgLeuProHisThr 160
 QY 689 TTGCAGTGGCCACATCATCACTGATGACACGAGAGTGTGAGAACGCTTACCCCGGC 748
 DB 161 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaLarTyrProGly 180
 QY 749 AACATCACAGACACCATGCTGTGTGCGACGCTGCGAGGAAGGGGGACAGAGCTCTGCCAG 808
 DB 181 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 200
 QY 809 GGTGACTCGGGGGCCCTGTGGTGTGTAAACAGTCTCTTCAAGGCAATATCTCTGGGAC 868
 DB 201 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrPhe 220
 QY 869 CAGGATCCGTGTGCGATCAACCCGAAAGCTGTGTACACGAAAGTCTGCAATATGTG 928
 DB 221 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValLysLysTyrVal 240
 QY 929 GACTGATCCAGGAGACGATGAGAAACAAT 958
 DB 241 AspThrIleGlnGlnThrMetLysAsn 250

RESULT 8
 AAU12424 ID AAU12424 standard; Protein: 250 AA.
 AC AAU12424;
 DT 24-OCT-2001 (first entry)
 XX Human PRO1279 polypeptide sequence.
 DE Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 KM breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
 KM cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
 KW adipocyte; A-peptide; factor VIIA; gene therapy.
 XX Homo sapiens.
 OS

XX WO200140466-A2.
 PN 07-JUN-2001.
 XX 01-DEC-2000; 2000MO-US32678.
 PD 01-DEC-1999; 99MO-US28301.
 XX 01-DEC-1999; 99MO-US28634.
 PR 02-DEC-1999; 99MO-US28551.
 PR 02-DEC-1999; 99MO-US28564.
 PR 09-DEC-1999; 99MO-US28565.
 PR 16-DEC-1999; 99MO-US170262.
 PR 20-DEC-1999; 99MO-US30911.
 PR 20-DEC-1999; 99MO-US30999.
 PR 30-DEC-1999; 99MO-US31243.
 PR 06-JAN-2000; 2000MO-US00277.
 PR 06-JAN-2000; 2000MO-US00376.
 PR 11-FEB-2000; 2000MO-US03565.
 PR 18-FEB-2000; 2000MO-US04341.
 PR 18-FEB-2000; 2000MO-US04342.
 PR 22-FEB-2000; 2000MO-US04414.
 PR 24-FEB-2000; 2000MO-US04914.
 PR 24-FEB-2000; 2000MO-US05004.
 PR 01-MAR-2000; 2000MO-US05601.
 PR 20-MAR-2000; 2000MO-US07377.
 PR 21-MAR-2000; 2000MO-US07532.
 PR 30-MAR-2000; 2000MO-US08439.
 PR 17-MAY-2000; 2000MO-US13705.
 PR 22-MAY-2000; 2000MO-US14042.
 PR 30-MAY-2000; 2000MO-US14941.
 PR 02-JUN-2000; 2000MO-US15264.
 PR 10-NOV-2000; 2000MO-US30873.
 PA (GENTH) GENENTECH INC.
 XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI: 2001-408281/43.
 DR N-PSDB: AAS21496.
 XX Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical
 XX Claim 12; Fig 506; 813pp; English.
 PS AAU12172-AAU12446 represent novel human secretory and transmembrane
 XX PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, or the release of a cytokine from peripheral blood
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.
 XX Sequence 250 AA;
 SQ

Alignment Scores:

Pred. No.: 2,686-97 Length: 250
 Score: 1355.00 Matches: 250
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 57.17% Indels: 0
 DB: 22 Gaps: 0

US-09-856-320A-1 (1-1301) x AAB6139 (1-250)

```

QY 209 ATGAGATTTCGACGTTAATCTGCTGCTGCGCAACAGGGGCTTGAGGGGAGAGACC 268
    |||||||
Db 1 MetArgIleLeuGlnIleuIleuLeuAlaLeuAlaThrGlyLeuValGlyGlyIuThr 20
QY 269 AGGATCATCAAGGGGTTGAGTGCAGAGCCCTACCTCCAGCCCTGGCAGGACGCTGTTC 328
    |||||||
Db 21 ArgIleIleuGlyPheGlnCysGlyProHisSerGlnProThrPrgIAlaAlaLeuPhe 40
QY 329 GAGAAAGCGGGCTACTCTGTGGGGGCGACGCTCATCGCCCGGAGATGGCTCTGACAGCA 388
    |||||||
Db 41 GluIysThrArgIleuLeuGlyAlaThrIleuIleAlaProArgIleuLeuThrAla 60
QY 389 GCCCACTGCTCAAGCCCGCTACATAGTTCACTGGGGGAGCAGCAACCTCCAGAAAGAG 448
    |||||||
Db 61 AlaHisCysLeuIysProAlaGlyTyrIleValHisIleuGlyGlnHisAsnLeuGlnGly 80
QY 449 GAGGGCTGTGAGCAGACCCGAGACAGCCAGTGAATCTTCCCGACCCGCTTCAACAC 508
    |||||||
Db 81 GluIleGlyGlnGlnIleuArgThrAlaThrIleuSerPheProHisProGlyPheAsnAsn 100
QY 509 AGCCTCCCAACAAAGACCCGAGACAGCCAGTGAATCTGCTGGAAGATGGCATCCGACATC 568
    |||||||
Db 101 SerIleuProAsnIysAspHisArgAsnAspIleuMetLeuValIysMetAlaSerProVal 120
QY 569 TCCATCACTGGGTGTGCGACCCCTCACTCTCTCTCACTGCTGTGCTGTGCGAC 628
    |||||||
Db 121 SerIleuThrIleuAlaValArgProIleuThrIleuSerSerArgCysValThrAlaGlyThr 140
QY 629 AGCTGCTCATATTCGCGCTGGGGGAGCAGCAGTGCAGCCCGGATTAAGCCTGCTGACACC 688
    |||||||
Db 141 SerCysIleuIleSerGlyTyrGlySerThrSerSerProGlnIleuArgLeuProHisThr 160
QY 689 TTGGGATGGCGCAACATCAACATCATGATGAGACAGCAAGTGTGAGAACGCTTACC 748
    |||||||
Db 161 LeuArgCysAlaAsnIleuThrIleuGlnHisGlnIysCysGlnAsnAlaTyrProGly 180
QY 749 AACATCAAGACACCATGATGTGTGCGAGCGTGCAGAAAGGGGAGAGACTCTGCGCAG 808
    |||||||
Db 181 AsnIleuThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGln 200
QY 809 GGTGATCCCGGGGCGCTGTGCTGTGTGAACAGTCTTCAAGGCAATTAATCTCTGGGCGC 868
    |||||||
Db 201 GlyAspSerGlyGlyProLeuValCysAsnGlnSerIleuGlnGlyIleIleSerTyrGly 220
QY 869 CAGATCCGTTGGTGCATCCGCAAGCCGCTGCTCTACACAGAAAGCTCGAATAATGTG 928
    |||||||
Db 221 GlnAspProCysAlaIleuThrArgLysProGlyValTyrThrIysValCysLysTyrVal 240
QY 929 GACTGATCCAGAGAGATGAAGACAAT 958
    |||||||
Db 241 AspTyrIleGlnGlnIuThrMetLysAsnAsn 250
  
```

RESULT 9

AAB6139 ID AAB6139 standard; protein: 250 AA.

AC AAB6139;

DT 02-APR-2001 (first entry)

DE Protein of the invention #51.

KM Secreted; transmembrane; gene therapy.

XX Unidentified.

XX WO200078961-A1.

XX 28-DEC-2000.

XX 18-FEB-2000; 2000WO-US04342.

XX 23-JUN-1999; 99US-0141037.

XX 20-JUL-1999; 99US-0144758.

XX 26-JUL-1999; 99US-0145698.

XX 01-SEP-1999; 99WO-US20111.

XX 29-OCT-1999; 99US-0162506.

XX 30-NOV-1999; 99WO-US28313.

XX 02-DEC-1999; 99WO-US28551.

XX 16-DEC-1999; 99WO-US30095.

XX 05-JAN-2000; 2000WO-US00219.

XX 06-JAN-2000; 2000WO-US00376.

XX (GENTH) GENENTECH INC.

XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;

XX Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;

XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D;

XX Watanabe CK, Williams PM, Wood WI;

XX WPI; 2001-071395/08.

XX Claim 1; Fig 102; 787pp; English.

XX The present invention relates to secreted and transmembrane proteins.

XX These proteins and the DNA encoding them may be used as hybridization

XX probes, in chromosome and gene mapping and in the generation of

XX anti-sense RNA and DNA. They may also be used to generate either

XX transgenic animals or knockout animals which are in turn useful for

XX development and screening of therapeutically useful reagents.

XX The nucleic acids may also be used in gene therapy.

XX Sequence 250 AA;

Alignment Scores:

Pred. No.: 2,686-97 Length: 250
 Score: 1355.00 Matches: 250
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 57.17% Indels: 0
 DB: 22 Gaps: 0

US-09-856-320A-1 (1-1301) x AAB6139 (1-250)

```

QY 209 ATGAGATTTCGACGTTAATCTGCTGCTGCGCAACAGGGGCTTGAGGGGAGAGACC 268
    |||||||
Db 1 MetArgIleLeuGlnIleuIleuLeuAlaLeuAlaThrGlyLeuValGlyGlyIuThr 20
QY 269 AGGATCATCAAGGGGTTGAGTGCAGAGCCCTACCTCCAGCCCTGGCAGGACGCTGTTC 328
    |||||||
Db 21 ArgIleIleuGlyPheGlnCysGlyProHisSerGlnProThrPrgIAlaAlaLeuPhe 40
QY 329 GAGAAAGCGGGCTACTCTGTGGGGGCGACGCTCATCGCCCGGAGATGGCTCTGACAGCA 388
    |||||||
Db 41 GluIysThrArgIleuLeuGlyAlaThrIleuIleAlaProArgIleuLeuThrAla 60
QY 389 GCCCACTGCTCAAGCCCGCTACATAGTTCACTGGGGGAGCAGCAACCTCCAGAAAGAG 448
    |||||||
Db 61 AlaHisCysLeuIysProAlaGlyTyrIleValHisIleuGlyGlnHisAsnLeuGlnGly 80
QY 449 GAGGGCTGTGAGCAGACCCGAGACAGCCAGTGAATCTTCCCGACCCGCTTCAACAC 508
  
```

```

Db      81 GluGlyCysGluInlThraThrAlaThrGluSerPheProHisProGlyPheAsnAsn 100
QY      509 AGGCTCCCAACAAAGACACCCGAAATGACATCATGCTGGTGAAGATGGCATGCCAGTC 568
Db      101 SerLeuProAsnLysAspHisAsnAspIleMetLeuValLysMetAlaSerProVal 120
QY      569 TCCATCATCCTGGGCTGTGGACCCCTACCCCTCTCTCTCAAGCTGTGTCACTGTGGCACC 628
Db      121 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgGlyValThrAlaGlyThr 140
QY      629 AGCTGCTCATTTCCGGCTGGGGCAGCAGCTCCAGCCCACTTAAGCCCTGCTCACACC 688
Db      141 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 160
QY      689 TTGCGATGGCCCAACATCAATCATTTGAGACACCAAGATGTGAGAACGCTTACCCGGC 748
Db      161 LeuArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTrpProGly 180
QY      749 AACATCAACAGACACCATGTGTGTGTGCGACGCTGCAGGAAGGGGCAAGACTCTCCAG 808
Db      181 AsnIleThrAspThrMetValCysAlaSerValGlnGlyGlyLysAspSerCysGln 200
QY      809 GGTGACTCGGGGGCCCTCTGCTGCTTAACACAGCTCTTCAAGGCAATTATCTCTGGGCG 868
Db      201 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 220
QY      869 CAGGATCCGTGTGCGATCAACCCGAAAGCCTGTGTCTACACGAAATCTGCAATATGTG 928
Db      221 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTrpVal 240
QY      929 GACTGGATCCAGAGACGATGAAGAACAAT 958
Db      241 AspTrpIleGlnGlnThrMetLysAsnAsn 250

RESULT 10
ABG61816
ID      ABG61816 standard; Protein; 250 AA.
XX
AC      ABG61816;
XX
DT      15-AUG-2002 (first entry)
XX
DE      Prostate cancer-associated protein #17.
XX
KM      Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
XX
OS      Mammalia.
XX
PN      WO200230268-A2.
XX
PD      18-APR-2002.
XX
PF      12-OCT-2001; 2001WO-US32045.
XX
PR      13-OCT-2000; 2000US-0687576.
XX
PR      08-DEC-2000; 2000US-0733288.
XX
PR      08-DEC-2000; 2000US-0733742.
XX
PR      24-JAN-2001; 2001US-263957P.
XX
PR      16-MAR-2001; 2001US-276791P.
XX
PR      16-MAR-2001; 2001US-276888P.
XX
PR      06-APR-2001; 2001US-281922P.
XX
PR      24-APR-2001; 2001US-286214P.
XX
PR      30-APR-2001; 2001US-0847046.
XX
PR      04-MAY-2001; 2001US-288589P.
XX
PA      (E05B-) EOS BIOTECHNOLOGY INC.
PI      Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX
DR      WPI; 2002-471335/50.
XX
DR      N-PSDB; ABK92131.
XX

```

```

PT      Detecting a prostate cancer-associated transcript in a cell in a
PT      patient, useful for diagnosing prostate cancer (PC) or screening
PT      modulators of PC, by determining if prostate cancer-associated genes
PT      are expressed in a prostate tissue
XX
PS      Claim 27; Page 314; 436pp; English.
XX
CC      The present invention relates to methods of detecting a prostate
CC      cancer-associated transcript in a cell from a patient. The method
CC      comprises contacting a biological sample from the patient with
CC      prostate cancer-associated polynucleotides (designated PC genes) that
CC      selectively hybridise to a sequence that is at least 80% identical
CC      to them. The prostate cancer-associated polynucleotide sequences
CC      are differentially expressed in prostate tumour tissue or in
CC      prostate cancer and are derived from the tissues of various
CC      organisms such as humans or other mammals (e.g. mice, sheep and dogs).
CC      The methods of the invention are useful for diagnosing and treating
CC      prostate cancer in mammals. The prostate cancer-associated genes are
CC      useful for diagnosing or treating prostate cancer, as well as for
CC      identifying modulators of prostate cancer or agents that inhibit
CC      prostate cancer. The nucleic acid sequences are particularly useful
CC      in gene therapy, as a vaccine or in antisense applications.
CC      ABG61800-ABG61944 represent prostate cancer-associated proteins.
XX
SQ      Sequence 250 AA:

Alignment Scores:
Pred. No.: 2,68e-97 Length: 250
Score: 1355.00 Matches: 250
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.17% Indels: 0
DB: 23 Gaps: 0

US-09-856-320a-1 (1-1301) x ABG61816 (1-250)
QY      209 ATGAGGATTCCTGAGTAATCTCTGCTGTGGAACAAGGCTTGAAGGAGAGACC 268
Db      1 MetArgIleLeuGlnIleuIleLeuAlaLeuAlaThrGlyLeuValGlyGlyIuThr 20
QY      269 AGGATCATCAAGGGGTTCAGTGCAGCCCTCACTCCAGCCCTGGAGAGAGCCCTGTTC 328
Db      21 ArgIleIleLysGlyPheGlyCysLysProHisSerGlnProTrpIleAlaIlePhe 40
QY      329 GAGAAAGCCGCGTACTCTGTGGGGGAGCGCTCATGCGCCCAAGTGGCTCTGACAGCA 388
Db      41 GlyLysThrArgLeuLeuGlyGlyAlaThrIleIleAlaProArgTrpLeuLeuThrAla 60
QY      389 GCCCACTGCCCTCAAGCCCGCTACATAGTTCACCTGGGGCAGCAACACTCCAGAGAG 448
Db      61 AlaHisCysLeuLysProArgTrpGlyIleValIleHisLeuGlyIleHisAsnLeuGlnLys 80
QY      449 GAGGCTGTGAGACACCCGGACAGCCACTGAGTCTTCCGCCACCCCGGCTTCAACAC 508
Db      81 GluGlyCysGluInlThraThrAlaThrGluSerPheProHisProGlyPheAsnAsn 100
QY      509 AGGCTCCCAACAAAGACACCCGAAATGACATCATGCTGGTGAAGATGGCATGCCAGTC 568
Db      101 SerLeuProAsnLysAspHisAsnAspIleMetLeuValLysMetAlaSerProVal 120
QY      569 TCCATCATCCTGGGCTGTGGACCCCTACCCCTCTCTCTCAAGCTGTGTCACTGTGGCACC 628
Db      121 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgGlyValThrAlaGlyThr 140
QY      629 AGCTGCTCATTTCCGGCTGGGGCAGCAGCTCCAGCCCACTTAAGCCCTGCTCACACC 688
Db      141 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 160
QY      689 TTGCGATGGCCCAACATCAATCATTTGAGACACCAAGATGTGAGAACGCTTACCCGGC 748
Db      161 LeuArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTrpProGly 180
QY      749 AACATCAACAGACACCATGTGTGTGTGCGACGCTGCAGGAAGGGGCAAGGACTCTCCAG 808

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Db      181 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerGln 200
QY      809 GGTGACTCCGGGGCCCTGTGTCGTAAACAGTCTTCAAGGCAATATCTCCGAGGC 868
Db      201 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 220
QY      869 CAGGATCCGTGTGCATACCCGGAAGCCTGTGTCACAGAAAGTCTGCAATATGTG 928
Db      221 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 240
QY      929 GACTGATCCAGAGAGATGAGACAAAT 958
Db      241 AspTrpIleGlnGlnThrMetLysAsn 250

RESULT 11
ABR95526
ID      ABR95526 standard; Protein; 250 AA.
XX      ABR95526;
AC      19-JUL-2002 (first entry)
DE      Human angiogenesis related protein PRO1279 SEQ ID NO: 208.
XX      19-JUL-2002 (first entry)
DE      Human, angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW      atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW      cardiac; cytosolic; antiangiogenic; hypotensive; vulnary;
KW      antiarteriosclerotic.
OS      Homo sapiens.
XX      Wo200208284-A2.
XX      31-JAN-2002.
PD      09-JUL-2001; 2001WO-US21735.
XX      20-JUL-2000; 2000US-219556P.
XX      25-JUL-2000; 2000US-220624P.
XX      28-JUL-2000; 2000US-220664P.
XX      02-AUG-2000; 2000WO-US20710.
XX      17-AUG-2000; 2000US-222695P.
XX      23-AUG-2000; 2000US-0643657.
XX      24-AUG-2000; 2000WO-US23522.
XX      07-SEP-2000; 2000US-230978P.
XX      15-SEP-2000; 2000US-000000P.
XX      18-SEP-2000; 2000US-0664610.
XX      24-SEP-2000; 2000US-0655350.
XX      24-OCT-2000; 2000US-242922P.
XX      08-NOV-2000; 2000US-0709238.
XX      10-NOV-2000; 2000WO-US30952.
XX      01-DEC-2000; 2000WO-US30873.
XX      20-DEC-2000; 2000US-0747259.
XX      20-DEC-2000; 2000WO-US34956.
XX      22-JAN-2001; 2001US-0767609.
XX      28-FEB-2001; 2001US-0796498.
XX      01-MAR-2001; 2001WO-US06520.
XX      09-MAR-2001; 2001US-0802706.
XX      14-MAR-2001; 2001US-0808689.
XX      22-MAR-2001; 2001US-0816744.
XX      05-APR-2001; 2001US-0828366.
XX      10-MAY-2001; 2001US-0854208.
XX      10-MAY-2001; 2001US-0854280.
XX      25-MAY-2001; 2001US-0866028.
XX      25-MAY-2001; 2001US-0866034.
XX      30-MAY-2001; 2001US-0870574.
XX      30-MAY-2001; 2001WO-US17443.
XX      01-JUN-2001; 2001WO-US17800.

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PR      20-JUN-2001; 2001WO-US19692.
PR      28-JUN-2001; 2001WO-US00000.
XX      (GETH ) GENENTECH INC.
PA      (BAKE) BAKER K P.
PA      (FERR) FERRARA N.
PA      (GERB) GERBER H.
PA      (GERR) GERRITSEN M E.
PA      (GODD) GODDARD A.
PA      (GODO) GODOWSKI P J.
PA      (GUEN) GUENEY A L.
PA      (HILL) HILLAN K J.
PA      (MARS) MARSTERS S A.
PA      (PANU) PAN J.
PA      (PAON) PAONI N F.
PA      (STEP) STEPHAN J F.
PA      (WATA) WATANABE C K.
PA      (WILL) WILLIAMS P M.
PA      (WOOD) WOOD W I.
XX      Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
XX      Godowski PJ, Gueney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
XX      Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX      WPI: 2002-171999/22.
XX      DR      N-PSDB; ABL95664.
XX      PT      One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX      useful in diagnosis and treatment of cardiovascular (e.g myocardial
XX      infarction), endothelial or angiogenic disorders in a mammal -
XX      Claim 11; Fig 208; 567PP; English.
XX      PS      The present invention provides the protein and coding sequences of human
XX      CC      PRO proteins. These are useful for treating or diagnosing a
XX      CC      cardiovascular, endothelial or angiogenic disorder, including cardiac
XX      CC      hypertrophy, trauma, cancer, age-related macular degeneration,
XX      CC      atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
XX      CC      angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
XX      CC      angiogenesis (such as breast carcinoma and liver carcinoma) and wound
XX      CC      healing. The present sequence is a PRO protein of the invention.
XX      SQ      Sequence 250 AA;

Alignment Scores:
Pred. No.: 2,68e-97 Length: 250
Score: 1355.00 Matches: 250
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.17% Indels: 0
DB: 23 Gaps: 0

US-09-856-320A-1 (1-1301) x ABR95526 (1-250)
QY      209 ATGAGGATTCGCGAGTTAATCTCTGCTTGGCAACAGGGCTTGTAGGGGAGAGACC 268
Db      1 MetArgIleLeuGlnIleuIleLeuLeuAlaLeuAlaThrGlyLeuValGlyGlnThr 20
QY      269 AGGATCATCAAGGGGGTTCGAGTGCAGACCTTCACCTCCAGGCCCTGGCAGGAGCCCTGTC 328
Db      21 ArgIleIleLeuGlyPheGlnCysLysProHisSerIleProTrpGlnAlaAlaLeuPhe 40
QY      329 GAGAAGACGGGGCTACTCTGTGGGGCAGCCTCATCGCCGCCAGATGGCTCTGACAGCA 388
Db      41 GlnLysThrArgLeuLeuLeuGlyAlaThrLeuIleAlaProArgTrpLeuThrAla 60
QY      389 GCCCAGTCGCTCAAGCCCCCGCTACATAGTTCACCTGGGGGAGCAGCAACCTCCAGAGGAG 448
Db      61 AlaHisCysLeuLysProArgTyrIleValAlaHisLeuGlnGlnHisAsnLeuGlnLysGln 80
QY      449 GAGGGCTGTGAGCAGACCGGAGACGACCATGAGCTTCCGCCACCCGGGCTTCACCAAC 508
Db      81 GluGlyCysGlnGlnIleThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsn 100

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QY 509 AGCTTCCCAACAAAGACCGCAATGATCATCTCTGTGAAGTGGCATGCCAGTC 568
DB 101 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 120
QY 569 TCCATACCTGGGCGCTGGAGCCCTCACCCTCTCTCAGCGTGGTCACTGCTGGCACC 628
DB 121 SerIleThrTrpAlaAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 140
QY 629 AGCTGCCATATTCGCGTGGGAGCAGACGTCAGCCGCCAGTATACGCTGCGTCAACC 688
DB 141 SerCysLeuIleSerCylTrpGlySerThrSerProGlnLeuArgLeuProHisIleThr 160
QY 689 TTGCGATGCGCCAAACATCACCATCATTTAGACACACAGAGTGTGAGAGCCCTACCCGGC 748
DB 161 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrProGly 180
QY 749 AACATCAGACAGACCATGTGTGTGGCAGCGTCAGAGAGGGGGGAGAGACATCTCCAG 808
DB 181 AsnIleThrAspThrMetValCysAlaSerValGlnGlyLysAspSerCysGln 200
QY 809 GGTGACTCCGGGGGCGCTCTGCTGTAAACAGTCTCTCAAGGCAATATCTCTGGGCGC 868
DB 201 GlyAspSerCylGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 220
QY 869 CAGGATCCGTGTGCGATCACCCGAAAGCCTGTGTCTACAGAAAGTGTCAAAATATGTC 928
DB 221 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 240
QY 929 GACTGATCCAGAGACGATGAAGAACAT 958
DB 241 AspTrpIleGlnGlnIleThrMetLysAsnAsn 250

RESULT 12
ABR84920
ID ABR84920 standard; Protein; 250 AA.
XX
XX ABR84920;
XX
DE 16-MAY-2002 (first entry)
XX
XX Human PRO1279 protein sequence SEQ ID NO:208.
XX
KW Human; angiogenesis; cardiant; cytosolic; antiangiogenic; hypotensive;
KW vulnerability; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping.
XX
XX Homo sapiens.
XX
XX MO200200690-A2.
XX
PD 03-JAN-2002.
XX
XX 20-JUN-2001; 2001WO-US19692.
XX
XX 23-JUN-2000; 2000US-213637P.
XX
XX 20-JUL-2000; 2000US-219556P.
XX
XX 25-JUL-2000; 2000US-220624P.
XX
XX 28-JUL-2000; 2000WO-US2064P.
XX
XX 02-AUG-2000; 2000US-222695P.
XX
XX 17-AUG-2000; 2000US-064365P.
XX
XX 23-AUG-2000; 2000WO-US23522.
XX
XX 24-AUG-2000; 2000WO-US23328.
XX
XX 07-SEP-2000; 2000US-230978P.
XX
XX 18-SEP-2000; 2000US-066410.
XX
XX 18-SEP-2000; 2000US-0665350.
XX
XX 24-OCT-2000; 2000US-242922P.

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PR 08-NOV-2000; 2000US-0709238.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0806889.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 30-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 01-JUN-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
XX
PA (GENT) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gertlisen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Masters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-090516/12.
DR N-PSDB; ABL88175.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX infarction), endothelial or angiogenic disorders in a mammal -
XX
XX Claim 11; Fig 208; 565pp; English.
XX
XX ABL88072 to ABL88258 encode the PRO proteins given in ABR84817 to
XX ABR85003. The PRO proteins and polynucleotides have cardiant, cytosolic,
XX antiangiogenic, hypotensive, vulnerability and antiarteriosclerotic
XX activities, and can be used in gene therapy. The PRO polynucleotides,
XX proteins, agonists and antagonists are useful for treating or diagnosing
XX a cardiovascular, endothelial or angiogenic disorder in a mammal,
XX e.g. cardiac hypertrophy, trauma, cancer, age-related macular
XX degeneration, atherosclerosis, hypertension, arterial restenosis,
XX rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
XX lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
XX carcinoma) and wound healing. The PRO polynucleotides have applications
XX in molecular biology, including use as hybridisation probes, and in
XX chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
XX probes used in the exemplification of the present invention.
XX
XX Sequence 250 AA:
XX
XX Alignment Scores:
XX Pred. No.: 2.68e-97 Length: 250
XX Score: 1355.00 Matches: 250
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 57.17% Indels: 0
XX DB: 23 Gaps: 0
XX
XX US-09-856-320A-1 (1-1301) x ABR84920 (1-250)
QY 209 ATGAGATCTCTGCAATATCTCTGCTGTGGCAGACGGGCTTGTAGGGAGAGACC 268
DB 1 MetArgIleLeuGlnLeuIleLeuAlaLeuAlaThrGlyLeuValGlyIleGlyThr 20
QY 269 AGCATCATCAAGGGGTTCAGTGTGCAAGCCTTCACCTCCAGGAGGAGCAGCCGTGTTTC 328
DB 21 ArgIleIleLeuGlyPheGlnCysLysProHisSerGlnProTrpGlnAlaLeuPhe 40

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OY 329 GAGAGAGCGCGCTACTGTGTGGGGCGACGCTCATCGCCCGCCAGATGGCTCTGTACAGCA 388
    |||||||
Db 41 GlutylthraArgLeuLeuCySGlYAlaThrLeuIleAlaProArgTyrPLeuLeuThrAla 60
    |||||||
OY 389 GCCACATCCCAAGACCGCCGCTACATAGTACCGGGGCGACCACTCCAGAGAGAG 448
    |||||||
Db 61 AlaHisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnHisGlu 80
    |||||||
OY 449 GAGGGCTGTGAGCAGACCGGACGACGCACTAGTCTCTCCCGCCCGGCTTCAACAC 508
    |||||||
Db 81 GluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnHis 100
    |||||||
OY 509 AGCTCTCCCAACAAAGACACCGCAATACATCATCTGCTGGGAGATGGATCCGCAATC 568
    |||||||
Db 101 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 120
    |||||||
OY 569 TTCATACACTGGGCTGTGCGACCGCTCACCTCTCCCTGCTGCTGCTGCTGCTGCTGCTG 628
    |||||||
Db 121 SerIleThrTrpAlaValArgProLeuThrLeuSerSerAlaGlyValThrAlaGlyThr 140
    |||||||
OY 629 AGCTGCTCATTTCCGCTGGGCGACGACGCTCACGCCCCCGGTTACGCTTCCCTCACACC 688
    |||||||
Db 141 SerCysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThr 160
    |||||||
OY 689 TTGGGATCGCCGCAACATACCATCATATGAGACACGAGAGTGTGAGAACGCTTACCCGCGC 748
    |||||||
Db 161 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaIleTyrProGly 180
    |||||||
OY 749 AACATCAGACAGACCATGCTGTGTCCAGCTGACGAGAAAGGGGCGCAAGCTCCGCGCAG 808
    |||||||
Db 181 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGln 200
    |||||||
OY 809 GGTGACTCCGGGGGCGCTGTGTGTGTATACAGTCTCTTCAAGGCATTATCTCTGGGGC 868
    |||||||
Db 201 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrPly 220
    |||||||
OY 869 CAGATCCGCTGGTGGATACCCGGAAGCTGTCTCTACAGAAAGTCTGCAAAATATATGTG 928
    |||||||
Db 221 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 240
    |||||||
OY 929 GACTGATCCAGAGACGATGAGAACAAAT 958
    |||||||
Db 241 AspTrpIleGlnGluThrMetLysAsnHis 250
    |||||||

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RESULT 13

AA083684
ID AA083684 standard; Protein; 250 AA.

AA083684;

08-MAY-2002 (first entry)

Human PRO protein, Seq ID No 186.

Human: secreted protein: PRO; tumour; lung cancer; colon cancer;

pericyte cell proliferation; chondrocyte cell proliferation;

tumour necrosis factor-alpha.

Homo sapiens.

MO200208288-A2.

31-JAN-2002.

29-JUN-2001; 2001WO-US21066.

20-JUL-2000; 2000US-219556P.

25-JUL-2000; 2000US-220585P.

25-JUL-2000; 2000US-220605P.

25-JUL-2000; 2000US-220607P.

25-JUL-2000; 2000US-220624P.

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PR 25-JUL-2000; 2000US-220664P.
PR 25-JUL-2000; 2000US-220666P.
PR 25-JUL-2000; 2000US-220683P.
PR 28-JUL-2000; 2000WO-US20710.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 15-SEP-2000; 2000US-000000P.
PR 10-NOV-2000; 2000WO-US30873.
PR 28-NOV-2000; 2000US-253646P.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001WO-US17092.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2002-172001/72.
XX N-PSDB; ABK33628.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
PI useful for treating a PRO related disorder and for diagnosing tumours
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
PT tumour or liver tumour -
XX
XX Claim 11; Figure 186; 359pp; English.
XX
XX The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression in, pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. AA083592-AA083713 represent human PRO
CC protein sequences of the invention.
XX
XX Sequence 250 AA;
SQ

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Alignment Scores:

Pred. No.: 2,68e-97 Length: 250
Score: 1355.00 Matches: 250
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.17% Indels: 0
DB: 23 Gaps: 0

US-09-856-320A-1 (1-1301) x AA083684 (1-250)

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OY 209 ATGAGGATTCGCGAGTTATCTCTGCTGTGGCAACAGGGCTTGTAGGGGAGAGACC 268
    |||||||
Db 1 MetArgIleLeuGlnIleuIleLeuLeuAlaLeuAlaThrGlyLeuValGlyGlyGluThr 20
    |||||||
OY 269 AGATCATCAAGGGGTTGAGTGCAGCTTCACCTCCAGCCCGGCGAGGAGGAGCCCTTC 328
    |||||||
Db 21 ArgIleIleLysGlyPheGlyCysLysProHisSerGlnProTrpGlnAlaAlaLeuPhe 40
    |||||||
OY 329 GAGAGAGCGCGCTACTGTGTGGGGCGACGCTCATCGCCCGCCAGATGGCTCTGTACAGCA 388
    |||||||
Db 41 GlutylthraArgLeuLeuCySGlYAlaThrLeuIleAlaProArgTyrPLeuLeuThrAla 60
    |||||||
OY 389 GCCACATCCCTCAAGACCGCCGCTACATAGTTCACCTGGGGGAGCAACAACCTCCAGAGAGAG 448
    |||||||

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Db 61 AlaHisCysLeuIysProAlaGlyTyrIleValHisLeuGlyClnHisAsnLeuGlnIysGln 80
QY 449 GAGGGCTGTGACAGACCCGACAGCCGACTGATGCTCTTCCGCCACCCGGCTTCAACAC 508
Db 81 GluGlyCysGluGlnIthrArgThrAlaTrpGlnUserPheProHisIstroIlyPheAsn 100
QY 509 AGCGTCCCAACAAAGACACCGCAATGACATCATGCTGGTAAAGATGGCATCGCCATC 568
Db 101 SerLeuProAsnIlysPheHisArgAsnAspIleMetLeuValIysMetAlaSerProVal 120
QY 569 TGCATCACCTGGGCTGTGGACCCCTCACCCTCTCTCAAGCTGTGTCACTGTGGACAC 628
Db 121 SerIleThrTrpAlaValArgProLeuThrIleSerSerArgCysValThrAlaGlyThr 140
QY 629 ACCTGCTCATTTCCGGCTGGGAGACAGCATCGACGCCACAGTACGCTGCCTCACACC 688
Db 141 SerCysLeuIleSerClyTrpIleSerThrSerProGlnLeuArgLeuProHisThr 160
QY 689 TTGCGATGCGCCAACTACATCATTTGAGCACACAGAGTGTGAGAACGCTAACCCGGC 748
Db 161 LeuAlaGysAlaAsnIleThrIleIleGlnHisGlnIlyCysGlnAsnAlaTrpProGly 180
QY 749 AACATCACAGACACCATGTGTGTGTGACACCTGCGACGAGGAGGGGCAAGACTCTCCAG 808
Db 181 AsnIleThrAspThrMetValCysAlaSerValGlnGluGlyClyLysAspSerCysGln 200
QY 809 GGTGACTCCGGGGGCCCTGTGCTGTATACAGTCTCTTCAAGGCTTATCTGCTGGGAC 868
Db 201 GlyAspSerClyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 220
QY 869 CAGATCCGTGTGCGATCACCCGAAAGCCTGTGTCTACACAGAAAGTGTGCAAAATATGTG 928
Db 221 GlnAspProCysAlaIleThrArgLysProGlyValIlyThrIlyValCysIlySTyVal 240
QY 929 GACTGGATCCAGAGACGATGAAGAACAT 958
Db 241 AspTrpIleGlnIleThrMetLysAsnAsn 250

RESULT 14
ABU66822
ID ABU66822 standard; Protein; 250 AA.
XX
AC ABU66822;
XX
DT 23-MAY-2003 (first entry)
XX
DE Human PRO polypeptide #253.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW differentiation; chondrocyte; tumour; genetic disorder;
KW cytosolic.
XX
OS Homo sapiens.
XX
PN US2003036180-A1.
XX
PD 20-FEB-2003.
XX
PF 09-MAY-2002; 2002US-0143114.
XX
PR 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1998; 98WO-US12456.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.

PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 22-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US23052.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0803706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0826366.

PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866034.
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 PR 01-JUN-2001; 2001US-0872035.
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 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 PR (GENTH) GENENTECH INC.
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 PI Baker RP, Beresini M, DeForge L, Desnoyers L, Flivaroff E, Gao W;
 PI Gerltsen ME, Goddard A, Godowski PJ, Gunney AL, Sherwood S,
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WT, Zhang Z;
 XX WPI: 2003-332040/31.
 DR N-PSDB; ACA03855.
 XX
 PT New secreted and transmembrane PRO nucleic acids, useful for gene
 PT therapy, in chromosome and gene mapping, as chromosome markers, in
 PT tissue typing, and in chromosome identification -
 XX
 PS Claim 12; Fig 506; 660pp; English.
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for
 CC linking bioactive molecules to cells expressing PRO polypeptides,
 CC for modulating biological activities of cells expressing PRO
 CC polypeptides, and for identifying agonists or antagonists.
 CC The PRO polypeptides are useful for stimulating the release of
 CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating
 CC the proliferation or differentiation of chondrocytes, and detecting the
 CC presence of tumours. The polynucleotide sequences encoding PRO
 CC polypeptides are useful as hybridisation probes, in chromosome and
 CC gene mapping, in the generation of antisense RNA and DNA, in the
 CC preparation of PRO polypeptides, for generating transgenic animals or
 CC knockout animals, for the genetic analysis of individuals with genetic
 CC disorders, and in gene therapy. AB06570-AB066844 represent the human
 CC PRO polypeptides of the invention.
 CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at
 CC seqdata.uspto.gov/psipdsidentity.html.
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Db 41 GluylstrhraryleuLeuCySgLYAlaThrleuilelaProAdgtrPleuileThrAla 60
 QY 389 GGGCAGCTGCTCAAGCCCCGGCTACATAGTTACCTGGGGGAGCAACCTCCACAGAGAG 448
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 QY 449 GAGGAGCTGTAGCAGACCCGGAGCAGCCAGTACGTCTCCSCACCCCGGCTTCACACAC 508
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 QY 509 AGCTCCGCCAACAAAGACACCCGAAAGACATGACATGCTGCTGGTGAAGATGSGATGSC 568
 Db 101 SerleuProAsnLysAspNHLSArgAsnAspIleMetleuValLysMetAlaSerProVal 120
 QY 569 TCCATCAGCTGGGCTGTGCGACCCCTGACCTCTCTCCAGCTGTGACGTGGGACG 628
 Db 121 SerlethrtrpAlaValArgProleuThrleuSerSerArgcysValThrAlaGlyThr 140
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 DT 27-MAY-2003 (first entry)
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 KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
 KW infertility; birth defects; premature aging; AIDS; biosensor;
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;
 KW bioreactor; tumour.
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 OS Homo sapiens.
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 PN US2003032155-A1.
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 PD 13-FEB-2003.
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 PF 03-MAY-2002; 2002US-0137865.
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 XX 31-MAR-1997; 97WO-US05230.
 PR 12-JUN-1998; 98WO-US12456.
 PR 14-JUL-1998; 98WO-US14552.
 PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.

PR 14-SEP-1998: 98WO-US19094.
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 PR 17-SEP-1998: 98WO-US19437.
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 PR 01-MAR-2000: 2000WO-US05004.
 PR 02-MAR-2000: 2000WO-US05601.
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 PR 30-MAY-2000: 2000WO-US14042.
 PR 02-JUN-2000: 2000WO-US14941.
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 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI: 2003-331925/31.
 DR N-PFSDB: NCA04276.
 XX
 PT New secreted and transmembrane nucleic acids and polypeptides,
 PT designated as PRO, useful for treating inflammation, organ failure,
 PT atherosclerosis, cardiac injury, infertility, birth defects, premature
 PT aging, AIDS, or cancer
 PS
 XX
 PS Claim 12: Fig 506; 655pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising, or which is
 CC at least 80% identical to, or the full-length coding sequence of, any of
 CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid
 CC further comprises the full-length coding sequence of the DNA deposited
 CC under American Type Culture Collection (ATCC) accession number in a list
 CC given in the specification. Also included are vectors and host
 CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO
 CC antibodies, PRO extracellular domains and mature sequences, methods
 CC of detecting PRO proteins, methods for stimulating the release of
 CC TNF-alpha (tumour necrosis factor alpha) from human blood,
 CC (and the proliferation of differentiation of chondrocyte cells, the
 CC proliferation of, or gene expression in pericyte cells, the release or
 CC proteoglycans from cartilage, proliferation of inner ear utricular
 CC supporting cells, the proliferation of T-lymphocyte cells, the release
 CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the
 CC proliferation of endothelial cells), a method for modulating the uptake
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
 CC a method for inhibiting the binding of A-peptide to factor VIIA,
 CC or the differentiation of adipocyte cells, a method for detecting the
 CC presence of a tumour in a mammal and an oligonucleotide probe derived
 CC from any of the nucleotide sequences cited above. The nucleic acids and
 CC polypeptides are useful for treating inflammatory diseases, organ
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
 CC diabetic complications. The nucleic acids are useful as hybridisation
 CC probes, in chromosome and gene mapping, and in generating antisense RNA
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
 CC biosensors or bioreactors. Both are useful in tissue typing.
 CC The present sequence represents a PRO protein of the invention.
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GenCore version 5.1.6
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SUMMARIES

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2	1355	57.2	250	4	US-09-205-258-427 Sequence 427, Appl
3	1324	55.9	248	4	US-08-944-483-24 Sequence 24, Appl
4	1279	54.0	246	4	US-09-205-258-1149 Sequence 1149, Ap
5	1232	52.0	289	4	US-09-386-642-14 Sequence 14, Appl
6	1197	50.5	228	4	US-09-205-258-1150 Sequence 1150, Ap
7	698.5	29.5	260	3	US-09-025-059-3 Sequence 3, Appl1
8	690	29.1	260	4	US-09-070-526-2 Sequence 2, Appl1
9	689	29.1	288	4	US-09-386-642-13 Sequence 13, Appl
10	682	28.8	260	4	US-09-008-271A-7 Sequence 7, Appl1
11	650.5	27.4	293	4	US-09-996-243-309 Sequence 309, Appl
12	608.5	23.7	268	2	US-08-824-874-1 Sequence 1, Appl1

13	608.5	25.7	268	3	US-09-210-084-1 Sequence 1, Appl1
14	608.5	25.7	268	4	US-09-764-762-1 Sequence 1, Appl1
15	604.5	25.5	263	2	US-08-790-137-4 Sequence 4, Appl1
16	604.5	25.5	263	2	US-08-824-874-5 Sequence 5, Appl1
17	604.5	25.5	263	3	US-08-807-151-5 Sequence 5, Appl1
18	604.5	25.5	263	3	US-09-210-084-5 Sequence 5, Appl1
19	604.5	25.5	263	4	US-09-478-957-5 Sequence 5, Appl1
20	604.5	25.5	263	4	US-09-764-762-5 Sequence 5, Appl1
21	600.5	25.3	246	2	US-08-978-404B-44 Sequence 44, Appl
22	596.5	25.2	261	3	US-08-768-859A-6 Sequence 6, Appl1
23	596.5	25.2	261	3	US-08-767-820A-6 Sequence 6, Appl1
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25	596.5	25.2	261	3	US-09-100-264-7 Sequence 7, Appl1
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37	585.5	24.7	244	3	US-08-622-046B-16 Sequence 16, Appl
38	585.5	24.7	244	3	US-09-100-264-5 Sequence 5, Appl1
39	585.5	24.7	244	4	US-08-843-076D-5 Sequence 5, Appl1
40	582.5	24.6	244	4	US-08-622-046B-5 Sequence 5, Appl1
41	581.5	24.5	244	5	PCT-US95-06157-10 Sequence 10, Appl
42	580	24.5	262	2	US-08-790-137-1 Sequence 1, Appl1
43	580	24.5	262	2	US-08-790-137-3 Sequence 3, Appl1
44	580	24.5	262	2	US-08-681-151-4 Sequence 4, Appl1
45	580	24.5	262	2	US-08-824-874-4 Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-09-025-059-1
; Sequence 1, Application US/09025059
; Patent No. 6075136
GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,059
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0481 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166

MOLECULE TYPE: No. 6232456e
US-08-944-483-24

Alignment Scores:
Pred. No.: 7,78e-105 Length: 248
Score: 1324.00 Matches: 248
Percent Similarity: 99.20% Conservative: 0
Best Local Similarity: 99.20% Mismatches: 0
Query Match: 55.86% Indels: 2
Gaps: 3

US-09-856-320a-1 (1-1301) x US-08-944-483-24 (1-248)

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1 MetArgIleLeuGlnIleuIleLeuLeuAlaLeuAlaThrGlyLeuValIGlyGlnThr 20
269 AGGATTCATCAGGGGTTTGAGTGTGACAGCTCCTCCAGCCCTGGCAGGAGCCCTGTC 328
21 ArgIleIleLysGlyPheGlyLys--ProHisSerGlnProTyrGlnAlaLeuPhe 39
329 GAGAGAGCGCGCTACTCTGTGGGCGACGCTCATCGCCCGCCAGATGGCTCTGACAGCA 388
40 ---LysThrArgLeuLeuLeuGlyAlaLeuThrLeuIleAlaProAlaGlyIleuLeuThrAla 58
389 GCCCACTGCTCAAGCCCCGCTACATAGTTCACTGGGGGAGCAGCAACCTCCAGAAAGAG 448
59 AlaHisCysLeuLysProAlaGlyTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGln 78
449 GAGGGGTGTGAGAGACCGGAGCAGCAGCTGAGTCCTTCCCGCCCGGCTTCAAGAC 508
79 GlnIleLysGlnGlnIleThrAlaGlnAlaThrIleSerPheProHisProGlyPheAsn 98
509 AGCCTCCCAACAAAGACACCCGCAATGACATCATGCTGTGATGAGATGGCATGCCAGTC 568
99 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 118
569 TCCATACCTGGGCTGTGGCAGCCCTGACCTCTCTCAGCTGTGTACTGTGGCAGCC 628
119 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 138
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159 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaLysProGly 178
749 AACATCAGACAGACCATGCTGTGTCAGCCTGACAGAGGGGCGAAGAGACTCCTGCCAG 808
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809 GGTGACTCGGGGGGCGCTGTGCTGTAAACAGTCTTTCAAGCATTAATCTCTGGGCGC 868
199 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrPhe 218
869 CAGGATCCGTTGCGATCAGCCGGAAGCCTGTGTACAGAGAAGTGTGAATATGATG 928
219 GlnAspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTyrVal 238
929 GACTGATCCAGAGAGCAGATGAGACAAAT 958
239 AspTrpIleGlnGlnIleThrMetLysAsnAsn 248

RESULT 4
US-09-205-258-1149
Sequence 1149, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1

CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
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EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
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EARLIER APPLICATION NUMBER: 60/048,882
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EARLIER APPLICATION NUMBER: 60/048,899
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EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
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EARLIER APPLICATION NUMBER: 60/048,875
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EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877


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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1149
; LENGTH: 246
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-205-258-1149

Alignment Scores:
Pred. No.: 5,29e-101 Length: 246
Score: 1279.00 Matches: 244
Percent Similarity: 98.79% Conservative: 0
Best Local Similarity: 98.79% Mismatches: 2
Query Match: 53.97% Indels: 1
DB: 4 Gaps: 0

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QY 269 AGATATCAACAGGGGTTCAGTGCAGACCTCCACCTCCAGGAGGAGCCCTGTTTC 328
Db 21 ArgIleIleLeuGlyPheGlyLeuGlyLeuHisSerGlnProTyrPheIleAlaLeuPhe 40
QY 329 GAGAGAGCCGCGCTACTCTGTGGGGGAGGCGTCATGCCGCCAGATGGCTCTGCAGACA 388
Db 41 GlnLysThrArgLeuLeuLeuGlyAlaThrIleuIleAlaProArgTyrLeuThrAla 60
QY 389 GCCCACTGCGCTAAGCCCGCTACATAGTTCACCTGGGCGAGACCAACCTCCAGAGAGAG 448
Db 61 AlaHisCysLeuLeuProArgTyrIleValHisLeuGlyGlnHisLeuGlnLysGln 80
QY 449 GAGGGCTGTGAGCAGACCCGAGACAGGCACTGAGTCCCTCCACCCCGGCTTCAACAC 508
Db 81 GlnGlyCysGlnGlnThrArgThrAlaThrGlnUserPheProHisProGlyPheAsnAn 100
QY 509 ACCCTCCCAACAAAGACACCGCAATGATCATATGCTGTGAAGATGGCATCGCCAGTC 568
Db 101 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProAl 120
QY 569 TCCATCACTGGGCTGTGGAGCCCGCTCACCTCTCCAGGCTGTGCTCACTGCTGGCAGC 628
Db 121 SerIleThrThrAlaValArgProLeuThrIleSerSerArgCysValThrAlaGlyThr 140
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QY 689 TTGGCGATGGCCCAACATCAATCATTTGAGCACAGAAATGTGAGAACCCCTAACCCGGC 748
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QY 809 GGTGACTCCGGGGGCGCTGTGGTGTGTAACAGATCTTCAAGCAATTAATCTGTGGGC 868
Db 200 gValThrProGlyAlaLeuThrSerValThrSerLeuPheLysAlaLeuSerProGlyAl 220
QY 869 CAGGATCCGTGTGGCATCACCCGAAAGCCTGGTGTATACAGCAAGTCTGCAATATGTG 928
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RESULT 5
US-09-386-642-14
; Sequence 14, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Dartow, Andrew
; APPLICANT: Qi, Jensen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 289
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: With homo sapien serine protease catalytic domain
US-09-386-642-14

Alignment Scores:
Pred. No.: 5,57e-97 Length: 289
Score: 1232.00 Matches: 233
Percent Similarity: 86.12% Conservative: 9
Best Local Similarity: 82.92% Mismatches: 17
Query Match: 51.98% Indels: 22
DB: 4 Gaps: 3

US-09-856-320A-1 (1-1301) x US-09-386-642-14 (1-289)
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QY 254 GTAGGG----- 259
Db 28 ValSerAspTyrLysAspAspAspValAspAlaAlaLeuAlaAlaProPheAsp 47
QY 260 GGAAGACCAAGATCATCAAGGGGTTCAGATGC---AAGCTTCATCCAGCCCTGGCAG 316
Db 48 AspAspAspLysIleValGlyGlyTyrAsnCysLeuGlnLysHisSerGlnProTyrGln 67
QY 317 GGAAGCCCTGTGAGAAGACGCGGCTACTGTGGGGGAGCAGCTCATCGCCCAATAGG 376
Db 68 AlaAlaLeuPheGlnLysThrArgLeuLeuGlyAlaThrIleuIleAlaProArgTyr 87
QY 377 CTCCTGACAGCAGCCCATGCTCAAGCCCGCTACATAGTTACCTGGGGGAGCAGCAAC 436
Db 88 LeuLeuThrAlaAlaHisCysLeuLysProArgTyrIleValHisLeuGlnHisAsn 107
QY 437 CTCACAGAGAGAGAGGGCTGTGAGCAGACCCCGAGACGCACTGATGCTTCCGCCACCC 496
Db 108 LeuGlnLysGlnGlnLysGlnGlnGlnThrArgThrAlaThrGlnUserPheProHisPro 127
QY 497 GGCTTCACACACAGCTCCCGCAACAAAGACCAACCGCAATGATCATGCTGTGGGAAGAG 556
Db 128 GlnPheAsnAsnSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMet 147
QY 557 GCATGCGCATGCTCATCACTGTGGGCTGTGCGACACCCCTCACTCTCCTCAGCTGTGTC 616
Db 148 AlaSerProValSerIleThrThrAlaValArgProLeuThrIleuSerSerArgCysVal 167
QY 617 ACTGCTGGCAGCAGCTGCTCATTTCCGGCTGGGGGAGCAGACGTCACAGCCCGCAATTAACG 676
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QY 797 GACTCTCCAGAGGAGTCTCCGGGGGCGCTGTGCTGTACACGATCTTCTCAAGGCAAT 856
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QY 857 ATCTCTGGGGCCAGATCCGTGTGCGATCACCCGAAAGCCTGTGTCTACACGAAAGTC 916
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QY 917 TGCAATATGTGACTGATCGAGAGCATGAGAGCAATTAACCTGGACCCACCCAC 976
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QY 977 CAC 979
Db 288 His 288

RESULT 6
US-09-205-258-1150
; Sequence 1150, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER APPLICATION NUMBER: 1998-12-04
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
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; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
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; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
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; EARLIER APPLICATION NUMBER: 60/048,974
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; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
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; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
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; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 228
; TYPE: PRT
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US-09-205-258-1150

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Pred. No.: 4,99e-94 Length: 228
Score: 1197.00 Matches: 226
Percent Similarity: 98.69% Conservative: 0
Best Local Similarity: 98.69% Mismatches: 2
Query Match: 50.51% Indels: 1
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QY 383 ACACGAGCCGCTGCTCAAGCCCGCTACATAGTTCACCTGGGGCGACGACCACTCCAG 442
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; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1020091
; US-09-025-059-3

Alignment Scores:
Pred. No.: 1,49e-51 Length: 260
Score: 698.50 Matches: 129
Percent Similarity: 66.13% Conservative: 35
Best Local Similarity: 52.02% Mismatches: 77
Query Match: 29,47% Indels: 7
DB: 3 Gaps: 3

US-09-856-320A-1 (1-1301) x US-09-025-059-3 (1-260)
QY 227 ATCCCTGCTGCTCTGCGACACAGGCTTGTAGGGGAGAGACCG----- 271
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    |||
Db 13 IleLeuLeuLeuLeuPheMetGlyAlaThrAlaGlyLeuThrArgAlaGlnGlySerLys 32
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    |||
QY 272 ATCATCAAGGGGTTGAGTGCAGAGCTCACTCCACGCTGGCAGGACAGCCCTGTTCGAG 331
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    |||
    |||
Db 33 IleLeuGlnGlyArgGlnLysIleProHisSerGlnProThrGlnAlaAlaLeuPheGln 52
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    |||
    |||
QY 332 AAGACGGCTACTCTGTGGGGGAGCGCTATCGCCCAAGATGCTCTGACAGCAGCC 391
    |||
    |||
    |||
Db 53 GlyLysArgLeuLeuLeuLecysGlyGlyValLeuValGlyAspArgThrValLeuThrAlaAla 72
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    |||
    |||
QY 392 CACTGCTCAAGCCCGCTAAGTCAATGTCACCTGGGGGACACACACCTCCAGAGAGAG 451
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    |||
Db 73 HisCysLysLysGlnLysIleLysThrSerValArgLeuGlyAspHisSerLeuGlnSerArgAsp 92
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    |||
QY 452 GGCCTGTGACAGACCCGACAGCGCTAGTCTTCCGCCACCCGGCTTCACAAACACAG 511
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    |||
Db 93 GlnProGluGlnGlnIleGlnValAlaGlnSerIleGlnHisProCysThrAsnAsnSer 112
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    |||
QY 512 CTCGCCACAAAGACACCGCAATGATCATCTCTGTGAAGATGGCATGCCAGTCTCC 571
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    |||
Db 113 AsnPro--GlnAspHisSerHisAspIleMetLeuIleArgLeuGlnAsnSerAlaAsn 131
    |||
    |||
    |||
QY 572 ATCACCTGGGCTGTGGACCCCTCACCCCTCTCTACGCTGCTGCTGCTGCTGCTGCTGCT 631
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    |||
Db 132 LeuGlyAspLysValLysProValGlnLeuAlaAsnLeuCysProLysValGlyGlnLys 151
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    |||
QY 632 TGCTTCATTTCCGGCTGGGGGACAGCAGCTCCAGCCCAAGTTAGCCTGCTCACACCTTG 691
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    |||
    |||
Db 152 CysIleIleSerGlyThrProGlyThrValThrSerProGlnGlnAsnThrProAsnThrLeu 171
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    |||
QY 692 CGATGCGCCACATCATCATTCATGACACAGAGATGTGAGAGACCTTACCCCGGCAAC 751
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    |||
    |||
Db 172 AsnCysAlaGlnValLysIleLysThrSerGlnAsnLysCysGlnArgLysThrProGlyLys 191
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    |||
QY 752 ATCAGACAGACCATGCTGTGCTGCGACGCGGAGGAGGCGCAAGGCTCCGCCAGGCT 811
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    |||
Db 192 IleThrGluGlyMetValCysAlaGly---SerSerAsnGlyAlaAspThrCysGlnGly 210
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QY 812 GACTCCGGGGGCTGTGCTGTGTACAGTCTTCACAGGATTTATCTCCGGGGGCGAG 871
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    |||
Db 211 AspSerGlyGlyProLeuValCysAspGlyMetLeuGlnGlyIleThrSerThrProLysSer 230
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    |||
QY 872 GATCGGTGCGATCACCCGAAAGCCTGTGTCTACAGAAAGTGTGCAAAATGTGTGAC 931
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Db 231 AspProCysGlyLysProGlnLysProGlyValLysThrLysIleCysArgThrThrThr 250
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QY 932 TGGATCCAGGAGACGATGAAGAAC 955
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Db 251 ThrIleLysLysThrMetAspAsn 258
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RESULT 8
US-09-070-526-2
; Sequence 2, Application US/09070526
; Patent No. 6100059
; GENERAL INFORMATION:
; APPLICANT: SOUTHAN, CHRISTOPHER
; APPLICANT: CLINKENBEARD, HELEN
; APPLICANT: BURGESS, NICOLA
; TITLE OF INVENTION: No. 6100059e1 Compounds
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P. O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070.526
; FILING DATE: 30-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9711952.3
; FILING DATE: 9-JUN-1997
; APPLICATION NUMBER: EP 97309646.4
; FILING DATE: 1-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-30353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-070-526-2

Alignment Scores:
Pred. No.: 7,92e-51 Length: 260
Score: 690.00 Matches: 125
Percent Similarity: 66.93% Conservative: 45
Best Local Similarity: 49.21% Mismatches: 80
Query Match: 29.11% Indels: 4
DB: 3 Gaps: 3

US-09-856-320a-1 (1-1301) x US-09-070-526-2 (1-260)
QY 188 CGCTCTCCCTCCAGCCATGAGATTCGAGTTAATCTGCTT-----GCTCTG 241
Db 3 ArgProArgProArgAlaAlaLysThrTrpMetHeuLeuLeuGlyAlaIrr 22
QY 242 GCACAGGGCTTGTAGGGGAGACACAGATCATCAAGGGCTTCAGATGACCTTAC 301
Db 23 AlaGlyHisSerArgAlaGlnGluAspLysValLeuGlyHisGlyCysGlnProHis 42
QY 302 TCCAGCCCTGCGAGCAGCCCTGTGAGAAAGAGCGGCTACTGTGGGGGAGAGCTC 361
Db 43 SerLInProTrpGlnAlaAlaLeuPheGlnGlnGlnLeuLeuGlyGlyValLeu 62
QY 362 ATGCCCCCAGATGGCTCTGACAGACCCACTGCTCAAGCCCGCTACATAGTTTAC 421
Db 63 ValGlyLysAsnTrpValLeuThrAlaAlaHisCysLysLysProLysTyrThrValArg 82
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QY 422 CTGGGGCAGACACACCTCCAGAGAGAGGCTGTGACAGACCCGGACACCTGAG 481
Db 83 LeuGlyAspHisSerLeuGlnAsnLysAspGlyProGlnGlnGlnIleProValValGln 102
QY 482 TCCTTCCCCCAGCCCGGCTTGAACAACAGCCTCCCAACAAGACACCCAGATGAC 541
Db 103 SerLInProHisProCysTyrAsnSerSer---AspValGluAspHisAsnHisLeu 121
QY 542 ATGTGTGTAAGATGATCCAGCTCCATCCATCCATCCATCCATCCATCCATCCAT 601
Db 122 MetLeuLeuGlnLeuArgAspGlnAlaSerLeuGlnSerLysValLysProIleSerLeu 141
QY 602 TCCTCAGCCTGTGTCATGCTGGCAGCAGCTCCCTCATTCCTCCGCTGGGGAGAC 661
Db 142 AlaAspHisCysThrGlnProGlyGlnLysCysThrValSerGlyTyrGlyThrValThr 161
QY 662 AGCCCCCAGTTACCGCTCCCTACACCTTCGGAGATGCCCAACATCCATATGAGCAC 721
Db 162 SerProArgGluAsnProAspThrLeuAsnGlyAlaGluValLysIlePheProGln 181
QY 722 CAGAAGTGTGAGAACGCTTACCCGCAATCATACAGACACCATGCTGTGCCAGCTG 781
Db 182 LysLysCysGluAspAlaTyrProGlyGlnIleThrAspGlyMetValCysAlaGlySer 201
QY 782 CAGGAGGGGCGAAGACTCCTGCCAGGGTACTCCGGGGCCCTTGTGTTAACCGAG 841
Db 202 SerLysGlyAlaA---AspThrCysGlnGlnLysAspSerGlyGlyProLeuValCysAsp 220
QY 842 TCCTTCAAGCATTAATCTCGTGGGGCCAGAGATCGGTGGGAGACACCCGAAACCTG 901
Db 221 AlaLeuGlnGlyIleThrSerTrpLysSerAspProCysGlyLysSerAspLysProGly 240
QY 902 GTCTACAGAAAGTCTGCAATATATGTGACTGTGATCCAGGAG 943
Db 241 ValTyrThrAsnIleCysArgTyrLeuAspTrpIleLysLys 254

RESULT 9
US-09-386-642-13
; Sequence 13, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jemson
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386.642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-13

Alignment Scores:
Pred. No.: 9.91e-51 Length: 288
Score: 689.00 Matches: 129
Percent Similarity: 62.81% Conservative: 50
Best Local Similarity: 45.26% Mismatches: 79
Query Match: 29.07% Indels: 27
DB: 4 Gaps: 6

US-09-856-320a-1 (1-1301) x US-09-386-642-13 (1-288)
QY 203 CAGCCCATGAGATTCGAGTTAATCTG-----CTTGCTGCGCAACAGGCTT 253
Db 8 GlnLysSerArgLeuLeuLeuValValSerAsnLeuLeuLeuGlyGlnGlyVal 27
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QY 254 GTAGG----- 259
Db 28 ValSerAspTyrIlysAspAspAspValAspAlaAlaAlaLeuAlaAlaProPheAsp 47
QY 260 GGAGAGACACGAGTCAATCAAGGGTCCGAGTGC---AAGCTTACATCCCAAGCCCTGGCAG 316
Db 48 AspAspAspIlysIleValIleGlyIlyrAsnCysLeuGlnProHisSerGlnProIlePrgln 67
QY 317 GCAGCCCTGTTCGAGAGACGCGCTACTCTGTGGGCGAGCGCTCAATCCGCGCCCAAGATGG 376
Db 68 AlaAlaLeuPheGlnIleGlnIleGlnIleLeuGlnCysGlyIleValLeuValIleGlyIleAsnTyr 87
QY 377 CTCTTCAGACAGACCCCACTGCTCAAGCCCGCTACATAGTATCACTGGGGGAGACAC 436
Db 88 ValLeuThrAlaAlaHisCysIlySlysProIySlyTyrThrValArgLeuGlnIlyAspHisSer 107
QY 437 CTCACAAAGAGAGAGGGCTGTGTGACGACCGGACGACCACTGACATGCTTCCCAACCC 496
Db 108 LeuGlnAsnIlySAspIlyProGlnGlnIleProValIleGlnSerIleProHisPro 127
QY 497 GCGTTCACACACGAGCTCCCAACAAAGACACCGGACATGATCATGCTGGTGGAGAGAG 556
Db 128 CysTyrAsnSerSer---AspValIleIlyAspHisAsnHisAspLeuLeuGlnLeu 146
QY 557 GCATCGCCAGTCTCCATCACTGGGCTGTGCGACCCCTCAACCCCTCTCTACGCTGTATC 616
Db 147 ArgAspGlnAlaSerLeuGlnIlySerIlySlysValIlySProIleSerLeuAlaAspHisCysThr 166
QY 617 ACTGCTGGGACGACGCTGCTCATTTCCGGCTGGGGGAGACGACGACCCCAAGTACGC 676
Db 167 GlnProGlnIlyIlySerThrValSerGlyTyrPheIlyThrValIlySerProIleGlnIlyAsn 186
QY 677 CTGCTTCACACCTTGGGATCGCCCAACATCACCATCATTCATGAGCAGAGAGTGTGAGAC 736
Db 187 PheProAspPheIleAsnIlySAspIlyValIlySlePheProGlnIlySlysGlnIlyAsp 206
QY 737 GCGTACCCCGGACATCAACAGACACCATGCTGTGCGACGCTGCAGAGAGGGGCAAG 796
Db 207 AlaTyrProGlnIlyIleThrAspGlyMetValCysAlaGlySerSerIlySlysAla--- 225
QY 797 GACTCGTGCAGGATGACGCCGCGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 856
Db 226 AspThrIlyCysGlnIlyAspSerGlyIlyProLeuValCysAspIlyLeuLeuGlnIlyIle 245
QY 857 ATCTCTGGGCGGAGAGCTGCTGTGGCATCACCCGAAAGCCTGTGTATACAGGAAGTC 916
Db 246 ThrSerTyrPheIlySerAspProCysGlyIlySerAspIlyProGlyIlyThrAsnIle 265
QY 917 TGCAAATATGTGACTGTGATCCAGAGAGATGAAAGACATTAATGACTGAGCCACCCAC 976
Db 266 CysArgTyrLeuAspIlyIleIlySlysIleIleGlySerIlyS---GlySerArgHis 283
QY 977 CACAGCCCATCAC 989
Db 284 HisHis-HisHis 287

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RESULT 10
US-09-008-271A-7
; Sequence 7, Application US/09008271A
; Patent No. 6203979
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Yue, Henry
; Guegler, Karl J.
; Corley, Neil C.
; Tang, Tom Y.
; Shah, Puri
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.

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; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,271A
; FILING DATE: 16-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohan-Peterson, Sheela
; REGISTRATION NUMBER: 41,201
; REFERENCE/DOCKET NUMBER: PF-0458 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: COLN00727
; CLONE: 1798496
; SEQUENCE DESCRIPTION: SEQ ID NO: 7 :
;
US-09-008-271A-7
;
Alignment Scores:
Pred. No.: 3,8e-50 Length: 260
Score: 682.00 Matches: 124
Percent Similarity: 66.54% Conservative: 45
Best Local Similarity: 48.82% Mismatches: 81
Query Match: 28.78% Indels: 4
DB: 3 Gaps: 3
US-09-856-320A-1 (1-1301) x US-09-008-271A-7 (1-260)
QY 188 CGTCTCTCCCGCTCCAGGCGCATGAGATTCCTGCAATTCCTGCT-----GCTCTG 241
Db 3 ArgProIArgProIArgAlaAlaIlySThrTyrMetPheLeuLeuLeuGlnIlyGlyAlaTyr 22
QY 242 GCACACAGGAGCTGTAGGAGGAGAGACACGATCATCAAGGGTTCGAGTGCAGAGCTCAC 301
Db 23 AlaGlnHisSerIlyArgAlaGlnIlyAspIlySValIleGlyIlyHisGlnIlySglnProHis 42
QY 302 TCCACGCGCTTGGAGGACGCGCTGTTCGAAAGACGCGCTACTGTGTGGGCGGAGCTC 361
Db 43 SerGlnProIlePrglnAlaAlaIleuSerGlnGlnIleuLeuGlnIlySglnIlyVal 62
QY 362 ATCGCGCCGAGATGGCTCTGACAGAGCGGCTGCTCAAGCCCGCTACATAGTTCAC 421
Db 63 ValIleGlyIlyAsnTyrAlaLeuThrAlaAlaHisCysIlySAspIlySProIySlyThrValArg 82
QY 422 TCGGGGACACACAACTCCAGAGAGAGAGGGCTGTGACACGCGGACGACGACCATGAG 481
Db 83 LeuGlnIlyAspHisSerLeuIlyAsnIlySAspIlyProGlnIleProValIleGln 102
QY 482 TCCCTCCCGACCGCGGCTTCACAAACAGCTCCCAACAAAGACCGCATGATCATC 541
Db 103 SerIleProHisProCysTyrAsnSerSer---AspValIleIlyAspHisAsnHisPhe 121
QY 542 ATGCGGTGAAGATGGCATCGGACATGCTCCATCACTGGGCTGTGCGACCCCTCAACCTC 601
Db 122 MetLeuLeuGlnIleuIlyAspIleAlaSerLeuGlnIlySlysValIlySProIleSerIleu 141

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QY 602 TCCTACCGCTGTGTCACCTGCTGGCACACAGCTGCTCATTTCCGGGTGGGGACGACGCTCC 661
Db 142 Alaaprhscysthglpnrpogllyglntyscsthvalserglytrpdllythrvalthr 161
QY 662 AGCCCCAGTTCAGGCTGCTGCACACCTTGCGATCGGCACATCACCATCATTCATGAGCNC 721
Db 162 Serprroaigluasphetrroasphrleuanscysalaglualylslleheproglin 181
QY 722 CAGAAAGTGTAGACAGCGCTTACCCGGGACATCAGACAGCAGCAGTGTGTCCAGCGTG 781
Db 182 lylslscysgluasphalatyprpogllyglntierthaspglymetvalcysalalyser 201
QY 782 CAGAAAGGCGGACGCTCCGACGAGGTGACCTCGGGGGCCCTGCTGTATACAGC 841
Db 202 Serlysglyala--Asprthrcysglnglyaspserglyglyprolevalcysaspgly 220
QY 842 TCTCTTCAAGGATATATCTCTGAGGCGGATCCGCTGCGATCACCAGAAAGCTGTGT 901
Db 221 Alaleugnglylierhsertrpdllyserasprrocysgllyargserasplysprodly 240
QY 902 GTCTACACGAAAGTGTGCAAATATGTGAGCTGATCCAGGAG 943
Db 241 ValtyrthAsnlllecysargtyrleuasprriletylsls 254
RESULT 11
US-09-996-243-309
Sequence 309, Application US/0996243
Patent No. 6478825
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C13
CURRENT APPLICATION NUMBER: US/09/996, 243
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
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PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR APPLICATION NUMBER: 60/088217
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PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
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PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
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PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
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PRIOR FILING DATE: 1998-06-16
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PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17

IMMEDIATE SOURCE:
LIBRARY: KERANOT02
CLONE: 820694
US-09-210-084-1

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	6,98e-44	268	125	42	83	28
Percent Similarity:	60.29%					
Best Local Similarity:	45.13%					
Query Match:	25.68%					

US-09-856-320A-1 (1-1301) x US-09-210-084-1 (1-268)

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OY 171 CCAGAGAACCTGGGCGCCCTCCCTCCAGGAGATTCAGATTGAGTTAATCC 230
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Db 4 ProthmMetMetPheProValThrThrProLeuThrPro----- 16
OY 231 TCGTTGCTC-----TGCACAGAGGCTGTGAGGGGAGAGACCAGAG--- 272
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 17 CysProLeuGlyAlaThrArgThrTrpGluLeuGlyPro---GlyLysThrProGlyArg 35
OY 273 -----TCATCAAGGGGCTTGAGTGCAGAGCCTCAGTCCAGCCCTGGC 314
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Db 36 MetThrAlaAlaAlaAlaLaserSerMetAspProThrAlaIleCysThrProSerArgGly 55
OY 315 AG-----GCAGCCCTGTTCGAGAAGACGGCTACTCTGTGGGGCGAGCTCATCGCCCC 370
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Db 56 GlnAlaIleLeuLeuLeuArgProAsnGlnLeuTyrcysGlyAlaValLeuValHisPro 75
OY 371 AGATGGCTCTTCAGACAGACCCAGCTGCTCAAGCCCGCTACATAGTTCACCTGGGGCAG 430
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Db 76 GlnTrpLeuLeuThrAlaAlaHisCysArgGlyLysValPheArgValArgLeuGlyHis 95
OY 431 CACAACCTGCAGAG---GAGGAGGGCTGTGAGACGCCGAGACCCCATAGTCCTTC 487
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Db 96 TyrSerLeuSerProValTyrglnSerGlyGlnGlnMetPheGlnGlyValLysSerIle 115
OY 488 CCCCACCCCGGCTTCACACMACAGCCTCCCAACAAAGACCCGATGATCATGCTG 547
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Db 116 ProHisProGlyLysSer-----HisProGlyHisSerAsnSerLeuMetLeu 131
OY 548 GTGAAGATGGCATGCCAGCTGCATACACCTGGGCTGTGAGACCCCTCAGCTTCCTCA 607
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 131 IleLysLeuAsnArgArgIleArgProThrLysAspValArgProIleAsnValSerSer 151
OY 608 CGCTGTGCACCTGCGGAGCAGACGCTGCTCATTTCCGGTGGGGAGCAGCAGTCCAGCCC 667
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 152 HisCysProSerAlaGlyThrLysCysLeuValSerGlyTrpGlyThrThrLysSerPro 171
OY 668 CAGTTACGCTGCTCAGACACTTGCAGTGCAGCAGCAGCATCATCATTTGAGCAGAGAG 727
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 172 GlnValHisPheProLysValLeuGlnCysLeuAsnIleSerValLeuSerIleLysArg 191
OY 728 TGTGAGAACGCTTACCCCGGAGCAATCAGACACCATGTTGTGCGACCGTGCAGGAA 787
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 192 CysGlnAspAlaLysProArgGlnIleAspAspThrMetPheCysAlaGly---AspLys 210
OY 788 GGGGCAAGAGACTCGTCGACGGGTGACTCCGGGGGCGCTGCTGTGTAACCAAGTCTGT 847
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 211 AlaGlyAlaGlyAspSerCysGlnIleLysPserGlyGlyProValValCysAsnGlySerLeu 230
OY 848 CAAGGATATATCTCTGGGGCCAGAGATCCGTGTGAGTACACCCGAGAGGCTGTGCTAC 907
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 231 GlnGlyLeuValSerTrpGlyAspTyrrProCysAlaArgProAsnArgProGlyValTyrr 250
OY 908 ACGAAAGTCTGCAAAATATGTGAGCTGATCCAGAGACAGATGAAGACAAT 958
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 251 ThrAsnLeuCysLysPheThrLysTrpIleGlnGlnIleGlnAlaAsn 267

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RESULT 14
US-09-764-762-1

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? Sequence 1, Application US/09764762
? Patent No. 6472195
? GENERAL INFORMATION:
? APPLICANT: Hillman, Jennifer L.
? Invt, Preeti
? TITLE OF INVENTION: NOVEL KALLIKREIN
? NUMBER OF SEQUENCES: 5
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Incyte Pharmaceuticals, Inc.
? STREET: 3174 Porter Drive
? CITY: Palo Alto
? STATE: CA
? COUNTRY: USA
? ZIP: 94304
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FastSeq for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/764,762
? FILING DATE: 16-Jan-2001
? CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 09/210,084
? FILING DATE: <Unknown>
? ATTORNEY/AGENT INFORMATION:
? NAME: Billings, Lucy J.
? REGISTRATION NUMBER: 36,749
? REFERENCE/DOCKET NUMBER: PF-0252 US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-855-0555
? TELEFAX: 415-845-4166
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 268 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? LIBRARY: KERANOT02
? CLONE: 820694
? SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-856-320A-1 (1-1301) x US-09-764-762-1 (1-268)

Alignment Scores:
Pred. No.: 6,98e-44 Length: 268
Score: 608.50 Matches: 125
Percent Similarity: 60.29% Conservative: 42
Best Local Similarity: 45.13% Mismatches: 83
Query Match: 25.68% Indels: 28
Gaps: 8

OY 171 CCAGAGAACCTGGGCGCCCTCCCTCCAGGAGATTCAGATTGAGTTAATCC 230
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4 ProthmMetMetPheProValThrThrProLeuThrPro----- 16
OY 231 TCGTTGCTC-----TGCACAGAGGCTGTGAGGGGAGAGACCAGAG--- 272
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 17 CysProLeuGlyAlaThrArgThrTrpGluLeuGlyPro---GlyLysThrProGlyArg 35
OY 273 -----TCATCAAGGGGCTTGAGTGCAGAGCCTCAGTCCAGCCCTGGC 314
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 36 MetThrAlaAlaAlaAlaLaserSerMetAspProThrAlaIleCysThrProSerArgGly 55
OY 315 AG-----GCAGCCCTGTTCGAGAAGACGGCTACTCTGTGGGGCGAGCTCATCGCCCC 370
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 56 GlnAlaIleLeuLeuLeuArgProAsnGlnLeuTyrcysGlyAlaValLeuValHisPro 75
OY 371 AGATGGCTCTTCAGACAGACCCAGCTGCTCAAGCCCGCTACATAGTTCACCTGGGGCAG 430
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 76 GlnTrpLeuLthrAlaAlaHisCysArgLysValPheArgValArgLeuGlyHis 95
Oy 431 CACAACCTCCAGAG---GAGGAGGGCTGTGAGCAGACCCGACAGCCACTGAGCTCTTC 487
Oy 96 TyrSerLeuSerProValTyrGluSerGlyGlnGlnMetPheGlnGlyValIleSerIle 115
Oy 488 CCCCACCCCGGCTTCACACACAGCCTCCCAACAAAGCCACCGCATGATCATCTGCTG 547
Oy 116 ProHisProGlyTyrSer-----HisProGlyHisSerAspAspLeuMetLeu 131
Oy 548 GTGAAGATGATGCATGCCATCTCCATCTGAGCTGGGCTGACCCCTGACCTCTCTCA 607
Db 132 IleLysLeuAsnAlaArgGlyIleArgProThrLysAspValArgProIleAsnValSerSer 151
Oy 608 CGCTGTGTACCTGTGGCAGCAGCCTGCCCTCATTTCCGGCTGGGAGCAGCAGCTCCAGCCC 667
Db 152 HisCysProSerAlaGlyThrLysCysLeuValSerGlyTyrPglYThrThrLysSerPro 171
Oy 668 CAGTTAGCCCTGCTGCACACCTTGCGATGCGCCCAACATCACCATTCATTGACACCAAG 727
Db 172 GlnValHisPheProLysValLeuGlnCysLeuAsnIleSerValLeuSerGlnLysArg 191
Oy 728 TGTGAGAGCGCTACCCCGGACATCAGACACCAACCATGCTGTGAGGAGGAGGAGGAA 787
Db 192 CysLysAspAlaTyrProArgGlnIleAspAspThrMetPheCysAlaGly---AspLys 210
Oy 788 GGGGCAAGAGACTCCTGCGCAGGAGTACTCCGGGGCCCTCTGTGTATACAGATCTCTT 847
Db 211 AlaGlyArgAspSerCysGlnGlyAspSerGlyGlyProValValCysAsnGlySerLeu 230
Oy 848 CAAGGCATTAATCTCTGGGGCCAGAGATCCGTGTGCGATCACCCGAAGCCTGGTGTAC 907
Db 231 GlnLysLeuValSerTyrPglYAspTyrProCysAlaArgProAsnAlaProGlyValTyr 250
Oy 908 AGCAAGTCTCAATATATGTGATGATCCAGGAGGAGAGATGAGAACAT 958
Db 251 ThrAsnLeuCysLysPheThrLysTyrPheGlnGlnThrIleGlnAlaAsn 267

RESULT 15
US-08-790-137-4
; Sequence 4, Application US/08790137
; Patent No. 5840871
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL PROSTATE-ASSOCIATED
; TITLE OF INVENTION: KALLIKREIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,137
; FILING DATE: Filed Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0195 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555

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; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 55527
; US-08-790-137-4

Alignment Scores:
Pred. No.: 1.52e-43 Length: 263
Score: 604.50 Matches: 111
Percent Similarity: 62.02% Conservative: 49
Best Local Similarity: 43.02% Mismatches: 85
Query Match: 25.51% Indels: 13
Gaps: 3

US-09-856-320A-1 (1-1301) x US-08-790-137-4 (1-263)

Oy 224 TTAATCCCTGCTGTGTCGCAACAGCGCTGTAGGGGA-----GAGACCAAG 271
Db 5 IleLeuPheLeuAlaLeuPheLeuGlyLysLeuAlaAlaProProValGlnSerArg 24
Oy 272 ATCATCAAGGGGTTTGAAGTGCAGCCTTCACCTCCAGCCCTGGCAGCAGCCCTGTGAG 331
Db 25 IleIleGlyGlyPheAsnCysGlnLysAsnSerGlnProThrPheValAlaValTyrArg 44
Oy 332 AAGAGCGGCTACTCTGTGGGGCAGCCTCATGCCCCCAGATGGCTCTGTACAGACCC 391
Db 45 PheAlaArgTyrGlnCysGlyGlyValLeuLeuAspAlaAsnTyrValLeuThrAlaAla 64
Oy 392 CAGTGCCTCAAGCCCGCTACATGATTCACCTGGGGGAGCAGCAACCTCCAAAGAGAG 451
Db 65 HisCysTyrAsnArgLysTyrGlnValThrLeuGlyLysAsnAlaArgPheGlnAspLys 84
Oy 452 GGTGTGTGACAGACCCGGCAGCAGCCTGAGTCTCTCCGCCAGCCCGCTTCAACAGAC 511
Db 85 ProSerAlaGlnHisGlnIleuIleSerLysAlaIleProHisProGlyPheAsnMetSer 104
Oy 512 CTCGCCAACAAGACAC-----CGCATGACATCATGCTG 547
Db 105 LeuLeuAsnLysAspHisThrProHisProGlnAspArgTyrSerAsnAspLeuMetLeu 124
Oy 548 GTGAAGATGATGCATGCCATGATCCAGGAGTCCGCTGGGAGCAGCAGCTCTCCGCA 607
Db 125 ValArgLeuLysLysProAlaGlnIleThrAspValValLysProIleAspLeuProThr 144
Oy 608 CGCTGTGTACTGTGCGCAGCAGCCTGCCCTCATTTCCGGCTGGGAGCAGCAGCTCC---AGC 664
Db 145 GlnGluProThrValGlySerArgCysLeuAlaSerGlyTyrPglYThrThrProThr 164
Oy 665 CCCCAGTTAGCCCTGCTGCACACCTTGCGATGCGCCCAACATCACCATTCATTGACACAG 724
Db 165 GlnLysPheGlyTyrSerHisAspLeuGlnCysValTyrLeuGlnLeuLeuSerAsnGln 184
Oy 725 AAGTGTGAGACAGCGCTACCCCGGCAACATCAACACCAATGCTGTGCGCAGGCTCAG 784
Db 185 ValCysAlaLysAlaHisThrGlnLysValThrAspThrMetLeuCysAlaGlyGlnMet 204
Oy 785 GAAGGGGCAAGAGACTCCTGCCAGGAGTACTCCGGGGCCCTGTGCTGTAAACAGACT 844
Db 205 AspGlyGlyLysAspThrLysValGlyAspSerGlyGlyProLeuIleCysAspGlyVal 224
Oy 845 CTTCAGGCATTAATCTCTGGGGCCAGAGATCCGTGTGCGATCACCCAAAGCTGTGTC 904
Db 225 LeuGlnGlyIleThrSerTyrPglYProThrProCysAlaLeuProAsnValProGlyIle 244
Oy 905 TACAGGAAGTCTCAATATATGTGATGATGATGATGATGATGATGATGATGATGATGAT 958
Db 245 TyrThrLysLeuIleGlyTyrArgSerThrIleLysAspValMetAlaAsnAsn 262

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Thu Oct '16 09:48:32 2003

us-09-856-320a-1.rai

Page 15

Search completed: October 15, 2003, 20:28:58
Job time : 29.2321 secs

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; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 211
; LENGTH: 1186
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-211

Alignment Scores:
Pred. No.: 5,17e-162 Length: 1186
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-856-320a-2 (1-282) x US-10-205-823-211 (1-1186)
QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
DB 26 ATGCAGAGGTTGAGTGCGCTGGCGAGCTGGAGATCATCGGGCAGAGTCTCACAGCAGCC 85
QY 21 LysGluProGluValArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleu 40
DB 86 AAGGAACCTGGGCCCGCTCTCCCTCCCTCCAGGCGCATGGCATGGCATGTTAACTCG 145
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgIleIleLysGlyPheGlyCys 60
DB 146 CTTCCTCTGGCAACAGGGCTTTAGGGGGAGAGACCATCATCAAGGGGTTGAGTGC 205
QY 61 LysProHisSerLeuProTrpGlnAlaAlaLeuPheGluLysThrArgLeuLeuGly 80
DB 206 AACCCCTACCTCCAGCCCTGGCAGGCGCCCTGTGAGAGAAAGCGGGCTACTCTGTGG 265
QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
DB 266 GCGACCTCATCGCCCCCAGATGGCTCTGCACAGCAGCCACCTCCTCAAGCCCCCGTAC 325
QY 101 IleValHisLeuGlyLysHisAsnLeuGlnLysGlyGlyLysGlnGlnThrArgThr 120
DB 326 ATAGTTCACCTGGGCGAGCACAACCTCCAGAAAGAGAGGGCTGTGAGCAGACCGGACA 385
QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB 386 GGCACCTGAGTCTTCCCCACCCCGGCTTCAMACAGGCTCCCAACAAAGACCCAGC 445
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValAlaPro 160
DB 446 AATGACATCATGTGGTGAAGATGGCATGGCCAGTCTCATATCCCTGGGGTGGCAGCC 505
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrGly 180
DB 506 CTCACCCCTCCCTCAGCGTGTGTCATGCTGGGACCAAGCTGCCCTATTCCGGCTGGGG 565
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
DB 566 AGCAGCTCCAGCCCAAGTTACCCCTGCACACCTTGGAGTGGCCCAACATCACACATC 625
QY 201 IleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
DB 626 ATTGACACCAAGAGTGTGAAGAGCGCTACCCCGGCAACATCAACACCATGATGTGT 685
QY 221 AlaSerValGlnGlnLysGlyLysAspSerCysGlnGlyLysAspSerGlyLysProLeuVal 240
DB 686 GCCAGCGTGCAGGAAGGGGCAAGGACCTCTGCGAGGGTACTCCGGGGGCCCTCTGTGTC 745
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QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
DB 746 TGTAAACAGCTCTTCAAGGCAATTATCTCTGGGCCAGAGATCCGTGCGATCACCCCA 805
QY 261 LysProGluValIleThrLysValCysLysTyrValAspTrpIleGlnLeuThrMetLys 280
DB 806 AACCTGTGTCTACAGAAAGTCTCAATATGTGACTGATGATCCAGAGAGATGAAG 865
QY 281 AsnAsn 282
DB 866 AACAAAT 871

RESULT 2
US-09-946-374-169
; Sequence 169, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Rong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099336
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
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Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 11      Gaps: 0

US-09-856-320a-2 (1-282) x US-09-946-374-169 (1-1204)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
    |||||||
DB 10 ATGCAAGAGGTGGAGGTGGCTGCGGAGCTGAGAGTCAATCGGGGAGAGTCTCACAGAGACC 69
QY 21 LysGluProGluValAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnIleLeu 40
    |||||||
DB 70 AAGGAACCTGGGGCCCGCTCTCCCTCCAGGCCATGAGATTCTGCGATTAACTCTG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGluThrArgIleIleLeysGlyPheGlyCys 60
    |||||||
DB 130 CTGTGCTCTGGCAACAGGGCTTGTAGGGGGAGAGACCAAGATCATCAAGGGGTTGAGTGC 189
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLeuGlyGly 80
    |||||||
DB 190 AACCTCTACTCCAGCCCTGGAGGAGGAGCCCTGTGGAGAAAGCGGGGTACTCTGTGGG 249
QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
    |||||||
DB 250 GCGACGCTCATCCCGCCAGATGGCTCTCTGACAGCAGCCACTGCTCAAGCCCGCTAC 309
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlyCysGluGlnThrArgThr 120
    |||||||
DB 310 ATAGTTCACCTGGGGAGGACACACCTCCAGAAAGAGAGGGGTGTGAGAGACCGGACA 369
QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
    |||||||
DB 370 GCCAGTGAAGCTTCTCCCGCCAGCCGCTTCACACAGCCCTCCCAACAAAGACCCAGC 429
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
    |||||||
DB 430 AATGACATCATGCTGTGGAGATGGCATGCCAGTCTCCATCACTCGGGGTGTGCCAGCC 489
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrGly 180
    |||||||
DB 490 CTCACCTCTCTCTCAAGCTGTGTCACTGTGTCGACACAGCTGCTCATTTCCGGCTGGGG 549
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
    |||||||
DB 550 AGCAGCTGACGCCCCAGATGATGAGCTGCTCCTCACACCTGGATGCGCAACATCACCATC 609
QY 201 IleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
    |||||||
DB 610 ATTAGACACACAGAAAGTGTAGAGACGCTACCCCGGCAACATCACAGACACCATGATGTGT 669
QY 221 AlaSerValGlnGluGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
    |||||||
DB 670 GCCAGCTGTGAGAAAGGGGGCAAGAGACTCTGCGCAAGGTGACCTCGGGGGCTCTGTGGTC 729
QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
    |||||||
DB 730 TGTAAACCAAGCTCTTAAAGGCATTATCTCTGGGGCAGAGATCCGATGTGACACCCGA 789
QY 261 LysProGluValLysThrLysValCysLysTyrValAspTrpIleGlnGluThrMetLys 280
    |||||||
DB 790 AAGCCGTGTCTACACGAAAGCTCAATATGTGACTGATTCAGAGAGCATGAGAAC 849
QY 281 AsnAsn 282
    |||||||
DB 850 AACAAAT 855
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RESULT 3
US-10-015-387A-169
; Sequence 169, Application US/10015387A
; Publication No. US20030135034A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
```

```
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoul, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC54
; CURRENT APPLICATION NUMBER: US/10/015,387A
; CURRENT FILING DATE: 2001-12-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 169
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-387A-169

Alignment Scores:
Pred. No.: 5,286-162      Length: 1204
Score: 1523.00      Matches: 282
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 12      Gaps: 0

US-09-856-320a-2 (1-282) x US-10-015-387A-169 (1-1204)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
    |||||||
DB 10 ATGCAAGAGGTGGAGGTGGCTGCGGAGCTGAGAGTCAATCGGGGAGAGTCTCACAGAGACC 69
QY 21 LysGluProGluValAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnIleLeu 40
    |||||||
DB 70 AAGGAACCTGGGGCCCGCTCTCCCTCCAGGCCATGAGATTCTGCGATTAACTCTG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGluThrArgIleIleLeysGlyPheGlyCys 60
    |||||||
DB 130 CTGTGCTCTGGCAACAGGGCTTGTAGGGGGAGAGACCAAGATCATCAAGGGGTTGAGTGC 189
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLeuGlyGly 80
    |||||||
DB 190 AACCTCTACTCCAGCCCTGGAGGAGGAGCCCTGTGGAGAAAGCGGGGTACTCTGTGGG 249
QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
    |||||||
DB 250 GCGACGCTCATCCCGCCAGATGGCTCTCTGACAGCAGCCACTGCTCAAGCCCGCTAC 309
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlyCysGluGlnThrArgThr 120
    |||||||
DB 310 ATAGTTCACCTGGGGAGGACACACCTCCAGAAAGAGAGGGGTGTGAGCAGACCGGACA 369
QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
    |||||||
DB 370 GCCAGTGAAGCTTCTCCCGCCAGCCGCTTCACACAGCCCTCCCAACAAAGACCAAGCC 429
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
    |||||||
DB 430 AATGACATCATGCTGTGAAGATGGCATGCGCATGCTCCATCACTCGGGGTGTGCCAGCC 489
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrGly 180
    |||||||
DB 490 CTCACCTCTCTCTCAAGCTGTGTCACTGTGACACAGCTGCTCATTTCCGGCTGGGG 549
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
    |||||||
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Db 550 AGCAGTCACGCCCCCACTACGCGCTGCTCAGACCTTGCGATGCGCCACATCACCATC 609
Oy 201 ILeGIuHISgInLysCySgLUaSnAlaTyRProGlyAsnIleThrAspThrMetValCys 220
Db 610 ATTGAGCACCAGAAAGTGTGAGAAAGCCCTACCCCGGCACATCACAGACCATGGTGTGT 669
Oy 221 AlaSerValGIngluGlyGlyLysAspSerCysGIngluYAspSerGlyGlyProLeuVal 240
Db 670 GCCACGCTGCAGGAAGGGGGGCAAGGACTCTCCGCGGGGTGACTCCGGGGGCTCTGTGTC 729
Oy 241 CysAnGInSerLeuGIngluGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
Db 730 TGTAAACCACTCTCTTCAAGGCATATCTCTCGGGCCAGCATCCGTGTGCATCACCCGA 789
Oy 261 LysProGlyValTyRThrLysValCysLysTyRValAspTrpIleGIngluThrMetLys 280
Db 790 AAGCTGTGTCTCTACACGAAAGTCTGCMAATATGTGACTGGATCCAGAGACGATGAAG 849
Oy 281 AsnAsn 282
Db 850 AACAAAT 855

RESULT 4
US-10-137-870-505
; Sequence 505, Application US/10137870
; Publication No. US20030138883a1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C155
; CURRENT APPLICATION NUMBER: US/10/137, 870
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-137-870-505

Alignment Scores:
Pred. NO.: 5,28e-162 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
12

US-09-856-320A-2 (1-282) x US-10-137-870-505 (1-1204)
Oy 1 MetGlnArgLeuAlaGlyTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
Db 10 ATGAGAGAGTGTGAGTGTCTCGGAGACTGGAAGTCATCTCGGCAAGAGGTCTCACAGCAGCC 69
Oy 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnIleLeu 40

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Db 70 AAGGAACCTGGGGGCGCTCTCTCCCGCTCCAGGCCCATAGAGATTGTGACGTTAAATCTTG 129
Oy 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGlnThrArgIleIleLysGlyPheGluCys 60
Db 130 CTGTGCTGGCAACAGGGGCTGTAGGGGAGAGACAGATATCATAAAGGCTTCAGATTC 189
Oy 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLysThrArgLeuLeuGly 80
Db 190 AAGCTCACTCCACCCCTGTGGAGAGACCCCTGTTCGAGAGACCCGCTACTCTGTGGG 249
Oy 81 AlaThrLeuIleAlaProArgTrpLeuThrAlaAlaHisCysLeuLysProArgTrp 100
Db 250 GCGAGCTCATATGCCCCAGATGGCTCTGACAGCAGCCACTGCTCAAGCCCGCTAC 309
Oy 101 ILeValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlyCysGlyGlnThrArgThr 120
Db 310 ATAGTTCACCTGGGGCAGACACACACTCCAGAAAGAGAGAGGGGTGTGACAGACCCGACA 369
Oy 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Db 370 GCCACTGAGTCTTCCCTCCACCCCGGCTTCAACAACACCTCCCAACAAAGACACCGC 429
Oy 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
Db 430 AATGACATCATGCTGTGTAAGATGGCATGCGCAGCTCTCATACACTGGGGCTGTGGACCC 489
Oy 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
Db 490 CTCACCCCTCTCTACAGCTGTGTCTACTCTGTGGACACCACTGCTCTATTTCCGGCTGGGGC 549
Oy 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
Db 550 AGCAGCTCACAGCCCACTACAGCTACGCTGCTCACACTTGCGATGGGCCACATCAGCATC 609
Oy 201 ILeGIuHISgInLysCySgLUaSnAlaTyRProGlyAsnIleThrAspThrMetValCys 220
Db 610 ATTGAGCACCAGAAAGTGTGAGAAAGCCCTACCCCGGCACATCACAGACCATGGTGTGT 669
Oy 221 AlaSerValGIngluGlyGlyLysAspSerCysGIngluYAspSerGlyGlyProLeuVal 240
Db 670 GCCAGCGTGCAGGAAGGGGGGCAAGGACTCTCCGCGGGGTGACTCCGGGGGCTCTGTGTC 729
Oy 241 CysAnGInSerLeuGIngluGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
Db 730 TGTAAACCACTCTCTTCAAGGCATATCTCTCGGGCCAGCATCCGTGTGCATCACCCGA 789
Oy 261 LysProGlyValTyRThrLysValCysLysTyRValAspTrpIleGIngluThrMetLys 280
Db 790 AAGCTGTGTCTCTACACGAAAGTCTGCMAATATGTGACTGGATCCAGAGACGATGAAG 849
Oy 281 AsnAsn 282
Db 850 AACAAAT 855

RESULT 5
US-10-140-018-505
; Sequence 505, Application US/10140018
; Publication No. US20030138885a1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel

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; APPLICANT: Watanabe, Colin K
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P33081C158
; CURRENT APPLICATION NUMBER: US/10/140,018
; PRIOR APPLICATION removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO: 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-505

Alignment Scores:
Pred. No.: 5,286-162 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-856-320a-2 (1-282) x US-10-140-018-505 (1-1204)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
DB 10 ATGACAGAGCTTGTAGAGCTGGCGAGCTGAGCATCGGAGAGCTGCACAGCAGCC 69
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnIleLeu 40
DB 70 AAGAACCTGGGGCCCTCTCTCCCTCCAGGCAATGAGATTCGAGTTATCTG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyIleThrArgIleLeuGlyPheGlyCys 60
DB 130 CTGGCTCTGGCAACAGGGCTGTAGAGGGAGAGACCGAGTACATCAAGGGGTTGAGTGC 189
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnIleLysThrArgLeuLeuGly 80
DB 190 AACCTTCACCTCCAGAGCCCTGGAGGAGCCCTGTTCAGAAAGACGGGCTACTCTGTGGG 249
QY 81 AlaThrIleLeuAlaProArgTrpLeuThrAlaAlaHisCysLeuLysProArgTrp 100
DB 250 GCGAGCTCATCGCCCAATGAGCTCTCTCAGACAGCCCACTGCTCAAGCCCGGTAC 309
QY 101 IleValHisLeuGlnIleHisAsnLeuGlnLysGlnIleLysCysGlnIleThrArgThr 120
DB 310 ATAGTTCACTGGGGGAGCACAACCTCCAGAGAGAGGGCTGTGACAGACCCGAGACA 369
QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB 370 GCCACTGAGTCTCTCCCAACCCGGGCTTCACAAACAGCCCTCCCAACAAAGACCCGCG 429
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
DB 430 AATGACATCTGCTGCTGTAAGATGAGCATGCCAGTCTCCATCACTGGGGTGTGCAAGCC 489
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
DB 490 CTCACACCTCTCCACAGGCTGTGCACAGTGTGGGACACAGCTGCTCATTTCCGGCTGGGCG 549
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
DB 550 AGCAGCGCTGAGCCCGCAGTTACCGCTGCACACCTTGGATGCGCAACATCACACATC 609
QY 201 IleGlnHisGlnLysCysGlnAsnAlaTrpProGlyAsnIleThrAspThrMetValCys 220
DB 610 ATTGAGCAGCAGAGAGTGTGAAGAGCGCTACCCGCGCAACATCAACAACACATGAGTGTGT 669
QY 221 AlaSerValGlnIleGlyLysLysAspSerCysGlnIleLysAspSerGlyLysProLeuVal 240
DB 670 GCCAGCGCTGAGAGAGAGGGGCAAGAGACTCTGCGCAGGGTACTGCCGGGGCCCTGTGGTC 729
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QY 241 CysAsnGlnSerIleGlnIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
DB 730 TGTAAACAGCTCTCTCAAGGATTAATCTCTGGGGCAGAGATCGGTGGATCACCCGA 789
QY 261 LysProGlyAlaIleThrLysValCysLysValAspTrpIleGlnIleThrMetLys 280
DB 790 AACCTGTGTCTACAGAAAGTCTCAATATGTGAGTATCCAGAGAGCATGTAAG 849
QY 281 AsnAsn 282
DB 850 AACCAT 855

RESULT 6
US-10-140-021-505
; Sequence 505, Application US/10140021
; Publication No. US20030138886A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geo, Mei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Zhang, Zemin
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P33081C167
; CURRENT APPLICATION NUMBER: US/10/140,021
; PRIOR APPLICATION removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO: 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-021-505

Alignment Scores:
Pred. No.: 5,286-162 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-856-320a-2 (1-282) x US-10-140-021-505 (1-1204)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
DB 10 ATGACAGAGCTTGTAGAGCTGGCGAGCTGAGCATCGGAGAGCTGCACAGCAGCC 69
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnIleLeu 40
DB 70 AAGAACCTGGGGCCCTCTCTCCCTCCAGGCAATGAGATTCGAGTTATCTG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyIleThrArgIleLeuGlyPheGlyCys 60
DB 130 CTGGCTCTGGCAACAGGGCTGTAGAGGGAGAGACCGAGATCATCAAGGGTTCGAGTGC 189
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnIleLysThrArgLeuLeuGly 80
DB 190 AACCTTCACCTCCAGAGCCCTGGAGGAGCCCTGTTCAGAAAGACGGGCTACTCTGTGGG 249
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QY	81	AlaThrLeuIleAlaProArgTrpLeuThrAlaAlaHisCysLeuLysProArgTyr	100
Db	250	GGAGAGCTCATGCGCCCGCCAGATGGCTCTTGACAGCAGCCCACTGCTCAAGCCCGGTAC	309
QY	101	IleValHisLeuGlyGlnHisAsnLeuGlnIlySgluGlyCysgluGlnThrArgThr	120
Db	310	ATAGTTCACCTGGGGAGACAACTCCAGAAAGGAGAGGGCTGTAGCAGACCCGACA	369
QY	121	AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg	140
Db	370	GGCATGTAGTCTCTTCCCGCCACCCCGGCTTCACACAGCTCTCCCAACAAGACCAACGC	429
QY	141	AsnaPileMetLeuValLysMetalSerProValSerIleThrTrpAlaValArgPro	160
Db	430	AATGACATCATCTGTGTGAAGATGGCATGGCCAGTCTCATCATCTGGGTGTGGCAACC	489
QY	161	LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly	180
Db	490	CTCACCCCTCTCTCAACGCTGTCTACTGTGTGCACACAGCTGCTCTCTTCCCGCTGGGG	549
QY	181	SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle	200
Db	550	AGCAGCTCCAGGCCCGCCAGTTAGCCTGCGCTCACACCTTCGATGGCCCAATACACATC	609
QY	201	IleGluHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys	220
Db	610	ATTGAGCACCAAAAGTGTGAGAACGCTACCCCGGCAACATACACACACATGATGTGTG	669
QY	221	AlaSerValGlnGluGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal	240
Db	670	GCCACAGCTGCAGGAAGGGGGCAGAGACTCTTGCAGAGGTGACTCCGGGGCCCTTGAGTC	729
QY	241	CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg	260
Db	730	TGTACACGATCTCTTCAAGGCAATATCTCTGCGGCGCAGAGATCCGHTGCGATCACCCGA	789
QY	261	LysPProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnIleLuhThrMetLys	280
Db	790	AAGCTGTGTCTACACGAAAGTGTGCAATATGTGACTGATCCAGAGACGATGAAG	849
QY	281	AsnaAsn	282
Db	850	AAACAT	855
RESULT 7			
US-10-140-274-505			
: Sequence 505, Application US/10140274			
: Publication No. US20030143674A1			
: GENERAL INFORMATION:			
: APPLICANT: Baker, Kevin P.			
: APPLICANT: Beresini, Maureen			
: APPLICANT: Deforge, Laura			
: APPLICANT: Desnoyers, Luc			
: APPLICANT: Filvaroff, Ellen			
: APPLICANT: Gao, Wei-Jiang			
: APPLICANT: Gerritsen, Mary E.			
: APPLICANT: Goddard, Audrey			
: APPLICANT: Godowski, Paul J.			
: APPLICANT: Gurney, Austin L.			
: APPLICANT: Sherwood, Steven			
: APPLICANT: Smith, Victoria			
: APPLICANT: Stewart, Timothy A.			
: APPLICANT: Tumas, Daniel			
: APPLICANT: Watanabe, Colin K			
: APPLICANT: Wood, William			
: APPLICANT: Zhang, Zhen			
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NOCLEIC			
: FILE OF INVENTION: ACIDS ENCODING THE SAME			
: FILE REFERENCE: P333091C161			
: CURRENT APPLICATION NUMBER: US/10/140,274			
: PRIOR APPLICATION: 2002-05-06			
: Prior Application removed - See File Wrapper or Palm			

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; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-274-505

Alignment Scores:
Pred. No.:          5,28e-162
Score:              1523.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match:       100.00%
DB:                12

US-09-856-320A-2 (1-282) x US-10-140-274-505 (1-1204)
length: 1204
Matches: 282
Conservative: 0
Mismatches: 0
Indels: 0
Caps: 0

```

OY	MeGlnlnrGleuLrGrPrLeuArGAspTrpLysSerSerGlyArgGlyLeuThrAlaLa	20
Db	10 ATGCAGAGGTGTAGAGTGGCTGGCGGAGCTGGAAAGTCTCGGGAGAGAGTCTCACACAGACC	69
OY	21 LysGIuProGIyAlaArGSerSerProLeuGlnAlaMetArgPIleuGlnLeuIleLeu	40
Db	70 AAGGAACCTGGGGCGCGCTCTCCCTCCAGCGCATGAGGATTCTCGAGTTATCTCTG	122
OY	41 LeuAlaLeuAlaThrGlyLeuValIleGlyGlyIuThrArgPIleIleGlyGlyPheGluCys	60
Db	130 CTTCGCTCTGGCAACAGGGCTGTGAGGGGAGAGACCGAGCATATCAAGCGGTTCACATGTC	187
OY	61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnIleLysThrArgLeuLeuGlyGly	80
Db	190 AAGCTTACCTCCCAAGCCCTTGGACAGGACCCCTTGTGAAAGAACCGCGCTACTCTGTGGG	247
OY	81 AlaThrIleuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTrp	100
Db	250 GCGACGGCTCATCCGCCCCAGATGGCTCTCTGACAGCAGCCCATGGCTCTCAAGCCCGGTAC	308
OY	101 IleValHisIleuGlyGlnHisAsnLeuGlnIlyGlyGlnGlyCysGlnGlnThrArgThr	120
Db	310 ATATGTTTACCTGGGGGACGACAAACCTCCAGAAAGAGAGAGGCTGTGACACAGCCGGGACA	366
OY	121 AlaThrGlyuSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg	140
Db	370 GCCACGTAGTCTTCCGCCCCAGCCCGGCTTCACAAACAGGCTCTCCCAACAAAGACACACCGC	422
OY	141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValaArgPro	160
Db	430 AATGACATCATCTGCTGTGAAGATGGCATGGCAGATCTCCATCATCCTGGGCTGTGGACCC	488
OY	161 LeuThrIleuSerSerArgCysValIThrAlaGlyThrSerCysLeuIleIleSerGlyTrpGly	180
Db	490 CTACCCCTCTCCACAGCTGTGTGCATCGTGGACACAGTCGCTCATATTCGGCGTGGGGC	545
OY	181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle	200
Db	550 AGACAGTCCAGGCCCGCAGTTACGCTGGCTCTACACCTTGCGATGTGGCCAAATCACATC	607
OY	201 IleGlnHisGlnLysCysGluAsnAlaArgTrpProGlyAsnIleThrAspThrMetValCys	220
Db	610 ATTGAGTACCAGAAAGTGTAGAAAGCGCTCCCGCGCAACATCACAGACACCATGGTGTGT	665
OY	221 AlaSerValGlnGlnIuGlyLysAspSerCysGlnGlyAspSerGlyProLeuVal	240
Db	670 GCCAGGGGTGAGGAAGGGGCAAGGACATCTCCAGGGTGAATCCGGGGGCCCTCTGGTGC	722
OY	241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg	260
Db	730 TGTAAACAGACTCTTCAAGGATTTATCTCTGGGGCCAGATCCGTGTGGCATCACCCGA	789
OY	261 LysProGlyValaIlyThrLysValCysLysIlyTrValAspTrpIleGlnGlyIuThrMetLys	280
Db	790 AACCTCGGTGTATACGAAAGTGTGCAAATTTGTGGACTGTGATTCAGAGACATGATAG	849

QY 281 AsnAsn 282
Db 850 AACAAAT 855

RESULT 8
US-10-140-471-505
; Sequence 505, Application US/10140471
; Publication No. US2003013887A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C163
; CURRENT APPLICATION NUMBER: US/10/140,471
; PRIOR APPLICATION DATE: 2002-05-06
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-471-505

Alignment Scores:
Pred. No.: 5,28e-162 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-856-320a-2 (1-282) x US-10-140-471-505 (1-1204)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
Db 10 ATGCAGAGGTGGAGGTGGCTGGCGGACTGGAAGTCAATCGGGCGAGAGGTCTCACAGCAGCC 69
QY 21 LysGluProGlyValArgSerSerProLeuGlnAlaMetArgIleLeuGlnIleu 40
Db 70 AAGGAACCTGGGGCCGCTCTCCCTCCAGCCCATGGATGTGTGCAAGTAAATCCG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgIleIleLysGlyPheGlyCys 60
Db 130 CTGGCTGGCAACAGGGCTGTAGGGGGAGACACAGATCATCAAGGGTTCCAGTGC 189
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLeuCysGly 80
Db 190 AAGCCTCATCCAGCCCTGGCGAGCGCTGTGAGAAAGCGGGCTACTCTGTGG 249
QY 81 AlaThrLeuLeuLeuArgTrpLeuArgTrpLeuThrAlaAlaHisCysLeuLysProArgTyr 100
Db 250 GGACCCCTATGCCCCCAGATGGCTCTGCACAGCAGCCACCTGCTCAAGCCGCTAC 309
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyCysGlnGlnThrArgTyr 120
Db 310 ATAGTTCACCTGGGGCAGCACAACCTCCAGAAAGAGAGGGCTGTGACGACAGCCGAC 369

QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Db 370 GCCACTGAGTCTTCCCCACCCGGGCTTCAACACAGCTCCCAACAAAGACACCCG 429
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrPheAlaAlaPro 160
Db 430 AATGACATCATGTGTGAAGATGAGCATGCCAGTCTCATCACCCTGGGCTGTGCAGCC 489
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyr 180
Db 490 CTCACCTCTCCACAGCTGTGTGCTGCTGGACACAGCTGCCTCATTTCCGGCTGGGG 549
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
Db 550 AGCAGCTCCAGCCCGCCAGTTACGCTGCTCACACCTTCGATGCGCCAAATCACACATC 609
QY 201 IleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
Db 610 ATTGAGCACCCAGAAAGTGTGAAGAGCCTACCCCGGCAACATCACACACACATGTGT 669
QY 221 AlaSerValGlnGlnLysGlyLysAspSerCysGlnGlyAspSerGlyLysProLeuVal 240
Db 670 GCCAGGCTGAGGAAGGGGCAAGACTCTCTGCAGAGGTGACTCCGGGGCCCTGTGGTC 729
QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
Db 730 TGTAAACCACTCTTCAAGGCATTATCTCTGGGCGCAGAGATCCGTGTGCAACCCGA 789
QY 261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnLysThrMetLys 280
Db 790 AAGCCTGGTGTCTACACGAAAGTCTCAATATGTGACTGTGATCCAGAGAGATGAAG 849
QY 281 AsnAsn 282
Db 850 AACAAAT 855

RESULT 9
US-10-140-807-505
; Sequence 505, Application US/10140807
; Publication No. US2003013435A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C174
; CURRENT APPLICATION NUMBER: US/10/140,807
; PRIOR APPLICATION DATE: 2002-05-07
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-807-505

Alignment Scores:
Pred. No.: 5,28e-162 Length: 1204

Score: 1523.00 Matches: 282
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-09-856-320a-2 (1-282) x US-10-140-807-505 (1-1204)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
 DB 10 ATGAGAGAGTTGAGGTGGCTGGGGAGTGAAGTATCGGGGAGAGGCTCACACACACC 69
 QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetAlaGlyLeuGlnLeuLeu 40
 DB 70 AAGGAACCTGGGGCCGCTCTCCCTCCAGGCGCATGAGATTCTCAGTTAATCTCTG 129
 QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGluThrArgIleIleLysGlyPheGluLys 60
 DB 130 CTTCGCTGGGACACAGGCTTGTAGGGGAGAGACACGAGATCATCAAGGGGTTCGAGTGC 189
 QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLysThrArgLeuLysGly 80
 DB 190 AAGCTCAGCTCCAGCCCTGGCAGGACACCTGTTCCGAAAGACGGGCTACTGTGTGG 249
 QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
 DB 250 GCGACGCTCATCGCCGCCAGATGGCTCTGACAGACGCCCTCGTCAAGCCCGGCTAC 309
 QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCysGluGlnThrArgThr 120
 DB 310 ATAGTTCACTGGGGGACACACACCTCCGAAAGGAGGGCTGTGACAGACCCGGACA 369
 QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
 DB 370 GCCACTGAGTCTCTCCCGCCACCCGGGCTTCAACAACACCTCCCAACAAAGACACCGC 429
 QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
 DB 430 AATACATCATGCTGGGTGAGATGAGATGCCAGTCTTCATCACCCTGGCTGTGGACCC 489
 QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrGly 180
 DB 490 CTCACCCCTCTCTCACCGTGTGTACATCTGTGGACACACCTCTCTATTTCCGGCTGGGC 549
 QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
 DB 550 AGCAGCTCCAGCCGCCAGTACGCTGCTCACACCTTGCGATGGGCCAACATCATC 609
 QY 201 IleGluHisGlnLysCysGluAsnAlaIleThrProGlyAsnIleThrAspThrMetValCys 220
 DB 610 ATTGAGCACCGAAGGTGTGAGAACGCTTACCCCGGCAACATCACAGACCATGTGTGT 669
 QY 221 AlaSerValGlnGluGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
 DB 670 GCCAGCGTGCAGGAAGGGGGGCAAGGACTCTCCGCAAGGTGATCCGGGGGCGCTGTGTC 729
 QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
 DB 730 TGTAAACAGTCTCTTCAAGGCAATATCTCTGGGGGCGAGATCCGTTGCGATACCCGA 789
 QY 261 LysProGlyValIleThrTrpLysValCysLysThrValAspTrpIleGlnGlnThrMetLys 280
 DB 790 AAGGCTGGTGTCTACAGAAAGTCTGCAAAATATGTGACTGTGATCCAGAGACATGAG 849
 QY 281 AsnAsn 282
 DB 850 AACAAAT 855

RESULT 10
 US-10-140-922-505
 ; Sequence 505, Application US/10140922
 ; Publication No. US20030138889A1
 ; GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
 APPLICANT: Beresini, Maureen
 APPLICANT: DeForge, Laura
 APPLICANT: Desnoyers, Luc
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowsky, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Sherwood, Steven
 APPLICANT: Smith, Victoria
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zhenli
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3330R1C179
 CURRENT APPLICATION NUMBER: US/10/140,922
 PRIOR APPLICATION removed - See Palm or File Wrapper
 NUMBER OF SEQ ID NOS: 530
 SEQ ID NO 505
 LENGTH: 1204
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-10-140-922-505

Alignment Scores:
 Pred. No.: 5,286-162 Length: 1204
 Score: 1523.00 Matches: 282
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-09-856-320a-2 (1-282) x US-10-140-922-505 (1-1204)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
 DB 10 ATGAGAGAGTTGAGGTGGCTGGGGAGTGAAGTATCGGGGAGAGGCTCACACACACC 69
 QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetAlaGlyLeuGlnLeuLeu 40
 DB 70 AAGGAACCTGGGGCCGCTCTCCCTCCAGGCGCATGAGATTCTCAGTTAATCTCTG 129
 QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGluThrArgIleIleLysGlyPheGluLys 60
 DB 130 CTTCGCTGGGACACAGGCTTGTAGGGGAGAGACACGAGATCATCAAGGGGTTCGAGTGC 189
 QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLysThrArgLeuLysGly 80
 DB 190 AAGCTCAGCTCCAGCCCTGGCAGGACACCTGTTCCGAAAGACGGGCTACTGTGTGG 249
 QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
 DB 250 GCGACGCTCATCGCCGCCAGATGGCTCTGACAGACGCCCTGCTCAAGCCCGGCTAC 309
 QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCysGluGlnThrArgThr 120
 DB 310 ATAGTTCACTGGGGGACACACACCTCCGAAAGGAGGGCTGTGACAGACCCGGACA 369
 QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
 DB 370 GCCACTGAGTCTCTCCCGCCACCCGGGCTTCAACAACACCTCCCAACAAAGACACCGC 429
 QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
 DB 430 AATGACATCATGCTGGGTGAGATGAGATGCCAGTCTTCATCACCCTGGGCTGTGGACCC 489
 QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrGly 180

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DB      490 CTCACCTCTCCACAGCTGTGTACAGTGTGGACACGAGCTCATTTCCGGCTGGGGC
QY      181 SerThrsSerProGlnLeuArgLeuProHisThrlLeuArgCysAlaAsnIleThrIle
DB      550 AGACAGCTCCAGGCCCCAGTTACGGCTGCTCACAACCTTGGGATGCCCAATCACCATC
QY      201 IleGlnHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrAspThrMetValCys
DB      610 ATTGAGACACCAAGAGTGTGAGAACGGCTACCCGGCAACATCAAGACACCATGTTGTGT
QY      221 AlSerValGlnGlnLysGlyLysAspSerCysGlnGlnLysPserGlyGlyProLeuVal
DB      670 GCCAGGCTGACGAGAGGGGGCAAGAGACTCTGCCAGGGTGACTCCGGGGCCCTGTGTC
QY      241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg
DB      730 TGTAAACCAAGTCTTCAAGGCAATTATCTCTGGGGCCAGGATCCGTGTGGATCACCAG
QY      261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnIleThrMetLys
DB      790 AAGCTGTGTCTTACACGAAAGTGTCAATATGTGACTGATCCAGAGACAGATGAAG
QY      281 AsnAsp 282
DB      850 AACAAAT 855

RESULT 11
US-10-140-924-505
; Sequence 505, Application US/10140924
; Publication No. US20030134355A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C177
; CURRENT APPLICATION NUMBER: US/10/140,924
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Saplen
US-10-140-924-505

Alignment Scores:
Pred. No.: 5,28e-162      Length: 1204
Score: 1523.00      Matches: 282
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 12      Gaps: 0

US-09-856-320a-2 (1-282) x US-10-140-924-505 (1-1204)
QY      1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20

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DB      10 ATCAGAGGATGTGAGTGGCTGCGGAGCTGCAAGTCAATCGGGCAGAGTCTCACAGCAGCC
QY      21 LysGlnProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnIleLeu
DB      70 AAGGAACTGTGGGCGGCTCTCTCCCTCAGGCAATGAGATGTGTGAGTTAAATCTG
QY      41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgIleIleLysGlyPheGlnCys
DB      130 CTTCCTGTGGCAACAGGGGCTTGTAGGGGGAGAACACAGATCATCAAGGGTTCCAGTGC
QY      61 LysProHisSerLysProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLeuCysGly
DB      190 AAGCTTCACTCCAGCCCTGGCAGGAGCCCTGTGAGAAAGACGGGCTACTCTGTGGG
QY      81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr
DB      250 GCCAGCTCATGCCCCCGAGATGGCTCTGTACAGCAGCCACTGCTCAAGCCCGCTAC
QY      101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyCysGlnIleThrArgThr
DB      310 ATAGTTACCTGGGCGAGCACAACCTCCAGAAAGAGAGGGGCTGTGAGCAGACCCGAGCA
QY      121 AlaThrGlnSerPheProHisProGlyPheAsnSerLeuProAsnLysAspHisArg
DB      370 GCCACTGAGTCTTCCGCCACCCCGCTTCACACAGACCTCCCAACAAAGACACCCG
QY      141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro
DB      430 AATGACATCATGCTGTGGTGAAGATGCGATCCGAGTCTCCATCACTCGGGCTGTGCCACCC
QY      161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly
DB      490 CTCACCTCTCTCTCACAGCTGTGTCACTGTGGCAGCAGCTGCCTATTCGGCTGGGGC
QY      181 SerThrsSerProGlnLeuArgLeuProHisThrlLeuArgCysAlaAsnIleThrIle
DB      550 AGCAGCTCCAGGCCCCAGTTACGCTGTGCTCACACCTTGGAGTGCACCAATCACCATC
QY      201 IleGlnHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrAspThrMetValCys
DB      610 ATTGAGACACCAAGAGTGTGAGAACGGCTTACCCGGCAACATCACAACACATGAGTGTGT
QY      221 AlSerValGlnGlnLysGlyLysAspSerCysGlnGlnLysPserGlyGlyProLeuVal
DB      670 GCCAGGCTGACGAGAGGGGGCAAGAGACTCTGCCAGGGTGACTCCGGGGCCCTGTGTC
QY      241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg
DB      730 TGTAAACCAAGTCTTCAAGGCAATTATCTCTGGGGCCAGGATCCGTGTGGATCACCAG
QY      261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnIleThrMetLys
DB      790 AAGCTGTGTCTTACACGAAAGTGTCAATATGTGACTGATCCAGAGACAGATGAAG
QY      281 AsnAsp 282
DB      850 AACAAAT 855

RESULT 12
US-10-140-926-505
; Sequence 505, Application US/10140926
; Publication No. US20030134356A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

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Db      130 CTTCGCTCTGGCAACAGGGCTGTAGGGGGAGAGACCAAGATCATCAAGGGGTTGAGTGC 189
QY      61 LysProHisSerSerGlnProTrpGlnAlaAlaLeuPheGluIuysThrArgLeuLeuGly 80
      190 AACGCTCACTCCAGAGCCCTGGAGGAGAGCCCTGTGTGAGAAAGAGGGGCTACTGTGGG 249
QY      81 AlaThrLeuLeuLeuAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
      250 GCGAGCGTCATCCGCCCAATGAGTCTCTGACAGACACCCACGCTCCCAAGGCCCGGCTAC 309
Db      101 TLeValHisLeuGluGlnHisAsnLeuGlnLysGluGluGlnLysGlnGlnThrArgThr 120
QY      310 ATAGTTCACCTCGGGGGGAGCAACAACCTCCAGAAAGAGAGGGCTGTGAGCAGACCCGAGCA 369
QY      121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
      370 GCCACTGAGTCTTCCCGCCACCGGGCTTCACACAGAGCTCCCGCAACAAAGACACCGC 429
QY      141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
      430 AATGACATCATGCTGTGGAAAGATGGCATCGCAGTCTCCATCACTGGGCTGTGGCAGCC 489
Db      161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuLysSerGlyTrpGly 180
      490 CTCACCCCTCTCTCAGCGCTGTCTCACTGCTGGCAACAGCTGCTCATTTCCGGCTGGGC 549
QY      181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
      550 AGCAGCGTCAGCCCGCGGTAGCGCTGCTCACACCTGGCATGGCGCAACATCACACATC 609
Db      201 TLeGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
      610 ATTGAGACACCAAGAGTGTGAAAGCGCTACCGCGCAACATCACAGCACCATGCTGTGT 669
QY      221 AlaSerValGlnGlnLysGlnLysAspSerCysGlnLysAspSerGlyGlyProLeuVal 240
      670 GCGAGCGTGCAGAGAGGGGGGCAAGGACTCTGCCAGGGTACTCCGGGGCCCTCTGTGTC 729
Db      241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
      730 TGTAAACCAAGTCTTCAAGGCAATTAATCTCTGGGGGCGAGATCCGTGTGCAATCACCCGA 789
QY      261 LysProGlyValLysThrLysValLysLysTyrValAspTrpIleGlnGlnIuThrMetLys 280
      790 AACCGCTGGTGTCTACACGAAAGTCTGCAAAATATGTGACTGATCCAGGAGACATGAAG 849
Db      281 AsnAsn 282
      850 AACCAAT 855

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RESULT 14
US-10-141-702-505
; Sequence 505, Application US/10141702
; Publication No. US20030134358A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Mei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P330R1C208
; CURRENT APPLICATION NUMBER: US/10/141,702
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-141-702-505

Alignment Scores:
Pred. No.: 5.28e-162 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-856-320a-2 (1-282) x US-10-141-702-505 (1-1204)
QY      1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
      10 ATGCAAGAGGTGAGTGGCTGCGGACTGGAAATCATCGGGCAGAGTCTCACAGCAGCC 69
QY      21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40
      70 AAGGAACCTGGGGCCGCGCTCTCCCGCTCCAGCCATGAGATTCTGCAAGTTAACTCTG 129
Db      41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGluThrArgIleIleLysGlyPheGluCys 60
      130 CTTCGCTGTGCAACAGGGCTGTGAGGGGAGAACCAAGATCATCAAGGGGTTGCGAGTGC 189
QY      61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluIuysThrArgLeuLeuGly 80
      190 AACGCTCACTCCAGAGCCCTGGAGGAGAGCCCTTTTGAGAAAGCGGGCTACTGTGGG 249
Db      81 AlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
      250 GCGAGCGTCATCCGCCCAATGAGTCTCTGACAGACACCCACGCTCCCAAGGCCCGGCTAC 309
QY      101 TLeValHisLeuGlnGlnHisAsnLeuGlnLysGluGlnLysGlnGlnThrArgThr 120
      310 ATAGTTCACCTCGGGGGGAGCAACAACCTCCAGAAAGAGAGGGCTGTGAGCAGACCCGAGCA 369
Db      121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
      370 GCCACTGAGTCTTCCCGCCACCGGGCTTCACACAGAGCTCCCGCAACAAAGACACCGC 429
QY      141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
      430 AATGACATCATGCTGTGGAAAGATGGCATCGCAGTCTCCATCACTGGGCTGTGCGACCC 489
Db      161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuLysSerGlyTrpGly 180
      490 CTCACCCCTCTCTCAGCGCTGTCTCACTGCTGGCAACAGCTGCTCATTTCCGGCTGGGC 549
QY      181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
      550 AGCAGCGTCAGCCCGCGGTAGCGCTGCTCACACCTTGGCATGGCGCAACATCACACATC 609
Db      201 TLeGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
      610 ATTGAGACACCAAGAGTGTGAAAGCGCTACCGCGCAACATCACAGCATGAGTGTGT 669
QY      221 AlaSerValGlnGlnLysGlnLysAspSerCysGlnLysAspSerGlyGlyProLeuVal 240
      670 GCGAGCGTGCAGAGAGGGGGGCAAGGACTCTGCGCAGAGTACTCCGGGGCCCTCTGTGTC 729
Db      241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
      730 TGTAAACCAAGTCTTCAAGGCAATTAATCTCTGGGGGCGAGATCCGTGTGCAATCACCCGA 789

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QY 261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnGluThrMetLys 280
Db 790 AAGCTGTGCTCTACAGAAAGTCTGCATAATATGTGACTGTGATCCAGAGACGATGAA 849
QY 281 AsnAsn 282
Db 850 AACAAAT 855

RESULT 15
US-10-141-704-505
; Sequence 505, Application US/10141704
; Publication No. US20030134359A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Matanabe, Collin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P33081C209
; CURRENT APPLICATION NUMBER: US/10/141,704
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-141-704-505

Alignment Scores:
Pred. No.: 5,28e-162 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-856-320a-2 (1-282) x US-10-141-704-505 (1-1204)

QY 1 MetGlnArgLeuArgTyrPleuArgAspTyrLysSerSerGlyArgGlyLeuThrAlaAla 20
Db 10 ATGCAAGAGGTGAGTGGCTGCGGAGTCAATCGGCGACAGAGGCTTCACAGACGCC 69
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnIleLeu 40
Db 70 AAGCAACCTGGGGCCCTCTCCCTCCAGGCCATGAGGATTCGCACTTAATCTG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyIleuThrArgIleIleLysGlyPheGluCys 60
Db 130 CTTCCTCTGGCAACAGGGCTGTGAGGGGAGAGACAGCATCATCAAGGGGTTGAGAGTGC 189
QY 61 LysProHisSerGlnProTTPGlnAlaAlaLeuPheGluLysThrArgLeuLeuCysGly 80
Db 190 AAGCCTCACTCCAGCCCTGGCAGGACCCCTGTCAGAAAGACGCGCTACTCTGTGGG 249
QY 81 AlaThrLeuIleAlaProArgTyrPleuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
Db 250 GCGACGCTCATGCCCCACATGGCTCTCTGACAGACGCCCATGCTCAAGCCCCGCTAC 309

QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlyCysGlnGlnThrArgThr 120
Db 310 ATAGTTCACCTGGGGCAGACACACCTCCAGAAAGAGGAGGGCTGTGACAGACCCGAGCA 369
QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
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QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrPgly 180
Db 490 CTCACCTCTCTCTACGCTGTGTACTCTGTGACACACCTGCTCATTTCCGGGCTGGGG 549
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QY 201 IleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
Db 610 ATTGAGCACCAAGAGTGTGAGAACGCTTACCCCGGCACATCACAGACCATGGTGTGT 669
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Db 670 GCCAGCGTGCAGGAAGGGGGCAAGGACTCTGCCAGGGGTGACTCGGGGGCCCTGTGTC 729
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QY 281 AsnAsn 282
Db 850 AACAAAT 855

Search completed: October 15, 2003, 23:04:17
Job time : 318.352 secs

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GenCore version 5.1.6
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Run on: October 15, 2003, 20:58:42 ; Search time 78.364 Seconds

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Title: US-09-856-320A-2

Perfect score: 1523

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Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
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Listing first 45 summaries

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Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1523	100.0	1314	3	US-09-025-059-2
2	1519	99.7	1292	4	US-09-205-258-189
3	1410	92.6	1192	3	US-08-944-483-8
4	1398	91.8	1166	3	US-08-944-483-7
5	1284	84.3	1146	4	US-09-205-258-247
6	1233	81.0	833	2	US-08-790-137-2
7	1227	80.6	1052	4	US-09-386-642-10
8	916.5	60.2	618	4	US-09-280-116-3
9	739	48.5	472	4	US-09-280-116-136
10	690	45.3	944	3	US-09-070-526-1
11	682	44.8	994	3	US-09-008-271A-19
12	679	44.6	1049	4	US-09-386-642-9

13	650.5	42.7	1570	4	US-09-996-243-308	Sequence 308, App
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15	637.5	41.9	1476	3 <td>US-09-210-084-2</td> <td>Sequence 2, Appl1</td>	US-09-210-084-2	Sequence 2, Appl1
16	637.5	41.9	1476	4 <td>US-09-764-762-2</td> <td>Sequence 2, Appl1</td>	US-09-764-762-2	Sequence 2, Appl1
17	634.5	41.7	1364	4 <td>US-09-280-116-20</td> <td>Sequence 20, Appl</td>	US-09-280-116-20	Sequence 20, Appl
18	596.5	39.2	822	3 <td>US-09-100-264-8</td> <td>Sequence 8, Appl1</td>	US-09-100-264-8	Sequence 8, Appl1
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23	596.5	39.2	1341	4 <td>US-08-983-075D-6</td> <td>Sequence 6, Appl1</td>	US-08-983-075D-6	Sequence 6, Appl1
24	596.5	39.2	1358	4 <td>US-08-983-075D-8</td> <td>Sequence 8, Appl1</td>	US-08-983-075D-8	Sequence 8, Appl1
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26	593.5	39.0	832	3 <td>US-08-767-820A-20</td> <td>Sequence 20, Appl</td>	US-08-767-820A-20	Sequence 20, Appl
27	593.5	39.0	832	3 <td>US-08-767-820A-20</td> <td>Sequence 20, Appl</td>	US-08-767-820A-20	Sequence 20, Appl
28	593.5	39.0	832	3 <td>US-08-622-046B-4</td> <td>Sequence 4, Appl1</td>	US-08-622-046B-4	Sequence 4, Appl1
29	592.5	38.9	832	5 <td>PCT-US95-06157-5</td> <td>Sequence 5, Appl1</td>	PCT-US95-06157-5	Sequence 5, Appl1
30	587	38.5	897	2 <td>US-08-956-267A-1</td> <td>Sequence 1, Appl1</td>	US-08-956-267A-1	Sequence 1, Appl1
31	585.5	38.4	766	3 <td>US-08-768-859A-9</td> <td>Sequence 9, Appl1</td>	US-08-768-859A-9	Sequence 9, Appl1
32	585.5	38.4	766	3 <td>US-08-768-859A-9</td> <td>Sequence 9, Appl1</td>	US-08-768-859A-9	Sequence 9, Appl1
33	585.5	38.4	766	3 <td>US-08-622-046B-17</td> <td>Sequence 17, Appl</td>	US-08-622-046B-17	Sequence 17, Appl
34	585.5	38.4	766	3 <td>US-09-100-264-6</td> <td>Sequence 6, Appl1</td>	US-09-100-264-6	Sequence 6, Appl1
35	585.5	38.4	766	4 <td>US-08-843-076D-6</td> <td>Sequence 6, Appl1</td>	US-08-843-076D-6	Sequence 6, Appl1
36	583	38.3	1504	4 <td>US-09-280-116-1</td> <td>Sequence 1, Appl1</td>	US-09-280-116-1	Sequence 1, Appl1
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41	580	38.1	1089	5 <td>PCT-US96-04294-1</td> <td>Sequence 1, Appl1</td>	PCT-US96-04294-1	Sequence 1, Appl1
42	580	38.1	1089	5 <td>PCT-US96-04294-3</td> <td>Sequence 3, Appl1</td>	PCT-US96-04294-3	Sequence 3, Appl1
43	579.5	38.0	760	3 <td>US-08-768-859A-7</td> <td>Sequence 7, Appl1</td>	US-08-768-859A-7	Sequence 7, Appl1
44	579.5	38.0	760	3 <td>US-08-767-820A-7</td> <td>Sequence 7, Appl1</td>	US-08-767-820A-7	Sequence 7, Appl1
45	577.5	37.9	711	3 <td>US-08-622-046B-13</td> <td>Sequence 13, Appl</td>	US-08-622-046B-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-025-059-2
Sequence 2, Application US/09025059
Patent No. 6075136

GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,059
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0481 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-0555
TELEFAX: 650-845-4166

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TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1314 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LONGTUT10
; CLONE: 2723646
; US-09-025-059-2

Alignment Scores:
Pred. No.: 5.95e-144 Length: 1314
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
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Db 188 AAGGAACCTGGGGCCGCTCTCCCTCCAGGCGCATGAGATCTGCAAGTAAATCTG 247
QY 41 LeuAlaIleAlaThrGlyLeuValGlyGlyLeuThrArgIleIleLysGlyPheGlyLys 60
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Db 308 AAGCCTCAGCTCCAGGCGCTGGCGAGGAGCCCTGTTGAGAGAGCGGGCTACTGTGGG 367
QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTrp 100
Db 368 GCGACCTCATCCGCCAGATGGCTCCGACAGCAGCCACCTCAAGCCCGCTAC 427
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Db 428 ATAGTTCACCTGGGGGAGCACAACCTCCAGAAAGAGAGGGCTGTAGCAGACCCGGACA 487
QY 121 AlaThrGlySerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
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QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysIleuIleSerGlyTrpGly 180
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RESULT 2
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; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-12-18
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EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 189
LENGTH: 1292
TYPE: DNA
ORGANISM: Homo sapiens
US-09-205-258-189

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Score: 1519.00 Matches: 281
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QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLeuCysGly 80
Db 291 AAGCTCACTCCAGCCCTGGAGAGCCCTGTTGAGAAAGACGGGCTACTGTGGG 350
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Db 351 GCGAGGCTCATCGCCCAATGGCTCTGTGACAGACCCCACTCTCAAGCCCGCTAC 410
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlnGlyCysGlnGlnThrArgThr 120
Db 411 ATAGTTACCTGGGGGCGACACACCTCCAGAGGAGAGGGCTGTGAGACGACCGGACA 470
QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Db 471 GCCACGTAGTCCTTCCCCCAAGCCGGGCTTCAACAACAGCCCTCCCAACAAGACACCGC 530
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160

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QY 281 AsnAsn 282
Db 951 AACAAAT 956

RESULT 3
US-08-944-483-8
Sequence 8, Application US/08944483
Patent No. 6232456

GENERAL INFORMATION:
APPLICANT: COHEN, MAURICE
APPLICANT: COLPIPITS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183-US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623
 TELEEX:
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1192 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-944-483-8

Alignment Scores:

Pred. No.:	1,22e-132	Length:	1192
Score:	1410.00	Matches:	261
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	92.58%	Indels:	0
DB:	3	Gaps:	0

US-09-856-320a-2 (1-282) x US-08-944-483-8 (1-1192)

22 GIUProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuLeu 41
 |||||
 74 GAACCTGGGGCCCGCTCTCCCTCCAGGCCATGAGATTTCGAGTTAATCTGCTT 133
 |||||
 42 AAlaLeuAlaThrGlyLeuValGlyGlyIuThrArgIleIleLysGlyPheGlyCysLys 61
 |||||
 134 GCTCTGCAACAGAGCTGTAGGGGAGAGACCAGATCATCAAGGGGTTCGAGTCAAG 193
 |||||
 62 ProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLeuGlyAla 81
 |||||
 194 CCTCACTCCCAAGCTGGGAGGAGGAGGCTGTTCGAGAAGAGGGGTACTGTGGGGCG 253
 |||||
 82 ThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTrp 101
 |||||
 254 AGGCTATGCGCCCGGATGGCTCCGACAGCGCCGCTCAAGCCCGCTCAAG 313
 |||||
 102 ValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyCysGlnLysThrArgThrAla 121
 |||||
 314 GTTCACCTGGGGAGAGCAACCTCCAGAAAGAGAGGGCTGTAGAGAGACCCGAGACGC 373
 |||||
 122 ThrGlnSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 141
 |||||
 374 ACTGATCTTCCCTCCCAAGCCGCTTCACACAGCCCTCCCAACAAAGCACCGCAAT 433
 |||||
 142 AspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgProLeu 161
 |||||
 434 GACATCATGCTGGTGAAGATGGCATGCGCATCTCATACCTGGGCTGTGGACCCCTC 493
 |||||
 162 ThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGlySer 181
 |||||
 494 ACCCTCTCTCAGCGTGTCTACTGTGCACACAGTGCCTCATTTCCGGCTGGGGCAGC 553
 |||||
 182 ThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 201
 |||||
 554 AGCTCCAGGCCCGCATGTTACGCTGCTCACACCTTCGATGGCGCCCAACATCACCATCAT 613
 |||||
 202 GIUHisGlnLysCysGlnAsnAlaTrpProGlyAsnIleThrAspThrMetValCysAla 221
 |||||
 614 GAGCACCAAGAGTGAAGAACGCTACCCCGGCAACATACAGACACCATGGTGTGGC 673
 |||||
 222 SerValGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyLysProLeuValCys 241
 |||||
 674 AGCGTGCAGGAAGGGGCAAGGACTCTCCAGAGGTGACTCCGGGGGCTGTGCTGTG 733
 |||||
 242 AsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArgLys 261
 |||||
 734 AACCAATCTCTTCAAGGCAATATCTCTCTGGGGCAGAGATCCGTGTCGATCAACCCCAAG 793
 |||||
 262 ProGlyValIleTrpThrLysValCysLysTrpValAspTrpIleGlnGlnThrMetLysAsn 281
 |||||
 794 CCTGTGTCTACACGAAGTCTGCAAAATATGTGACTGATCCAGAGACGATGAAGAAC 853
 |||||

OY 282 Asn 282
 |||
 DB 854 AAT 856

RESULT 4

US-08-944-483-7

/ Sequence 7, Application US/08944483
 / Patent No. 6232456
 / GENERAL INFORMATION:
 / APPLICANT: COHEN, MAURICE
 / APPLICANT: COLETTIS, TRACEY L.
 / APPLICANT: FRIEDMAN, PAULA N.
 / APPLICANT: GRANADOS, EDWARD N.
 / APPLICANT: KLAAS, MICHAEL R.
 / APPLICANT: RUSSELL, JOHN C.
 / APPLICANT: STEWART, KENT D.
 / APPLICANT: STROUPE, STEVEN D.
 / TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
 / TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
 / TITLE OF INVENTION: OF THE PROSTATE
 / NUMBER OF SEQUENCES: 76
 / CORRESPONDENCE ADDRESSES:
 / ADDRESS: Abbott Laboratories
 / STREET: 100 Abbott Park Road
 / CITY: Abbott Park
 / STATE: IL
 / COUNTRY: USA
 / ZIP: 60064-3500
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette
 / COMPUTER: IBM compatible
 / OPERATING SYSTEM: DOS
 / SOFTWARE: FASTSEQ for Windows Version 2.0
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/944,483
 / FILING DATE:
 / CLASSIFICATION: 424
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER:
 / FILING DATE:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Becker, Cheryl L.
 / REGISTRATION NUMBER: 35,441
 / REFERENCE/DOCKET NUMBER: 6183.US.01
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 847/935-1729
 / TELEFAX: 847/938-2623
 / TELEX:
 / INFORMATION FOR SEQ ID NO: 7:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 1166 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / US-08-944-483-7

Alignment Scores:

Pred. No.:	1.9e-131	Length:	1166
Score:	1398.00	Matches:	259
Percent Similarity:	99.23%	Conservative:	0
Best Local Similarity:	99.23%	Mismatches:	2
Query Match:	91.79%	Indels:	0
DB:	3	Gaps:	0

US-09-856-320a-2 (1-282) x US-08-944-483-7 (1-1166)

22 GIUProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuLeu 41
 |||||
 70 GAACCTGGGGCCCGCTCTCCCTCCAGGCCATGAGATTTCGAGTTAATCTGCTT 129
 |||||
 42 AAlaLeuAlaThrGlyLeuValGlyGlyIuThrArgIleIleLysGlyPheGlyCysLys 61
 |||||
 130 GCTCTGCAACAGGCTGTAGGGGAGAGACCAGATCATCAAGGGGTTCGAGTCAAG 189
 |||||

[illegible]

Db	668	CCG6GGGGCCCTCTGTCCTTAACCAAGTCTCTCAAGGATATATCTCCGGGGCCAGATC	725
Oy	255	roCysalalIethrArGlySProGlyValTyrThLysValCysLysTyrValAspTri	275
Db	728	CGTGTCGATCACCCCAAGCCCTGGTCTACACGAAGTCTGCAAAATATGTGACTGGA	787
Oy	275	IeGIngluThrMetLysAsnAsn	282
Db	788	TCCAGGAGCATGAAGAACAAAT	810
RESULT 6			
US-08-790-137-2			
Sequence 2, Application US/08790137			
Patent No. 5840871			
GENERAL INFORMATION:			
APPLICANT: Hillman, Jennifer L.			
APPLICANT: Goli, Surya K.			
TITLE OF INVENTION: A NOVEL PROSTATE-ASSOCIATED			
TITLE OF INVENTION: KALLIKREIN			
NUMBER OF SEQUENCES: 4			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Incyte Pharmaceuticals, Inc.			
STREET: 3174 Porter Drive			
CITY: Palo Alto			
STATE: CA			
COUNTRY: USA			
ZIP: 94304			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Diskette			
COMPUTER: IBM compatible			
OPERATING SYSTEM: DOS			
SOFTWARE: FastSeq for Windows Version 2.0			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/790,137			
FILING DATE: Filed Herewith			
CLASSIFICATION: 424			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER:			
FILING DATE:			
ATTORNEY/AGENT INFORMATION:			
NAME: Billings, Lucy J.			
REGISTRATION NUMBER: 36,749			
REFERENCE/DOCKET NUMBER: PF-0195 US			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: 415-855-0555			
TELEFAX: 415-845-4166			
INFORMATION FOR SEQ ID NO: 2:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 833 base pairs			
TYPE: nucleic acid			
STRANDEDNESS: single			
TOPOLOGY: linear			
US-08-790-137-2			
Alignment Scores:			
Pred. No.: 4,67e-115			
Score: 1233.00			
Percent Similarity: 91.15%			
Best Local Similarity: 87.31%			
Query Match: 80.96%			
DB: 2			
Gaps: 1			
US-09-856-320A-2 (1-282) x US-08-790-137-2 (1-833)			
Oy	29	ProLeuGlAlaMetArGlieLeuGlInleuGlLeuAlaLeuAlaThrGlyLeuVal	48
Db	6	CCCGTGGACACCTCTCTACCACTGTGGTTCCTGGTCTCTGCTCGCCCTTCCTCGGG	65
Oy	49	GlIlyI-----GluthrArGlielelelysglyIyphelGlyCysLysPro	62
Db	66	GGGACTGTGTGCGGGCCCGCCGATTCAGTCCGGGATGTGGAGGCTGGAGTGTGACAG	125
Oy	63	HisSerGlnProTrpGlnAlaIaIeubheGluTyrThrArGleuLeuCysGlyAlaThr	82


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|||||
Db 126 CATCCAGCCCTGGACGGGCTGTACAGAAAGCGGGCTACTGTGGGGCAG 185
|||
Qy 83 Leu1leAlaProa1gTTPLeu1leuThra1Ala1h1Scy1leu1ysProa1gTyr1leVal 102
|||
Db 186 MTCATNGCCCAATGGTTCTGTGACAGCAGCCACTGCTTAAAGCCCCGGTACATAGTT 245
|||
Qy 103 His1eu1g1y1n1h1sa1n1leu1n1g1u1n1g1y1c1y1s1g1u1n1h1a1r1g1Thra1Ala1h 122
|||||
Db 246 CACCTGGGGCAGCAACCTCCAGAAAGAGAGGGCTGTGAGCAGACCGGAGACCCCT 305
|||
Qy 123 Glu1SerPhePro1h1s1Pro1g1y1Phe1a1n1a1n1Ser1leu1Pro1a1n1Lys1Asp1h1A1r1Asn1a1p 142
|||
Db 306 GAGTCCTTCCCAACCCCGGCTTCAACACAGCCTCCCAACAAAGACACCGCAATAGC 365
|||
Qy 143 Ile1Met1eu1Val1ys1Met1Ala1Ser1Pro1Val1Ser1Ile1Thr1Pala1Val1a1r1Pro1leu1Thr 162
|||
Db 366 ATCATGCTGTGAGAGATGGCATCCGACATCCATCACTGGGCTGTGCGACCCCTCAC 425
|||
Qy 163 Leu1Ser1e1Ar1g1Cy1Val1Thra1Ala1g1Y1Thr1Ser1Cy1leu1Ile1Ser1g1Y1Tyr1g1Ser1Thr 182
|||
Db 426 CTCCTCCACGCTGTGTACTGTGACGTGGCAGCAGCTGCTCATTTCCGGCTGGGGCAGCAGC 485
|||
Qy 183 Ser1Ser1Pro1Glu1e1u1Ar1g1leu1Pro1h1s1Thr1e1u1Ar1g1Cy1Ala1a1n1Ile1Thr1Ile1g1u 202
|||
Db 486 TCCAGCCCAAGCTTACAGCTCTGCTCTACACCTTGCGATGGCCACATCATCATATAG 545
|||
Qy 203 His1Glu1n1ys1Cy1Glu1a1n1a1Lys1Pro1Glu1a1n1Ile1Thr1a1s1P1h1r1Met1Val1Cy1Ala1Ser 222
|||
Db 546 CACCAAGAAAGTGTGAAGAGCGCTACCCGGCAACATCACAGACACATGCTGTGCGCAGC 605
|||
Qy 223 Val1Glu1n1Glu1g1Y1Lys1Asp1Ser1Cy1Glu1n1Lys1Ser1g1Y1G1Pro1leu1Val1Cy1Asn 242
|||
Db 606 GTGAGAGAAAGGGGCAAGAGACTCTGCGAGGGTACTCCGGGGCCCTCTGTGTGTAAAC 665
|||
Qy 243 Glu1Ser1eu1Glu1n1g1Y1Ile1Ser1Tyr1G1n1a1s1P1ro1Cy1Ala1Ile1Thr1Ar1g1Lys1Pro 262
|||
Db 666 CAGCTCTTCAAGGCATTAATCTCTGGGGCCAGCATCCGTTGCGATCACCCGAAAGCTT 725
|||
Qy 263 Gly1Val1Y1r1Thra1Lys1Val1Cy1Lys1Tyr1Val1a1s1P1r1Ile1Glu1n1h1r1Met1Lys1Asn 282
|||
Db 726 GGTTCTACAGAAAGTGTGCAATATGTGACTGTGATCCAGAGAGATGAAGAACAT 785
|||
RESULT 7
US-09-386-642-10
; Sequence 10, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Ol, Jensen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1052
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo saplen serine protease catalytic domain
US-09-386-642-10

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Alignment Scores:
Pred. No.: 2,666-114 Length: 1052
Score: 1227.00 Matches: 231
Percent Similarity: 87.59% Conservative: 9
Best Local Similarity: 84.31% Mismatches: 12
Query Match: 80.56% Indels: 22
DB: 4 Gaps: 3

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```

US-09-856-320a-2 (1-282) x US-09-386-642-10 (1-1052)
|||
Qy 31 Glu1a1Met1Ar1g1Ile1Leu1Glu1n1Leu1Ileu1-----Leu1Ala1Leu1Ala1Thr1Gly1Leu 47
|||
Db 34 CAGAAATCCCGCTCTCTCTGTGTGGTGGTGAATTAATCTTGTGTGCCAGGGTGTG 93
|||
Qy 48 Val1g1Y1----- 49
|||
Db 94 GTCTCCGACTCAAGAGAGACAGACAGCTGACAGCGCGCGCTCTGTGCCCCCTTTGAT 153
|||
Qy 50 Gly1u1Thra1r1g1Ile1Lys1Gly1r1Phe1Gly1Cy1---Lys1Pro1h1s1Ser1Glu1Pro1Tyr1Glu 68
|||
Db 154 GATGATGCAAGATGCTGTGGGGCTTACACAGCTGTGAAGAAAGCACTCCAGCCGCGGAG 213
|||
Qy 69 Ala1Ala1Leu1Phe1Glu1Lys1Thr1Arg1Leu1e1u1Cy1Glu1Ala1Thr1Leu1Ile1Ala1Pro1Arg1Trp 88
|||
Db 214 GCAGCCCTGTTCGAAAGACAGCGGCTACTCTGTGGGGCGAGCTCATGCCCCAGATGG 273
|||
Qy 89 Leu1e1u1Thra1Ala1Ala1h1s1Cy1Leu1Lys1Pro1Arg1Tyr1Ile1Val1His1Leu1Gly1n1His1Asn 108
|||
Db 274 CTCCTGACAGACAGCCCACTGCTCAAGCCCGCTACATAGTTCAACCTGGGGCAGACAC 333
|||
Qy 109 Leu1Glu1n1ys1Glu1n1Gly1Cy1Glu1n1h1a1r1g1Thra1Ala1Thr1Glu1Ser1Phe1Pro1h1s1Pro 128
|||
Db 334 CTCAGAAAGAGAGGGGCTGTGAGAGACCGGACAGCAGCTGAGTCTCCCAACCC 393
|||
Qy 129 Gly1Phe1a1n1a1n1Ser1leu1Pro1a1n1Lys1Asp1h1s1Ar1g1a1n1a1P1h1e1Met1Val1Lys1Met 148
|||
Db 394 GGCTTCAACAAACAGCTCTCCCAACAAAGACACCGCAATGACATATCTGTGTGAAGATG 453
|||
Qy 149 Ala1Ser1Pro1Val1Ser1Ile1Thr1Pala1Val1a1r1Pro1leu1Thr1Leu1Ser1Ser1Arg1Cy1Val 168
|||
Db 454 GCATCGCCAGCTCCATCATCACTGTGGCTGTGGACCCCTCACCCCTCTCTCAAGCTGTGTC 513
|||
Qy 169 Thr1Ala1Gly1Thra1Ser1Cy1leu1Ile1Ser1g1Y1Tyr1g1Ser1Thra1Ser1Pro1Glu1n1Arg 188
|||
Db 514 ACTCTGGCACCACTGTCTATTCTCGGCTGGGGCAGACAGCTCCAGCCCAAGTTAGC 573
|||
Qy 189 Leu1Pro1h1s1Thr1Leu1Ar1g1Cy1Ala1a1n1Ile1Thr1Ile1Glu1n1h1s1Glu1Lys1Cy1Glu1n 208
|||
Db 574 CTGCTCAACACCTTGCAGATGGCCCAACATCACTCATATTGAGACACAGAAATGTGAGAAC 633
|||
Qy 209 Ala1Tyr1Pro1Glu1a1n1Ile1Thr1a1s1P1h1r1Met1Val1Cy1Ala1Ser1Val1Glu1n1Gly1Lys 228
|||
Db 634 GCTTACCCCGGCAACATCACAGACACCATGTGTGTGCGACGTCAGAGAGGGGGCAG 693
|||
Qy 229 Asp1Ser1Cy1Glu1n1Gly1a1s1P1Ser1g1Y1G1Pro1leu1Val1Cy1a1n1Glu1n1Ser1Leu1Glu1n1Y1Le 248
|||
Db 694 GACTCTGCGCAGGGTGACTCCGGGGCCCTGTGCTGTAAACAGTCTCTTCAAGGCATT 753
|||
Qy 249 Ile1Ser1Tyr1G1n1a1s1P1ro1Cy1Ala1Ile1Thr1Arg1Lys1Pro1Glu1Val1Tyr1Thra1Lys1Val 268
|||
Db 754 ATCTCTCGGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGTGTCTACAGAAAGTC 813
|||
Qy 269 Cys1Lys1Tyr1Val1a1s1P1r1Ile1Glu1n1h1r1Met1Lys1Asn 282
|||
Db 814 TGCAAATATGTGAGCTGGATCCAGAGAGATGAAGAACAT 855
|||
RESULT 8
US-09-280-116-3
; Sequence 3, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 618

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: trypsin-like serine proteases
US-09-280-116-3

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Alignment Scores:
Pred. No.: 2,16e-83 Length: 618
Score: 916.50 Matches: 184
Percent Similarity: 90.78% Conservative: 3
Best Local Similarity: 89.32% Mismatches: 4
Query Match: 60.18% Indels: 16
DB: 4 Gaps: 2

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US-09-856-320a-2 (1-282) x US-09-280-116-3 (1-618)

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QY 76 ArgLeuLeuGlyGlyAlaThrLeuLeuAlaPro-ArgTyrPheLeuThrAlaAlaIscy 95
    |||||
DB 2 CGGCTACTGTGTGGGCGAC---TCATGCCCTCAATGCTCTTGCACAGCAGCCACTG 58
    |||||
QY 95 sLeuLysProArgTyrIleValHisLeuGlnHisAsnLeuGlnLysGlnLysGly 115
    |||||
DB 59 CCAAGAGCCCGGCTACATAGTTCACCTGGGCGAGCAGCAACCTCCAGAGAGAGGAGGCTG 118
    |||||
QY 115 sGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSerLeupr 135
    |||||
DB 119 TGGCAGAGCCCGGAGCCAGCCAGTGCCTCCCGCCAGCCCGGCTCAACAGCCCTCC 178
    |||||
QY 135 sAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal-SerIle 155
    |||||
DB 179 CACCAAGAGCCCGGAGCCAGCCAGTGCCTCCCGCCAGCCCGGCTCAACAGCCCTCC 238
    |||||
QY 155 hTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysAl 175
    |||||
DB 239 CCGGCGCTGTGGCAGCCCTCCAGCCCTCTCATGCTGTGCATGCTGTGCAGCCAGCTGCC 298
    |||||
QY 175 eutLeSerGlyTyrPglYserThrSerSerProGlnLeuArgLeuProHisThrLeuArgC 195
    |||||
DB 299 TCATTTCGGCTGGGCGAGCAGCTCCAGCCCGGAGTTCAGCCCTCCAGCCCTCCAGT 358
    |||||
QY 195 ysaAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsnIle 215
    |||||
DB 359 GCGCCAAAGCCAGCCAGCCAGTGCAGCCAGGAGTGCAGGAGTGCAGGAGTGCAGGAGT 418
    |||||
QY 215 hAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGlyAspS 235
    |||||
DB 419 CAGACACCAATGCTGTGTGCAGGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 471
    |||||
QY 235 eGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrp-GlyGlnAsp 254
    |||||
DB 472 -----GTCCTCTTC-AAAGGCATTATCTCCCTGGGCGCAGAGC 507
    |||||
QY 255 -ProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAspTr 274
    |||||
DB 508 TCGGTGTGGATACCCGGAAGGCTGTGTGTACAGAAAGTGTGCAAAATATGTGAGCTG 567
    |||||
QY 274 pIleGlnGlu 277
    |||||
DB 568 GATCCAGAA 577

```

RESULT 9
US-09-280-116-136

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; Sequence 136, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 136

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; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: trypsin-like serine proteases
US-09-280-116-136

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Alignment Scores:
Pred. No.: 1,06e-65 Length: 472
Score: 739.00 Matches: 138
Percent Similarity: 99.28% Conservative: 0
Best Local Similarity: 99.28% Mismatches: 1
Query Match: 48.32% Indels: 0
DB: 4 Gaps: 0

```

US-09-856-320a-2 (1-282) x US-09-280-116-136 (1-472)

```

QY 3 ArgLeuArgTyrPheLeuArgPrrPrrLysSerSerGlyArgGlyLeuThrAlaAlaLysGlu 22
    |||||
DB 56 AGGTTGAGGTGGTGGGAGCTGGAAGTCATCGGCGAGAGGTCTCACAGCAGCCAGAGAA 115
    |||||
QY 23 ProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeuLeuAla 42
    |||||
DB 116 CCGGCGCCCGGCTCTCCCGCCCGCCAGCCAGTGCAGTTCGCAATTCCTGCTTGT 175
    |||||
QY 43 LeuAlaThrGlyLeuValGlyGlyLutThrArgIleIleLysGlyPheGlnCysLysPro 62
    |||||
DB 176 CTGGCAAGAGGCTGTAGAGGAGAGACAGAGATCATCAAGGGGTTGAGTGCAGAGCC 235
    |||||
QY 63 HisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLeuGlyGlyAlaThr 82
    |||||
DB 236 CACTCCAGCCCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 295
    |||||
QY 83 LeuIleAlaProArgTyrPheLeuThrAlaAlaHisCysLeuLysProArgTyrIleVal 102
    |||||
DB 296 CTCATGCCCGCCAGATGGTCTCGACAGAGCCCACTGCTCAAGCCCGGCTACATAGT 355
    |||||
QY 103 HisLeuGlyGlnHisAsnLeuGlnLysGlnGlyLysGlnThrArgThrAlaThr 122
    |||||
DB 356 CACCTGGGCGAGCAGCAACTCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 415
    |||||
QY 123 GluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArgAsn 141
    |||||
DB 416 GAGTCTTCCCGCCAGCCCGGCTTCACACAGCTTCCACAAAGACAGCCAGAT 472
    |||||

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RESULT 10
US-09-070-526-1

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; Sequence 1, Application US/09070526
; Patent No. 6100059
; GENERAL INFORMATION:
; APPLICANT: SOOTHAN, CHRISTOPHER
; APPLICANT: CLINKENBEARD, HELEN
; APPLICANT: BURGESS, NICOLA
; TITLE OF INVENTION: No. 6100059el Compounds
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSER: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,526
; FILING DATE: 30-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9711952.3

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FILING DATE: 9-JUN-1997
 APPLICATION NUMBER: EP 97309646.4
 FILING DATE: 1-DEC-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: PRESTIA, PAUL F
 REGISTRATION NUMBER: 23,031
 REFERENCE/DOCKET NUMBER: GH-30353
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEFAX: 610-407-0701
 TELE: 846169
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 944 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-070-526-1

Alignment Scores:
 Pred. No.: 2.57e-60 Length: 944
 Score: 690.00 Matches: 129
 Percent Similarity: 64.81% Conservative: 46
 Best Local Similarity: 47.78% Mismatches: 82
 Query Match: 45.31% Indels: 14
 Gaps: 4

US-09-856-320A-2 (1-282) x US-09-070-526-1 (1-944)

QY 10 TTPlySerSerGlyAArgGlyLeuThrAlaAlaLysGluProGlyAlaArgSerPro 29
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 DB 91 TGGAAAGACCTCA-----CCATG-GGACGCCCGGCGACT 122
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 QY 30 LeuGlnAlaMetArgIleLeuGlnLeuIleLeuLeu-----AlaLeuAlaThrGlyLeu 47
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 DB 123 CGTCCGCCCAAGAGCGTGATGTTCTCTCTGGGGGAGCGCTGGGCGACACTCC 182
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 QY 48 ValGlyGlyLeuThrArgIleIleLysGlyPheGlyCysLysProHisSerGlnProTrp 67
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 DB 183 AGGCGACAGAGAGAGCAAGTGTGGGGGTCATGATGCCAACCCCATTCGACACCTTG 242
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 QY 68 GlnAlaAlaLeuPheGlyLysThrArgLeuLeuGlyAlaThrLeuIleAlaProArg 87
 |||||:|||||
 DB 243 CAGCGCGCTGTGTCCAGGGCGACCAATTACTGTGTGGCGGTGTCTGTGTGCGAAC 302
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 QY 88 TTPLeuLeuThrAlaAlaHisCysLeuLysProArgTyrIleValHisIleGlnHis 107
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 DB 303 TGGGTCCTTACAGCTGCCCACTGTAAACCCGAAATACACAGTACCGCTGGAGACCCAC 362
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 QY 108 AsnLeuGlnLysGluGlyLysGlyGluGlnThrArgThrAlaThrGlnSerPheProHis 127
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 DB 363 AGCTTACAGATAAAGATGCGCCAGACCAAGAAATACCTGTGTGATCCATCCACAC 422
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 QY 128 ProGlyPheAsnAsnSerLeuProHisAspHisArgAsnAspIleMetLeuValLys 147
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 DB 423 CCGCGATATACACACAC---GATGTGAGAGCACCAACCATGTGATGCTTCTCA 479
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 QY 148 MetAlaSerProValSerIleThrThrAlaValArgProLeuThrLeuSerArgCys 167
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 DB 480 CTGGGTACCAAGGATCCCTGGGGTCCAAAGTGAAGCCCATCAGCTGGGCGATCATTGC 539
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 QY 168 ValThrAlaGlyThrSerCysLeuIleSerGlyTyrPheLysThrSerSerProGlnLeu 187
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 DB 540 ACCAGCGCTGGCGAAGTGCACCGCTGAGGGGCGACTGTACACAGTCCCGGAGAG 599
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 QY 188 ArgLeuProHisThrLeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlu 207
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 DB 600 AATTTCCTACACTCTCACTGTGAGAGTAAATCTTCCCGAAGAAAGTGTGAG 659
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 QY 208 AsnAlaTyrProGlyAsnIleThrAspThrMetValCysAlaSerValGlnGlyGly 227
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 DB 660 GATGCTTACCGGGGCGAGATTCAGATGGCATGTGTGTGTGAGGCGACGCAAGAGGGGCT 719

QY 228 LysAspSerCysGlnGlyAspSerGlyLeuProLeuValCysAsnGlnSerLeuGlnGly 247
 |||||:|||||
 DB 720 --GACACGTGCCAGGGGATTCGTGAGAGCCCGCTGTGATGTGACACTCCAGGCG 776
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 QY 248 IleIleSerTTPGlyGlnAspProCysAlaIleThrArgLysProGlyValTyrThrLys 267
 |||||:|||||
 DB 777 ATCACATCCCTGGGGCTCAGACCCCTGTGGAGAGTCCGACAAACCTGCGCTCATACCAAC 836
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 QY 268 ValCysLysTyrValAspThrIleGlnGlu 277
 |||||:|||||
 DB 837 ATGTCCGCTACTGTGACTGATCAAGAG 866

RESULT 11
 US-09-008-271A-19
 : Sequence 19, Application us/09008271A
 : Patent No. 6203979
 : GENERAL INFORMATION:
 : APPLICANT: Bandman, Olga
 : Hillman, Jennifer L.
 : Yue, Henry
 : Guegler, Karl J.
 : Corley, Neil C.
 : Tang, Tom Y.
 : Shah, Purvi
 : STATE: CA
 : CITY: Palo Alto
 : COUNTRY: USA
 : ZIP: 94304
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: DOS
 : SOFTWARE: FastSeq for Windows Version 2.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/008,271A
 : FILING DATE: 16-Jan-1998
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: <Unknown>
 : FILING DATE: <Unknown>
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Mohan-Peterson, Sheila
 : REGISTRATION NUMBER: 41,201
 : REFERENCE/DOCKET NUMBER: PF-0458 US
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 650-855-0555
 : TELEFAX: 650-845-4166
 : INFORMATION FOR SEQ ID NO: 19:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 994 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : IMMEDIATE SOURCE:
 : LIBRARY: COLANOT27
 : CLONE: 1798496
 : SEQUENCE DESCRIPTION: SEQ ID NO: 19 :
 US-09-008-271A-19

Alignment Scores:
 Pred. No.: 1.77e-59 Length: 994
 Score: 682.00 Matches: 128
 Percent Similarity: 64.44% Conservative: 46
 Best Local Similarity: 47.41% Mismatches: 83
 Query Match: 44.78% Indels: 14
 Gaps: 4

US-09-856-320A-2 (1-282) x US-09-008-271A-19 (1-994)

RESULT 13
US-09-996-243-308
Sequence 308, Application US/09996243
Patent No. 6478825
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC13
CURRENT APPLICATION NUMBER: US/09/996.243
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
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PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
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PRIOR FILING DATE: 1998-06-17
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PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23


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REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1476 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KERANOT02
CLONE: 820694
US-08-824-874-2

Alignment Scores:
Pred. No.: 9.65e-55 Length: 1476
Score: 637.50 Matches: 118
Percent Similarity: 67.95% Conservative: 41
Best Local Similarity: 50.43% Mismatches: 67
Query Match: 41.86% Indels: 8
DB: Gaps: 4

US-09-856-320A-2 (1-282) x US-08-824-874-2 (1-1476)
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OY 71 -LeuPheGluLysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeu 90
DB 529 GTTGCTAAGGCCCAACAGCTCTACTGCGGGCGGTGGTGGATCCACAGTGGCTCT 588
OY 90 uThrAlaAlaHisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuG 110
DB 589 CACGCGCCGCCACGACGAGAGAAAGTTTCAGAGTCCGCTCCGCCACTCTCTCTC 648
OY 110 nLys---GluGluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProG 129
DB 649 ACCAGTTTATGATCTGGGCGAGAGTGTCCAGGGGGTCAAAATCATCCGCCACCTGG 708
OY 129 yPheAsnAsnSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAl 149
DB 709 CTACTCC-----CACCTGGCCACTCTACACCTCACTCACTCACTCACTCACTCA 756
OY 149 aSerProValSerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValTh 169
DB 757 CAGAGAAATTCGTCCTCAATAAGATGTCAGACCATCAAGCTCTCTCTCTCTCTCTC 816
OY 169 rAlaGlyThrSerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLe 189
DB 817 TGCTGGGCAAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 876
OY 189 uProHisThrLeuArgCysAlaAsnIleThrIleLeuGlnHisGlnLysCysGluAsnAl 209
DB 877 CCTCAAGGCTCTCAAGCTTGAATATCAGGCTCTAAGTCAAGAAAGTCCGAGGAGTC 936
OY 209 aTyProGlyAsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAs 229
DB 937 TTACCCGAGACATAGATGACACCATTTCTGCGCCGCT---GACAAAGACAGTAGAGA 993
OY 229 pSerCysGlnLysAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleAl 249
DB 994 CTCTGCGACAGGATCTCTGGGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1053
OY 249 eSerTrpGlyLysProCysAlaIleThrArgLysProGlyValYThrTrpLysValCy 269
DB 1054 GTCTGGGAGATTAACCTTGTGCCCGGCCCAACAGCCGGGTGTCTACAGAACCTCTG 1113
OY 269 sLysTyValAspTrpIleGlnGlnThrMetLysAsnAsn 282
DB 1114 CAAGTTTCAACAGTGTATCCAGAAACCATTCACAGCCCAAC 1153

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RESULT 15
US-09-210-084-2
Sequence 2, Application US/09210084
Patent No. 6197511
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
FLING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-4166
TELEFAX: 415-855-0555
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1476 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KERANOT02
CLONE: 820694
US-09-210-084-2

Alignment Scores:
Pred. No.: 9.65e-55 Length: 1476
Score: 637.50 Matches: 118
Percent Similarity: 67.95% Conservative: 41
Best Local Similarity: 50.43% Mismatches: 67
Query Match: 41.86% Indels: 8
DB: Gaps: 4

US-09-856-320A-2 (1-282) x US-09-210-084-2 (1-1476)
OY 52 ThrArgIleIleIleYsglyPheGluCysLysProHisSerGlnProTrp-GlnAlaAla-- 70
DB 469 AGCGGCATCATCATGATGATCGACTGCGATGATGCACACCGCGGTGGGAGCGCGCT 528
OY 71 -LeuPheGluLysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeu 90
DB 529 GTTGCTAAGGCCCAACAGCTCTACTGCGGGCGGTGGTGGATCCACAGTGGCTCT 588
OY 90 uThrAlaAlaHisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuG 110
DB 589 CACGCGCCGCCACGACGAGAGAAAGTTTCAGAGTCCGCTCCGCCACTCTCTCTC 648
OY 110 nLys---GluGluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProG 129
DB 649 ACCAGTTTATGATCTGGGCGAGAGTGTCCAGGGGGTCAAAATCATCCGCCACCTGG 708
OY 129 yPheAsnAsnSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAl 149

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QY      149 aserProValSerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValTh 169
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QY      169 rAlaGlyThrSerCysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLe 189
Db      817 TGCTGGGACAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 876
QY      189 uProH1sThrLeuArgCysAlaAsnIleThrIleIleGlnIleGlnIleGlnIleGlnIleGln 209
Db      877 CCCTAAGGTCTCTCCAGTCTTGAATATCAGCGTGTAGTCAGAAAAGTGCGAGGATGC 936
QY      209 aTyrProGlyAsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAs 229
Db      937 TTACCCGAGACAGATAGATGACACACATGTCTGTGCGCGGT---GACAAAGCAGGTAGAGA 993
QY      229 pSerCysGlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleI 249
Db      994 CTCCTGCCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1053
QY      249 eSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCy 269
Db      1054 GTCTGGGGAGATTACCTTGTGTGCCGGCCCAACAGACCGGTGTCTACAGAACTCTGTG 1113
QY      269 sLysTyrValAspTrpIleGlnGlnIleThrMetLysAsnAsn 282
Db      1114 CAAGTTCACCAAGTGGATCCAGAAACATCCAGGCCAAC 1153
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Search completed: October 15, 2003, 21:09:00
Job time : 84.364 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 15, 2003, 20:58:02 ; Search time 25.3855 Seconds

(without alignments)
1789.927 Million cell updates/sec

Title: US-09-856-320A-2

Perfect score: 1523

Sequence: 1 MQLRLMDKSGSGRLTAA.....GVYTKCKYVDIETMKN 282

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1355	89.0	250	12	US-10-137-870-506
4	1355	89.0	250	12	US-10-140-018-506
5	1355	89.0	250	12	US-10-140-021-506
6	1355	89.0	250	12	US-10-140-274-506
7	1355	89.0	250	12	US-10-140-471-506
8	1355	89.0	250	12	US-10-140-807-506
9	1355	89.0	250	12	US-10-140-822-506
10	1355	89.0	250	12	US-10-140-924-506
11	1355	89.0	250	12	US-10-140-926-506
12	1355	89.0	250	12	US-10-141-698-506
13	1355	89.0	250	12	US-10-141-702-506
14	1355	89.0	250	12	US-10-141-704-506
15	1355	89.0	250	12	US-10-142-421-506

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17	1355	89.0	250	12	US-10-142-767-506	Sequence 506, App
18	1355	89.0	250	12	US-10-143-033-506	Sequence 506, App
19	1355	89.0	250	12	US-10-144-994-506	Sequence 506, App
20	1355	89.0	250	12	US-10-145-628-506	Sequence 506, App
21	1355	89.0	250	12	US-10-145-631-506	Sequence 506, App
22	1355	89.0	250	12	US-10-145-633-506	Sequence 506, App
23	1355	89.0	250	12	US-10-145-746-506	Sequence 506, App
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26	1355	89.0	250	12	US-10-145-826-506	Sequence 506, App
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30	1355	89.0	250	12	US-10-146-724-506	Sequence 506, App
31	1355	89.0	250	12	US-10-146-725-506	Sequence 506, App
32	1355	89.0	250	12	US-10-146-795-506	Sequence 506, App
33	1355	89.0	250	12	US-10-147-495-506	Sequence 506, App
34	1355	89.0	250	12	US-10-147-501-506	Sequence 506, App
35	1355	89.0	250	12	US-10-147-504-506	Sequence 506, App
36	1355	89.0	250	12	US-10-147-509-506	Sequence 506, App
37	1355	89.0	250	12	US-10-147-509-506	Sequence 506, App
38	1355	89.0	250	12	US-10-147-510-506	Sequence 506, App
39	1355	89.0	250	12	US-10-147-511-506	Sequence 506, App
40	1355	89.0	250	12	US-10-147-529-506	Sequence 506, App
41	1355	89.0	250	12	US-10-152-397-506	Sequence 506, App
42	1355	89.0	250	12	US-10-153-586-506	Sequence 506, App
43	1355	89.0	250	12	US-10-158-783-506	Sequence 506, App
44	1355	89.0	250	12	US-10-158-786-506	Sequence 506, App
45	1355	89.0	250	12	US-10-006-130A-170	Sequence 170, App

ALIGNMENTS

RESULT 1
US-09-946-374-170
; Sequence 170, Application US/09946374
; Publication No. US20030073129A1
GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Olang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830P1C1
CURRENT APPLICATION NUMBER: US/09/946,374
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750

1	PRIOR FILING DATE: 1998-09-01
2	PRIOR APPLICATION NUMBER: 60/09880-0
3	PRIOR FILING DATE: 1998-09-02
4	PRIOR APPLICATION NUMBER: 60/09882-0
5	PRIOR FILING DATE: 1998-09-02
6	PRIOR APPLICATION NUMBER: 60/09884-0
7	PRIOR FILING DATE: 1998-09-02
8	PRIOR APPLICATION NUMBER: 60/09953-0
9	PRIOR FILING DATE: 1998-09-03
10	PRIOR APPLICATION NUMBER: 60/09956-0
11	PRIOR FILING DATE: 1998-09-03
12	PRIOR APPLICATION NUMBER: 60/09964-0
13	PRIOR FILING DATE: 1998-09-03
14	PRIOR APPLICATION NUMBER: 60/09974-0
15	PRIOR FILING DATE: 1998-09-10
16	PRIOR APPLICATION NUMBER: 60/09975-0
17	PRIOR FILING DATE: 1998-09-10
18	PRIOR APPLICATION NUMBER: 60/09976-0
19	PRIOR FILING DATE: 1998-09-10
20	PRIOR APPLICATION NUMBER: 60/09979-0
21	PRIOR FILING DATE: 1998-09-10
22	PRIOR APPLICATION NUMBER: 60/09980-0
23	PRIOR FILING DATE: 1998-09-10
24	PRIOR APPLICATION NUMBER: 60/09981-0
25	PRIOR FILING DATE: 1998-09-10
26	PRIOR APPLICATION NUMBER: 60/09981-0
27	PRIOR FILING DATE: 1998-09-10
28	PRIOR APPLICATION NUMBER: 60/10038-0
29	PRIOR FILING DATE: 1998-09-15
30	PRIOR APPLICATION NUMBER: 60/10039-0
31	PRIOR FILING DATE: 1998-09-15
32	PRIOR APPLICATION NUMBER: 60/10063-0
33	PRIOR FILING DATE: 1998-09-16
34	PRIOR APPLICATION NUMBER: 60/10064-0
35	PRIOR FILING DATE: 1998-09-16
36	PRIOR APPLICATION NUMBER: 60/10066-0
37	PRIOR FILING DATE: 1998-09-16
38	PRIOR APPLICATION NUMBER: 60/10068-0
39	PRIOR FILING DATE: 1998-09-17
40	PRIOR APPLICATION NUMBER: 60/10068-0
41	PRIOR FILING DATE: 1998-09-17
42	PRIOR APPLICATION NUMBER: 60/10070-0
43	PRIOR FILING DATE: 1998-09-17
44	PRIOR APPLICATION NUMBER: 60/10071-0
45	PRIOR FILING DATE: 1998-09-17
46	PRIOR APPLICATION NUMBER: 60/10084-9
47	PRIOR FILING DATE: 1998-09-18
48	PRIOR APPLICATION NUMBER: 60/10091-9
49	PRIOR FILING DATE: 1998-09-17
50	PRIOR APPLICATION NUMBER: 60/10093-0
51	PRIOR FILING DATE: 1998-09-17
52	PRIOR APPLICATION NUMBER: 60/10101-4
53	PRIOR FILING DATE: 1998-09-18
54	PRIOR APPLICATION NUMBER: 60/10106-8
55	PRIOR FILING DATE: 1998-09-18
56	PRIOR APPLICATION NUMBER: 60/10107-1
57	PRIOR FILING DATE: 1998-09-16
58	PRIOR APPLICATION NUMBER: 60/10127-9
59	PRIOR FILING DATE: 1998-09-22

1	PRIOR APPLICATION NUMBER: 60/1014471
2	PRIOR FILING DATE: 1998-09-23
3	PRIOR APPLICATION NUMBER: 60/1014472
4	PRIOR FILING DATE: 1998-09-23
5	PRIOR APPLICATION NUMBER: 60/1014474
6	PRIOR FILING DATE: 1998-09-23
7	PRIOR APPLICATION NUMBER: 60/1014475
8	PRIOR FILING DATE: 1998-09-23
9	PRIOR APPLICATION NUMBER: 60/1014476
10	PRIOR FILING DATE: 1998-09-23
11	PRIOR APPLICATION NUMBER: 60/1014777
12	PRIOR FILING DATE: 1998-09-23
13	PRIOR APPLICATION NUMBER: 60/101479
14	PRIOR FILING DATE: 1998-09-23
15	PRIOR APPLICATION NUMBER: 60/101738
16	PRIOR FILING DATE: 1998-09-24
17	PRIOR APPLICATION NUMBER: 60/1017411
18	PRIOR FILING DATE: 1998-09-24
19	PRIOR APPLICATION NUMBER: 60/101743
20	PRIOR FILING DATE: 1998-09-24
21	PRIOR APPLICATION NUMBER: 60/101915
22	PRIOR FILING DATE: 1998-09-24
23	PRIOR APPLICATION NUMBER: 60/101916
24	PRIOR FILING DATE: 1998-09-24
25	PRIOR APPLICATION NUMBER: 60/102007
26	PRIOR FILING DATE: 1998-09-25
27	PRIOR APPLICATION NUMBER: 60/102040
28	PRIOR FILING DATE: 1998-09-25
29	PRIOR APPLICATION NUMBER: 60/1020307
30	PRIOR FILING DATE: 1998-09-25
31	PRIOR APPLICATION NUMBER: 60/102330
32	PRIOR FILING DATE: 1998-09-25
33	PRIOR APPLICATION NUMBER: 60/102331
34	PRIOR FILING DATE: 1998-09-25
35	PRIOR APPLICATION NUMBER: 60/102484
36	PRIOR FILING DATE: 1998-09-30
37	PRIOR APPLICATION NUMBER: 60/102487
38	PRIOR FILING DATE: 1998-09-30
39	PRIOR APPLICATION NUMBER: 60/102570
40	PRIOR FILING DATE: 1998-09-30
41	PRIOR APPLICATION NUMBER: 60/102571
42	PRIOR FILING DATE: 1998-09-30
43	PRIOR APPLICATION NUMBER: 60/102664
44	PRIOR FILING DATE: 1998-10-01
45	PRIOR APPLICATION NUMBER: 60/102667
46	PRIOR FILING DATE: 1998-10-01
47	PRIOR APPLICATION NUMBER: 60/102965
48	PRIOR FILING DATE: 1998-10-02
49	PRIOR APPLICATION NUMBER: 60/103258
50	PRIOR FILING DATE: 1998-10-06
51	PRIOR APPLICATION NUMBER: 60/103314
52	PRIOR FILING DATE: 1998-10-07
53	PRIOR APPLICATION NUMBER: 60/103315
54	PRIOR FILING DATE: 1998-10-07
55	PRIOR APPLICATION NUMBER: 60/103328
56	PRIOR FILING DATE: 1998-10-07
57	PRIOR APPLICATION NUMBER: 60/103395
58	PRIOR FILING DATE: 1998-10-07
59	PRIOR APPLICATION NUMBER: 60/103396
60	PRIOR FILING DATE: 1998-10-07
61	PRIOR APPLICATION NUMBER: 60/103401
62	PRIOR FILING DATE: 1998-10-07
63	PRIOR APPLICATION NUMBER: 60/103449
64	PRIOR FILING DATE: 1998-10-06
65	PRIOR APPLICATION NUMBER: 60/103679
66	PRIOR FILING DATE: 1998-10-08
67	PRIOR APPLICATION NUMBER: 60/103711
68	PRIOR FILING DATE: 1998-10-08
69	PRIOR APPLICATION NUMBER: 60/104257
70	PRIOR FILING DATE: 1998-10-08

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; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
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Query Match      89.0%; Score 1355; DB 11; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.2e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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OY 33 MRLIQLILALATGIVGETRIKGFECCKPHSOPMOALFEKTRILLCGATLIAPRWLTA 92
DB 1 MRLIQLILALATGIVGETRIKGFECCKPHSOPMOALFEKTRILLCGATLIAPRWLTA 60
OY 93 AHCLKPRIVHLGQHNLOKEBCEQOTRATESFPHGFNNSLPNKDRNDIMLYMASPV 152
DB 61 AHCLKPRIVHLGQHNLOKEBCEQOTRATESFPHGFNNSLPNKDRNDIMLYMASPV 120
OY 153 SITMAVRPLTSSRCVTAAGTSCILISGWSSTSPQLRLPHTLRKANITIIIEHOKCENAYPG 212
DB 121 SITMAVRPLTSSRCVTAAGTSCILISGWSSTSPQLRLPHTLRKANITIIIEHOKCENAYPG 180
OY 213 NITDTMVCASVOEGKDCSQDGSGLPVCNOSLOGIISMGODPCAITRRPGVYTRVCXY 272
DB 181 NITDTMVCASVOEGKDCSQDGSGLPVCNOSLOGIISMGODPCAITRRPGVYTRVCXY 240
OY 273 DWIOETMKNN 282
DB 241 DWIOETMKNN 250
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RESULT 2

```
US-10-015-387A-170
; Sequence 170, Application US/10015387A
; Publication No. US20030135034A1
```

GENERAL INFORMATION:

```
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C54
; CURRENT APPLICATION NUMBER: US/10/015.387A
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 170
; LENGTH: 250
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-015-387A-170
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Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.2e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 33 MRLIQLILALATGIVGETRIKGFECCKPHSOPMOALFEKTRILLCGATLIAPRWLTA 92
DB 1 MRLIQLILALATGIVGETRIKGFECCKPHSOPMOALFEKTRILLCGATLIAPRWLTA 60
OY 93 AHCLKPRIVHLGQHNLOKEBCEQOTRATESFPHGFNNSLPNKDRNDIMLYMASPV 152
DB 61 AHCLKPRIVHLGQHNLOKEBCEQOTRATESFPHGFNNSLPNKDRNDIMLYMASPV 120
OY 153 SITMAVRPLTSSRCVTAAGTSCILISGWSSTSPQLRLPHTLRKANITIIIEHOKCENAYPG 212
DB 121 SITMAVRPLTSSRCVTAAGTSCILISGWSSTSPQLRLPHTLRKANITIIIEHOKCENAYPG 180
OY 213 NITDTMVCASVOEGKDCSQDGSGLPVCNOSLOGIISMGODPCAITRRPGVYTRVCXY 272
DB 181 NITDTMVCASVOEGKDCSQDGSGLPVCNOSLOGIISMGODPCAITRRPGVYTRVCXY 240
OY 273 DWIOETMKNN 282
DB 241 DWIOETMKNN 250
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RESULT 3

```
US-10-137-870-506
; Sequence 506, Application US/10137870
; Publication No. US20030138883A1
```

GENERAL INFORMATION:

```
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeGeorge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Stewart, Victoria
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Collin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C155
; CURRENT APPLICATION NUMBER: US/10/137.870
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-870-506
```

```
Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.2e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 33 MRLIQLILALATGIVGETRIKGFECCKPHSOPMOALFEKTRILLCGATLIAPRWLTA 92
DB 1 MRLIQLILALATGIVGETRIKGFECCKPHSOPMOALFEKTRILLCGATLIAPRWLTA 60
OY 93 AHCLKPRIVHLGQHNLOKEBCEQOTRATESFPHGFNNSLPNKDRNDIMLYMASPV 152
```

Db	61	AHCLKPRIVHIGOHNLQKEEGCEQTRATESFPHPGFNNSLPNKDHRNDIMLVMAASPV	120
QY	153	SITMAVRPLTSSRCVTAIGTSCILISGMGSTSSPOLRLPHTLRCANITITIEHOKCNAPG	212
Db	121	SITMAVRPLTSSRCVTAIGTSCILISGMGSTSSPOLRLPHTLRCANITITIEHOKCNAPG	180
QY	213	NITDPMVCASVOEGGKDCSQDSSGGLVCNCSLGGIISMGODPCAITRRKPGYTVKCYV	272
Db	181	NITDPMVCASVOEGGKDCSQDSSGGLVCNCSLGGIISMGODPCAITRRKPGYTVKCYV	240
QY	273	DMIOETMKN 282	
Db	241	DMIOETMKN 250	
RESULT 4			
US-10-140-018-506			
; Sequence 506, Application US/10140018			
; Publication No. US20030138885A1			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Beresini, Maureen			
; APPLICANT: Deforge, Laura			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Sherwood, Steven			
; APPLICANT: Smith, Victoria			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumei, Daniel			
; APPLICANT: Watanabe, Colin K			
; APPLICANT: Wood, William			
; APPLICANT: Zhang, Zhenli			
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
; TITLE OF INVENTION: ACIDS ENCODING THE SAME			
; FILE REFERENCE: P3330R1C158			
; CURRENT APPLICATION NUMBER: US/10/140,018			
; CURRENT FILING DATE: 2002-05-06			
; Prior Application removed - See Palm or File Wrapper			
; NUMBER OF SEQ ID NOS: 550			
; SEQ ID NO 506			
; LENGTH: 250			
; TYPE: PRT			
; ORGANISM: Homo Sapien			
US-10-140-018-506			
Query Match 89.0%; Score 1355; DB 12; Length 250;			
Best Local Similarity 100.0%; Pred. No. 1.2e-126;			
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	33	MRILQLILALATGIVGGEFTIINGFECKPHSQPQOALFEKTRILCGATILAPRWLTA	92
Db	1	MRILQLILALATGIVGGEFTIINGFECKPHSQPQOALFEKTRILCGATILAPRWLTA	60
QY	93	AHCLKPRIVHIGOHNLQKEEGCEQTRATESFPHPGFNNSLPNKDHRNDIMLVMAASPV	152
Db	61	AHCLKPRIVHIGOHNLQKEEGCEQTRATESFPHPGFNNSLPNKDHRNDIMLVMAASPV	120
QY	153	SITMAVRPLTSSRCVTAIGTSCILISGMGSTSSPOLRLPHTLRCANITITIEHOKCNAPG	212
Db	121	SITMAVRPLTSSRCVTAIGTSCILISGMGSTSSPOLRLPHTLRCANITITIEHOKCNAPG	180
QY	213	NITDPMVCASVOEGGKDCSQDSSGGLVCNCSLGGIISMGODPCAITRRKPGYTVKCYV	272
Db	181	NITDPMVCASVOEGGKDCSQDSSGGLVCNCSLGGIISMGODPCAITRRKPGYTVKCYV	240
QY	273	DMIOETMKN 282	
Db	241	DMIOETMKN 250	

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RESULT 5
US-10-140-021-506
: Sequence 506, Application US/10140021
: Publication No. US2003013886A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: DeForge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Elivaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerilsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NOCLEIC
: FILE REFERENCE: P3303R1C167
: CURRENT APPLICATION NUMBER: US/10/140, 021
: CURRENT FILING DATE: 2002-05-06
: Prior Application removed - See Palm or File Wrapper
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO: 506
: LENGTH: 250
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-140-021-506

Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. NO. 1,2e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 33 MRILQILILALATGLVGGETRIIKGFECCKPSQPMQAALEKTRRLCGATLIPRWLTA 92
Db 1 MRILQILILALATGLVGGETRIIKGFECCKPSQPMQAALEKTRRLCGATLIPRWLTA 60

QY 93 AHCLKRRYIVHLGQHNLDKEBCEQTRATSEFPHPGNNSLPRKDHNDIMLVKASPV 152
Db 61 AHCLKRRYIVHLGQHNLDKEBCEQTRATSEFPHPGNNSLPRKDHNDIMLVKASPV 120

QY 153 SITMAVRPILTLSSRCVTAAGTSCILISGWSSTSPQLRLPHLRLRCANITIIERHCENAPYG 212
Db 121 SITMAVRPILTLSSRCVTAAGTSCILISGWSSTSPQLRLPHLRLRCANITIIERHCENAPYG 180

QY 213 NITDTWVCASVQEGGKDCOGDSGGPLVNCNOSLGGIISMGDCPACATRRPGVYTKCKYV 272
Db 181 NITDTWVCASVQEGGKDCOGDSGGPLVNCNOSLGGIISMGDCPACATRRPGVYTKCKYV 240

QY 273 DWIQTETKNN 282
Db 241 DWIQTETKNN 250

RESULT 6
US-10-140-274-506
: Sequence 506, Application US/10140274
: Publication No. US2003014367A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: DeForge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Elivaroff, Ellen
: APPLICANT: Gao, Wei-Qiang

```

Query Match	89.0%;	Score 1355;	DB 12;	Length 250;
Best Local Similarity	100.0%;	Pred. No. 1.2e-126;		
Matches 250; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

RESULT 7
US-10-140-471-506
; Sequence 506, Application US/10140471

GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Beresini, Maureen
 APPLICANT: DeForge, Laura
 APPLICANT: Desnoyers, Luc
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerlitsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin I.
 APPLICANT: Sherwood, Steven
 APPLICANT: Smith, Victoria
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

Query Match	89.0%;	Score 1355;	DB 12;	Length 250;
Best Local Similarity	100.0%;	Pred. No. 1.2e-126;		
Matches 250; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

RESULT 8
US-10-140-807-506
; Sequence 506, Application US/10140807
; Publication No. US20030134354A1

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/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Beresini, Maureen
/ APPLICANT: DeRoche, Laura
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerlitsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Collin K
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3330R1C174
/ CURRENT APPLICATION NUMBER: US/10/140,807
/ CURRENT FILING DATE: 2002-05-07
/ Prior Application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 50
/ SEQ ID NO 506
/ LENGTH: 250
/ TYPE: PRT
/ ORGANISM: Homo Sapien
/ S-10-140-807-506

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Query Match	89.0%;	Score 1355;	DB 12;	Length 250;
Best Local Similarity	100.0%;	Pred. No. 1.2e-126;		


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; Publication No. US20030134356A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria A.
; APPLICANT: Stewart, Daniel
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C187
; CURRENT APPLICATION NUMBER: US/10/140,926
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-926-506
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Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.2e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 AHCLKPRYIVHLGQHNLOKEGCEOTRTATESFPHPGFNNSLPNKDHNDIMLVMAASPV 120
QY 153 SITMAVRPLTSSRCVTAGTSCSLISGWSSTSSPOLRLPHTLRKANITIIIEHQKCNAYPG 212
DB 121 SITMAVRPLTSSRCVTAGTSCSLISGWSSTSSPOLRLPHTLRKANITIIIEHQKCNAYPG 180
QY 213 NITDTMVCASVOEGKDCSQDGSGLPVCNOSLGGIISMGDPCAITRKPGYTVCKYV 272
DB 181 NITDTMVCASVOEGKDCSQDGSGLPVCNOSLGGIISMGDPCAITRKPGYTVCKYV 240
QY 273 DWIOETMKN 282
DB 241 DWIOETMKN 250
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RESULT 12
US-10-141-698-506
; Sequence 506, Application US/10141698
; Publication No. US20030134357A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven

```
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C206
; CURRENT APPLICATION NUMBER: US/10/141,698
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-141-698-506
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Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.2e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 33 MRLIQLILALATGIVGETRIIKGFECCKPHSQPQAALEFETRLLCGATTLIAPWMLTA 92
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QY 93 AHCLKPRYIVHLGQHNLOKEGCEOTRTATESFPHPGFNNSLPNKDHNDIMLVMAASPV 152
DB 61 AHCLKPRYIVHLGQHNLOKEGCEOTRTATESFPHPGFNNSLPNKDHNDIMLVMAASPV 120
QY 153 SITMAVRPLTSSRCVTAGTSCSLISGWSSTSSPOLRLPHTLRKANITIIIEHQKCNAYPG 212
DB 121 SITMAVRPLTSSRCVTAGTSCSLISGWSSTSSPOLRLPHTLRKANITIIIEHQKCNAYPG 180
QY 213 NITDTMVCASVOEGKDCSQDGSGLPVCNOSLGGIISMGDPCAITRKPGYTVCKYV 272
DB 181 NITDTMVCASVOEGKDCSQDGSGLPVCNOSLGGIISMGDPCAITRKPGYTVCKYV 240
QY 273 DWIOETMKN 282
DB 241 DWIOETMKN 250
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RESULT 13
US-10-141-702-506
; Sequence 506, Application US/10141702
; Publication No. US20030134358A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Daniel
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C208
; CURRENT APPLICATION NUMBER: US/10/141,702
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550

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; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-141-702-506

Query Match          89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.2e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 273 DWIOETMKNN 282
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Db 241 DWIOETMKNN 250

RESULT 14
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; Sequence 506, Application US/10141704
; Publication No. US20030134359A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC209
; CURRENT APPLICATION NUMBER: US/10/141,704
; PRIOR APPLICATION DATE: 2002-05-08
; PRIOR APPLICATION removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-141-704-506

Query Match          89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.2e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 273 DWIOETMKNN 282
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Db 241 DWIOETMKNN 250

RESULT 15
US-10-142-421-506
; Sequence 506, Application US/10142421
; Publication No. US20030134360A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC218
; CURRENT APPLICATION NUMBER: US/10/142,421
; CURRENT APPLICATION DATE: 2002-05-09
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-421-506

Query Match          89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.2e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MRILQILILALATGLVGGETRIIKGECKPHSOPMOALFEKTRILCGATLIPRWLLTA 92
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Db 1 MRILQILILALATGLVGGETRIIKGECKPHSOPMOALFEKTRILCGATLIPRWLLTA 60

QY 93 AHCLKPRYIVHLGOHNLQKEEGCEQTRTATESPFPHGFNNSLPNKDHRNDIMLVKMASPV 152
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Db 61 AHCLKPRYIVHLGOHNLQKEEGCEQTRTATESPFPHGFNNSLPNKDHRNDIMLVKMASPV 120

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    |||
Db 121 SITMAVRPLTSSRCVTAAGTSCGISGWSSTSPQLRPLPTLRKANITIIHOKCENAYPG 180

QY 213 NITDTWVCASVOEGKDSQCGDSGGLVNCNOSLOGIISWGODPCATIRKPGVYTKYCKYV 272
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Db 181 NITDTWVCASVOEGKDSQCGDSGGLVNCNOSLOGIISWGODPCATIRKPGVYTKYCKYV 240
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DB	241	DWIOETMKN	250

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Job time : 25.385 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 15, 2003, 20:55:12 ; Search time 16.0039 Seconds

(without alignments)
745.546 Million cell updates/sec

Title: US-09-856-320A-2

Perfect score: 1523

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Scoring table: BLOSUM62

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Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1227	80.6	289	4	US-09-386-642-14
5	748	49.1	246	4	US-09-205-258-1149
6	698.5	45.3	260	3	US-09-025-059-3
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8	682	44.8	260	3	US-09-008-271A-7
9	679	44.6	288	4	US-09-386-642-13
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13	604.5	39.7	263	2	US-08-824-874-5
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16	604.5	39.7	263	4	US-09-478-957-5
17	604.5	39.7	263	4	US-09-764-762-5
18	600.5	39.4	246	2	US-08-978-404B-44
19	600	39.4	268	2	US-08-824-874-1
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24	596.5	39.2	261	3	US-08-622-046B-14
25	596.5	39.2	261	4	US-09-100-264-7
26	596.5	39.2	261	4	US-08-983-075D-7
27	596.5	39.2	261	4	US-08-843-076D-3

28	594	39.0	244	1	US-08-361-395-1	Sequence 1, Appli
29	593.5	39.0	261	3	US-08-768-859A-19	Sequence 19, Appl
30	593.5	39.0	261	3	US-08-767-820A-19	Sequence 19, Appl
31	593.5	39.0	261	3	US-08-622-046B-3	Sequence 3, Appli
32	592.5	38.9	261	5	PCT-US95-06157-6	Sequence 6, Appli
33	588	38.6	260	4	US-08-983-075D-9	Sequence 9, Appli
34	587	38.5	247	2	US-08-956-267A-2	Sequence 2, Appli
35	585.5	38.4	244	3	US-08-768-859A-10	Sequence 10, Appl
36	585.5	38.4	244	3	US-08-767-820A-10	Sequence 10, Appl
37	585.5	38.4	244	3	US-08-622-046B-16	Sequence 16, Appl
38	585.5	38.4	244	3	US-09-100-264-5	Sequence 5, Appli
39	585.5	38.4	244	4	US-08-843-076D-5	Sequence 5, Appli
40	582.5	38.2	244	4	US-08-622-046B-5	Sequence 5, Appli
41	581.5	38.2	244	5	PCT-US95-06157-10	Sequence 10, Appl
42	580	38.1	262	2	US-08-790-137-1	Sequence 1, Appli
43	580	38.1	262	2	US-08-790-137-3	Sequence 3, Appli
44	580	38.1	262	2	US-08-681-151-4	Sequence 4, Appli
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ALIGNMENTS

RESULT 1
US-09-025-059-1
; Sequence 1, Application US/09025059
; Patent No. 6075136
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,059
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0481 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 282 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGFTU10
; CLONE: 273646
; US-09-025-059-1
Query Match 100.0%; Score 1523; DB 3; Length 282;
Best Local Similarity 100.0%; Pred. No. 1.9e-148;

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Db 1 MORLRIMDKSSGRGTTAAKEPGARSSPLQAMRIIQLILALATGVGETRIKQFEC 60
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Db 61 KPHSQPQOALFEKTRILCGATLIAPRWLTAAHCLKPRIVHLGQHNLOKEGCEQRT 120
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Db 121 ATSEFPHPGNNSLPKNDHNDIMLVKMASPVSIITWAVRPLTSSRCVTAGTSCILSGWG 180
QY 181 STSSPOLRPLHTRCANITITIEHOKCENAYPGNITDTWVCASVOEGKDSQGDGGPLV 240
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Db 181 STSSPOLRPLHTRCANITITIEHOKCENAYPGNITDTWVCASVOEGKDSQGDGGPLV 240
QY 241 CNOISLOGIISWGODPCATITRKPGVYTRKVCYVDMIOETMKN 282
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Db 241 CNOISLOGIISWGODPCATITRKPGVYTRKVCYVDMIOETMKN 282

RESULT 2
US-09-205-258-427
; Sequence 427, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
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; EARLIER APPLICATION NUMBER: 60/048,880
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; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 427
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-427

Query Match      89.0%; Score 1355; DB 4; Length 250;
Best Local Similarity 100.0%; Pred. No. 3e-131;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 33 MRILQILALATAGLVGETRIIKGFECKPHSQPQOALFEKTRILCGATLIAPRWLTAA 92
    33 MRILQILALATAGLVGETRIIKGFECKPHSQPQOALFEKTRILCGATLIAPRWLTAA 92
Db 1 MRILQILALATAGLVGETRIIKGFECKPHSQPQOALFEKTRILCGATLIAPRWLTAA 60
QY 93 AHCLKPRIVHLGQHNLOKEGCEQRTATESFPHPGFNNSLPKNDHNDIMLVKMASPV 152
    93 AHCLKPRIVHLGQHNLOKEGCEQRTATESFPHPGFNNSLPKNDHNDIMLVKMASPV 152
Db 61 AHCLKPRIVHLGQHNLOKEGCEQRTATESFPHPGFNNSLPKNDHNDIMLVKMASPV 120
QY 153 SITWAVRPLTSSRCVTAGTSCILSGWGSTSSPOLRPLHTRCANITITIEHOKCENAYPG 212
    153 SITWAVRPLTSSRCVTAGTSCILSGWGSTSSPOLRPLHTRCANITITIEHOKCENAYPG 212
Db 121 SITWAVRPLTSSRCVTAGTSCILSGWGSTSSPOLRPLHTRCANITITIEHOKCENAYPG 180
QY 213 NITDTWVCASVOEGKDSQGDGGPLVYNOSLOGIISWGODPCATITRKPGVYTRKCV 272
    213 NITDTWVCASVOEGKDSQGDGGPLVYNOSLOGIISWGODPCATITRKPGVYTRKCV 272
Db 181 NITDTWVCASVOEGKDSQGDGGPLVYNOSLOGIISWGODPCATITRKPGVYTRKCV 240
QY 273 DWIOETMKN 282
    273 DWIOETMKN 282
Db 241 DWIOETMKN 250
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1  RESULT 3
2  US-08-944-483-24
3  ; Sequence 24, Application US/08944483
4  ; Patent No. 6232456
5  ; GENERAL INFORMATION:
6  ; APPLICANT: COHEN, MAURICE
7  ; APPLICANT: COLPITS, TRACEY L.
8  ; APPLICANT: FRIEDMAN, PAULA N.
9  ; APPLICANT: GRANADOS, EDWARD N.
10 ; APPLICANT: KLASS, MICHAEL R.
11 ; APPLICANT: RUSSELL, JOHN C.
12 ; APPLICANT: STEWART, KENT D.
13 ; APPLICANT: STROUPE, STEVEN D.
14 ; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
15 ; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
16 ; TITLE OF INVENTION: OF THE PROSTATE
17 ; NUMBER OF SEQUENCES: 76
18 ; CORRESPONDENCE ADDRESS:
19 ; ADDRESSEE: Abbott Laboratories
20 ; STREET: 100 Abbott Park Road
21 ; CITY: Abbott Park
22 ; STATE: IL
23 ; COUNTRY: USA
24 ; ZIP: 60064-3500
25 ; COMPUTER READABLE FORM:
26 ; MEDIUM TYPE: Diskette
27 ; COMPUTER: IBM Compatible
28 ; OPERATING SYSTEM: DOS
29 ; SOFTWARE: FastSeq for Windows Version 2.0
30 ; CURRENT APPLICATION DATA:
31 ; APPLICATION NUMBER: US/08/944,483
32 ; FILING DATE:
33 ; CLASSIFICATION: 424
34 ; PRIOR APPLICATION DATA:
35 ; APPLICATION NUMBER:
36 ; FILING DATE:
37 ; ATTORNEY/AGENT INFORMATION:
38 ; NAME: Becker, Cheryl L.
39 ; REGISTRATION NUMBER: 35,441
40 ; REFERENCE/DOCKET NUMBER: 6183.US.01
41 ; TELECOMMUNICATION INFORMATION:
42 ; TELEPHONE: 847/935-1729
43 ; TELEFAX: 847/938-2623
44 ; TELEX:
45 ; INFORMATION FOR SEQ ID NO: 24:
46 ; SEQUENCE CHARACTERISTICS:
47 ; LENGTH: 248 amino acids
48 ; TYPE: amino acid
49 ; STRANDEDNESS: single
50 ; TOPOLOGY: linear
51 ; MOLECULE TYPE: No. 6232456e
52 ; US-08-944-483-24
53
54 Query Match 86.9%; Score 1324; DB 3; Length 248;
55 Best Local Similarity 99.2%; Pred. No. 4, 5e-128;
56 Matches 248; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
57
58 33 MRILQILALATGLVGGETRIITKIGECPSHPQMAALFETKRLICGATLLAPRWLTA 92
59 |||||
60 1 MRILQILALALATGLVGGETRIITKIGEC- PHSQPMQALP -KTRLICGATLLAPRWLTA 58
61 |||||
62 93 AHCLKPRYIVHLQHNMQKEGCEQTRTATESFPHPGFNNSLPNKDRHNDIMLVMAASPV 152
63 |||||
64 59 AHCLKPRYIVHLQHNMQKEGCEQTRTATESFPHPGFNNSLPNKDRHNDIMLVMAASPV 118
65 |||||
66 153 SITMAVAPLTLSSRCYTAGTSCILISGWSSTSPQLRPHTLRCANITIIHOKCENAYPG 212
67 |||||
68 119 SITMAVAPLTLSSRCYTAGTSCILISGWSSTSPQLRPHTLRCANITIIHOKCENAYPG 178
69 |||||
70 213 NITDTMVCASVQSGGSDSCGSGSGPFLVGNOSLOGITISMGDPCATTRRGVYTVKCYV 272
71 |||||
72 179 NITDTMVCASVQSGGSDSCGSGSGPFLVGNOSLOGITISMGDPCATTRRGVYTVKCYV 238

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Oy      273  DMIOTMKNN 282
        |||||
Db      239  DMIOTMKNN 248

RESULT 4
US-09-386-642-14
: Sequence 14, Application US/09386642
: Patent No. 6420157
: GENERAL INFORMATION:
: APPLICANT: Darrow, Andrew
: APPLICANT: Qi, Jensen
: APPLICANT: Andrade-Gordon, Patricia
: TITLE OF INVENTION: Zymogen Activation System
: FILE REFERENCE: ORT-1028
: CURRENT APPLICATION NUMBER: US/09/386,642
: CURRENT FILING DATE: 1999-08-31
: NUMBER OF SEQ ID NOS: 60
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 14
: LENGTH: 289
: TYPE: PRT
: ORGANISM: Artificial Sequence
FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
US-09-386-642-14
: OTHER INFORMATION: With homo sapien serine protease catalytic domain

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Query Match	Similarity	80.6%	Score 1227	DB 4	Length 269
Best Local Similarity	84.3%	Pred. No. 5.1e-118			
Matches 231	Conservative 9	Mismatches 12	Indels 22	Gaps 3	
QY	31 QAMRLDIL--LALATGLVG-----GETRIKGFEC-KPSPQWQ	68			
Db	8 QKSRLLLLLVSNLLCGGVSDYKDDDDVDAAALAFDDDDKIVGGYNCLERKISQWQ	67			
QY	69 AALEKRRLLCGATLIPARLLITAAHCLKPRYIYHLGHNLOKEGCEQTRATSPFHP	128			
Db	68 AALEKRRLLCGATLIPARLLITAAHCLKPRYIYHLGHNLOKEGCEQTRATSPFHP	127			
QY	129 GFNSLSPNKDHRNDIMLVKMAFPSITVAVPRILTSRCYTAGTSCILISGMSTSSPOLR	188			
Db	128 GFNSLSPNKDHRNDIMLVKMAFPSITVAVPRILTSRCYTAGTSCILISGMSTSSPOLR	187			
QY	189 LPHTLRCAITIIIEHOKCENAYPGNITDPMVCAVSQEGSKDSGGSGLVCNOSLOGI	248			
Db	188 LPHTLRCAITIIIEHOKCENAYPGNITDPMVCAVSQEGSKDSGGSGLVCNOSLOGI	247			
QY	249 ISMGDPCAIITRRKGGVYTKVCKRYDWIOETMKN	282			
Db	248 ISMGDPCAIITRRKGGVYTKVCKRYDWIOETMKN	281			
RESULT 5	US-09-205-258-1149				
	Sequence 1149, Application US/09205258				
	Patent No. 6525174				
	GENERAL INFORMATION:				
	APPLICANT: Young et al.				
	TITLE OF INVENTION: 207 Human Secreted Proteins				
	FILE REFERENCE: P2007P1				
	CURRENT APPLICATION NUMBER: US/09/205,258				
	CURRENT FILING DATE: 1998-12-04				
	EARLIER APPLICATION NUMBER: PCT/US98/11422				
	EARLIER FILING DATE: 1998-06-04				
	EARLIER APPLICATION NUMBER: 60/048,885				
	EARLIER FILING DATE: 1997-06-06				
	EARLIER APPLICATION NUMBER: 60/049,375				
	EARLIER FILING DATE: 1997-06-06				
	EARLIER APPLICATION NUMBER: 60/048,881				
	EARLIER FILING DATE: 1997-06-06				
	EARLIER APPLICATION NUMBER: 60/048,880				
	EARLIER FILING DATE: 1997-06-06				

EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1149

LENGTH: 246
TYPE: PRT
ORGANISM: Homo sapiens
US-09-205-258-1149
Query Match
Best Local Similarity 92.8%; Score 748; DB 4; length 246;
Matches 142; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
QY 33 MRLQLILALATGVLGGETRIIKGFCEKPHSQPMQAALEFKTRLLCGATLLAPRWLTA 92
DB 1 MRLQLILALATGVLGGETRIIKGFCEKPHSQPMQAALEFKTRLLCGATLLAPRWLTA 60
QY 93 AHCLEPRYIVHLCQHNLOKEEGCEQTRTATESPPHGFNNSLPKCDHRNDIMLVKMASPV 152
DB 61 AHCLEPRYIVHLCQHNLOKEEGCEQTRTATESPPHGFNNSLPKCDHRNDIMLVKMASPV 120
QY 153 SITWAVRPLTSSRCVTAGTSCFSPAGAAKPPD 153
DB 121 SITWAVRPLTSSRCVTAGTSCFSPAGAAKPPD 153

RESULT 6
US-09-025-059-3
Sequence 3, Application US/09025059
Patent No. 6075136
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,059
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0481 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 260 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1020091
US-09-025-059-3
Query Match
Best Local Similarity 45.9%; Score 698.5; DB 3; length 260;
Matches 129; Conservative 35; Mismatches 77; Indels 7; Gaps 3;

EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1150
LENGTH: 228
TYPE: PRT
ORGANISM: Homo sapiens
US-09-205-258-1150

Query Match 43.7%; Score 666; DB 4; Length 228;
Best Local Similarity 91.9%; Pred. No. 1.6e-60;
Matches 124; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 51 ETRIIRGECRPHSGPQMAAFEEKTRILGATLLAPRLLTAHRLKRYIVHGOHMLQ 110
|||||
DB 1 ETRIIRGECRPHSGPQMAAFEEKTRILGATLLAPRLLTAHRLKRYIVHGOHMLQ 60
QY 111 KEEGCEQRTATESPHPGFNNSLPKNDHRNDIMLVKASPVSLTMAVRPLTSSRCVTA 170
|||||
DB 61 KEEGCEQRTATESPHPGFNNSLPKNDHRNDIMLVKASPVSLTMAVRPLTSSRCVTA 120
QY 171 GTSCILSGWGSTSSP 185
|||||
DB 121 GTSCSPFAGARPP 135

RESULT 11
US-09-996-243-309
Sequence 309, Application US/09996243
Patent No. 6478825
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kiljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730P1C13
CURRENT APPLICATION NUMBER: US/09/996,243
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
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PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11


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ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0227 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 55527
US-08-807-151-5

Query Match          39.7%; Score 604.5; DB 3; Length 263;
Best Local Similarity 43.0%; Pred. No. 4e-54;
Matches 11; Conservative 49; Mismatches 85; Indels 13; Gaps 3;

QY 38 LILLALATGIVG---ETRIKGFCKPHSQPQALFEKTRILCGATLIAPRWLITAA 93
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 5 ILFLALFLGIDAPPVQSRILIGFNCCKNSQPMHVAAYRFARYCGGVLLDANWVLTAA 64
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 94 HCLAKPRYIHLGQHNLOKEEGCEQRTATSPFHPGFNNSLPNKDH-----RNDIML 145
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 65 HCYNDRYQVWLGNKNNFEDEPSAQHOLISKAIPHGFNNSLNKKDTPHPEDDYSDML 124
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 146 VKNASPVSTWAVRPLTISRCTAGTSCILSGWGSTS-SPOLRLPHTLRCAITIIHQ 204
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 125 VRLKRAEITDVYKPIIDLPTEPTVSRCLASGWSSTPTEPEYSHDLCVYLELSNE 184
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 205 KENAYPGNITDVMVCAVQEGGKDSQGDGSGPLVNCNLSLQIISWGDDPCAITRRPGV 264
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 185 VCAKAHTEKVTDMLCAGEWDGKDTGVGSLICDGLGITSWGPICALPVPPI 244
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 265 YTKVCKYVDMIOETMKN 282
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 245 YTKLIEYRSWIKDVANN 262
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 15
US-09-210-084-5
; Sequence 5, Application US/09210084
; Patent No. 6197511
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,084
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,874
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 55527
US-09-210-084-5

Query Match          39.7%; Score 604.5; DB 3; Length 263;
Best Local Similarity 43.0%; Pred. No. 4e-54;
Matches 11; Conservative 49; Mismatches 85; Indels 13; Gaps 3;

QY 38 LILLALATGIVG---ETRIKGFCKPHSQPQALFEKTRILCGATLIAPRWLITAA 93
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 5 ILFLALFLGIDAPPVQSRILIGFNCCKNSQPMHVAAYRFARYCGGVLLDANWVLTAA 64
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 94 HCLAKPRYIHLGQHNLOKEEGCEQRTATSPFHPGFNNSLPNKDH-----RNDIML 145
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 65 HCYNDRYQVWLGNKNNFEDEPSAQHOLISKAIPHGFNNSLNKKDTPHPEDDYSDML 124
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 146 VKNASPVSTWAVRPLTISRCTAGTSCILSGWGSTS-SPOLRLPHTLRCAITIIHQ 204
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 125 VRLKRAEITDVYKPIIDLPTEPTVSRCLASGWSSTPTEPEYSHDLCVYLELSNE 184
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 205 KENAYPGNITDVMVCAVQEGGKDSQGDGSGPLVNCNLSLQIISWGDDPCAITRRPGV 264
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 185 VCAKAHTEKVTDMLCAGEWDGKDTGVGSLICDGLGITSWGPICALPVPPI 244
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 265 YTKVCKYVDMIOETMKN 282
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 245 YTKLIEYRSWIKDVANN 262
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Search completed: October 15, 2003, 20:59:16
Job time : 16.0039 secs
```

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 15, 2003, 21:05:33 ; Search time 253.648 Seconds

(without alignments)
2342.665 Million cell updates/sec

Title: US-09-856-320a-2_COPY_54_282
Perfect score: 1258
Sequence: 1 IIKGPECKPHSQPMQALFE.....GVYTKCKYVDWIOETMKN 229

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1731049 seqs, 1297405648 residues

Total number of hits satisfying chosen parameters: 3462098

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-O=/cg2_1/USPTO_spool_P/US09855320/rnatat_15102003.105827.10080/app.query.fasta_1.846
-DB=Published Applications NA -OFMT=fasta -SUFFIX=rnpb -MINMATCH=0.1
-LOOEXT=0 -LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62
-TRANS=human40.cdi -LIST=43 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09855320.@CGN_1_1.129.@rnatat_15102003.105827.10080
-NCPU=6 -ICPU=3 -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA:
1: /cg2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cg2_6/ptodata/1/pubpna/PCIT_NEM_PUB.seq:*
3: /cg2_6/ptodata/1/pubpna/US06_NEM_PUB.seq:*
4: /cg2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cg2_6/ptodata/1/pubpna/PCITUS_PUBCOMB.seq:*
6: /cg2_6/ptodata/1/pubpna/PCITUS_PUBCOMB.seq:*
7: /cg2_6/ptodata/1/pubpna/US08_NEM_PUB.seq:*
8: /cg2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cg2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cg2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cg2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cg2_6/ptodata/1/pubpna/US09_NEM_PUB.seq:*
13: /cg2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cg2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cg2_6/ptodata/1/pubpna/US10_NEM_PUB.seq:*
16: /cg2_6/ptodata/1/pubpna/US60_NEM_PUB.seq:*
17: /cg2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match length	DB ID	Description
1	1258	100.0	1186 14	US-10-205-823-211 Sequence 211, App

2	1258	100.0	1204	11	US-09-946-374-169	Sequence 169, App
3	1258	100.0	1204	12	US-10-015-387A-169	Sequence 169, App
4	1258	100.0	1204	12	US-10-137-870-505	Sequence 505, App
5	1258	100.0	1204	12	US-10-140-018-505	Sequence 505, App
6	1258	100.0	1204	12	US-10-140-021-505	Sequence 505, App
7	1258	100.0	1204	12	US-10-140-274-505	Sequence 505, App
8	1258	100.0	1204	12	US-10-140-471-505	Sequence 505, App
9	1258	100.0	1204	12	US-10-140-807-505	Sequence 505, App
10	1258	100.0	1204	12	US-10-140-924-505	Sequence 505, App
11	1258	100.0	1204	12	US-10-140-924-505	Sequence 505, App
12	1258	100.0	1204	12	US-10-140-976-505	Sequence 505, App
13	1258	100.0	1204	12	US-10-141-658-505	Sequence 505, App
14	1258	100.0	1204	12	US-10-141-702-505	Sequence 505, App
15	1258	100.0	1204	12	US-10-141-704-505	Sequence 505, App
16	1258	100.0	1204	12	US-10-142-421-505	Sequence 505, App
17	1258	100.0	1204	12	US-10-142-432-505	Sequence 505, App
18	1258	100.0	1204	12	US-10-142-767-505	Sequence 505, App
19	1258	100.0	1204	12	US-10-143-033-505	Sequence 505, App
20	1258	100.0	1204	12	US-10-144-994-505	Sequence 505, App
21	1258	100.0	1204	12	US-10-145-628-505	Sequence 505, App
22	1258	100.0	1204	12	US-10-145-631-505	Sequence 505, App
23	1258	100.0	1204	12	US-10-145-633-505	Sequence 505, App
24	1258	100.0	1204	12	US-10-145-746-505	Sequence 505, App
25	1258	100.0	1204	12	US-10-145-748-505	Sequence 505, App
26	1258	100.0	1204	12	US-10-145-823-505	Sequence 505, App
27	1258	100.0	1204	12	US-10-145-826-505	Sequence 505, App
28	1258	100.0	1204	12	US-10-145-870-505	Sequence 505, App
29	1258	100.0	1204	12	US-10-145-876-505	Sequence 505, App
30	1258	100.0	1204	12	US-10-147-504-505	Sequence 505, App
31	1258	100.0	1204	12	US-10-147-506-505	Sequence 505, App
32	1258	100.0	1204	12	US-10-147-510-505	Sequence 505, App
33	1258	100.0	1204	12	US-10-146-725-505	Sequence 505, App
34	1258	100.0	1204	12	US-10-146-795-505	Sequence 505, App
35	1258	100.0	1204	12	US-10-147-495-505	Sequence 505, App
36	1258	100.0	1204	12	US-10-147-501-505	Sequence 505, App
37	1258	100.0	1204	12	US-10-147-504-505	Sequence 505, App
38	1258	100.0	1204	12	US-10-147-509-505	Sequence 505, App
39	1258	100.0	1204	12	US-10-147-510-505	Sequence 505, App
40	1258	100.0	1204	12	US-10-147-511-505	Sequence 505, App
41	1258	100.0	1204	12	US-10-147-529-505	Sequence 505, App
42	1258	100.0	1204	12	US-10-151-397-505	Sequence 505, App
43	1258	100.0	1204	12	US-10-151-566-505	Sequence 505, App
44	1258	100.0	1204	12	US-10-158-783-505	Sequence 505, App
45	1258	100.0	1204	12	US-10-158-786-505	Sequence 505, App

ALIGNMENTS

RESULT 1
US-10-205-823-211
; Sequence 211, Application US/10205823
; Publication No. US20030108963A1
GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbatcheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wansley, Angela M.
; APPLICANT: Glat, Xumel
; APPLICANT: Zhao, Xumel
; APPLICANT: Anderson, Dustin
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-044
CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314,356

; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 211
; LENGTH: 1186
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-203-823-211

Alignment Scores:
Pred. No.: 1,2e-134 Length: 1186
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-856-320a-2_COPY_54_282 (1-229) x US-10-203-823-211 (1-1186)

QY 1 ILeIleIySGLyPheGLyCysLysProHISerGlnProTrrpGlnAlaAlaLeuPheGlu 20
DB 185 ATCTCTCAAGGGGTTGAGTCCAGCCCTCACTCCAGCCCTGGCAGCAGCCCTGTTCGAG 244
QY 21 LysThrIrgLeuLeuGlyAlaThrLeuIleAlaProArgrTrrLeuLeuThrAlaAla 40
DB 245 AAGAGCGGGCTACTCTGTGGGGCAGCCCTCATCCGCCCAAGATGGCTGTGACAGCAGCC 304
QY 41 HIsCysLeuLysProArgrTrrIleValHIsLeuGlyLInHIsAsnLeuGlnLysGlu 60
DB 305 CACTGGCTCAAGCCCGCTCATATAGTTCACCTGGGGCAGACAACTCCGAAGAGGAGAG 364
QY 61 GLyCysGluGlnThrArgrTrrAlaThrGlnSerPheProHISProGlyPheAsnAsnSer 80
DB 365 GGGCTGTAGAGCAGACCCGAGCAGCCAGTCTCTCCCAACCCCGGCTTCACACAGC 424
QY 81 LeuProHISLysAspHISArgrAsnAspIleMetLeuValLysMetAlaSerProValSer 100
DB 425 CTCCCAACAAAGACCCCAATGACATGATGCTGTGAAGATGGATGCCAGTCTCC 484
QY 101 ILeThrTrrAlaValArgrProLeuThrLeuSerSerArgrCysValThrAlaGlyThrSer 120
DB 485 ATCACTGGGGCTGTGGCAGCCCTCACCTCTCTGACGCTGTGTCACACTGGTGGCAGCAGC 544
QY 121 CysLeuIleSerGlyTrrpGlySerThrSerSerProGlnLeuArgrLeuProHISThrLeu 140
DB 545 TGGCTCAATTCGCGCTGGGCGACACCTCCAGCCCGGCTTACGCTTCACACCTTG 604
QY 141 ArgrCysAlaAsnIleThrIleIleGlnHIsGlnLysCysGlnAsnAlaTrrProGlyAsn 160
DB 605 CGATGGCCCAACATCAACCATCATTTGACACACAGAGTGTAGAAGCGCTTACCCCGGAGC 664
QY 161 ILeThrAspThrMetValCysAlaSerValGlnGluLysLysAspSerCysGlnGly 180
DB 665 ATCAAGACACATGAGTGTGGCAGGCTCAGAAAGGGGGAAGAGACTCTGTCAGAGGT 724
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrrpGlyGln 200
DB 725 GACTCGGGGGCCCTCGCTGTAAACCACTCTTCMAAGCATTAATCTCGGGGCGAG 784
QY 201 AspProCysAlaIleThrArgrLysProGlyValTrrThrLysValCysLysTrrValAsp 220
DB 785 GATCCGCTGCTCGATCAACCCCAAGCCGTGGTGTCTACAGAAAGTGTGCAATATGTGGAC 844
QY 221 TrrpIleGlnGluThrMetLysAsnAsn 229
DB 845 TGGATCCAGAGAGCATGAAGAACAT 871

RESULT 2
US-09-946-374-169
; Sequence 169, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1c1
; CURRENT APPLICATION NUMBER: US/09/946,374
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15

PRIOR APPLICATION NUMBER: 60/100388
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100390
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100584
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100661
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100662
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100664
PRIOR FILING DATE: 1998-09-16
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PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100684
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PRIOR APPLICATION NUMBER: 60/100710
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100711
PRIOR FILING DATE: 1998-09-17
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PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102484

PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102487
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102570
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PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102684
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PRIOR APPLICATION NUMBER: 60/102687
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/102965
PRIOR FILING DATE: 1998-10-02
PRIOR APPLICATION NUMBER: 60/103258
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 60/103314
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103315
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PRIOR APPLICATION NUMBER: 60/103328
PRIOR FILING DATE: 1998-10-07
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PRIOR APPLICATION NUMBER: 60/104257
PRIOR FILING DATE: 1998-10-14
PRIOR APPLICATION NUMBER: 60/104987
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105000
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105002
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105104
PRIOR FILING DATE: 1998-10-21
PRIOR APPLICATION NUMBER: 60/105169
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105266
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105693
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105694
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105807

Alignment Scores:

Pred. No.:	1,23e-134	Length:	1204
Score:	1258.00	Matches:	229
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	11	Gaps:	0

US-09-856-320a-2_COPY_54_282 (1-229) x US-09-946-374-169 (1-1204)

QY 1 lletllysglypnehlucyslysefrohissertglnptpglnalalauleuphecln 20
|||||
DB 169 ATCATCAGGGGTTGAGTGCAGGCTCCTGAGCCCTGAGGAGCCCTGTGAG 228
QY 21 llystratgleuleucysgclyalathreullealapfoatgtrpleuleuthralala 40
|||||

APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C155
CURRENT APPLICATION NUMBER: US/10/137,870
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 505
LENGTH: 1204
TYPE: DNA
ORGANISM: Homo Sapien
US-10-137-870-505

Alignment Scores:
Pred. No.: 1,236-134 Length: 1204
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-856-320a-2_COPY_54_282 (1-229) x US-10-137-870-505 (1-1204)

QY 1 ILEIETLYSGLYPHGLUCYSYSPROHISERGINPROTRPGINLAALALEUPHEGLU 20
DB 169 ATCATCAAGGGGTTGAGTGCAGAGCTCCAGCCCTGGCAGGAGCCCTGTTCCAG 228
QY 21 LYSTHARGLEULEUCYSGLYALATHRLEULEALAPROATGTRPLEULEUTHRALA 40
DB 229 AAGAGCGGCTACTCTGTGGGCGAGCTCAGCTCCGCGGAGTGCTCTCGACACACCC 288
QY 41 HISCYSEULYSPROATGYRILEVALHISLEUGLYGNHISASINLEUGLINYSGLUGLU 60
DB 289 CACGTGCTCAAGCCCGCTACATAGTTCACCTGGGGCGAGCAACCTCCAGAGAGAGAG 348
QY 61 GLYCSGLUGINTHARGTRHIALATHRGLUSERPHEPROHISPROGLYPHEASNASNSER 80
DB 349 GGCTGTGAGCAGACCCGCGAGCCACTGATCTTCCGCCACCCGCTTCAACACAGC 408
QY 81 LEUPROASNLYSASPHISARGASNASPILLEMETLEUVALYSEMETALASERPROVALSER 100
DB 409 CTCCCAACAAAGACACCCGCAATGACATGCTGTGAAGATGGCATCGCCAGTCTCC 468
QY 101 ILEHTRPALAVALARGPROLEUTHRLEUTHRLEUSERSERARGCYVALTHRALAGLYTHRSER 120
DB 469 ATCAACCTGGGCTGTGGCGAGCCCTCAGCTCTCCAGCTGTGTACGTGGCGACAGC 528
QY 121 CYSLEULEISERGLYTPGLYSERTHRSERSETPROGLINLEUATGLENUPROHISTHREU 140
DB 529 TGCTTCATTTCCGGCTGGGGCGAGCAGTCCAGCCCGCTTAACGGCTCTCCACACCTTG 588
QY 141 ARGCSALASANIETHRIEILEGLIHISGLINYSYSGIUASALATYRPROGLYSN 160
DB 589 CGATGCCCAACATCACCATCATTTGAGCAGACAGAGTGTGAAGAGCGCTTACCCGCGAC 648
QY 161 ILEHTRAPTHRMETVALCYASLASERVALGINGLUGLYLYASPSERCYSGINGLY 180
DB 649 ATCAACAGACACCATGTTGTGCCAGGCTGCAGAGGAGGAGGAGGAGGAGGAGGAGG 708
QY 181 ASPERGGLYGLYPROLEUVALCYASNSGINSERLEUGINGLYLIELESERTTPGLYN 200
DB 709 GACTCCGGGGGCGCTGTGGTGTGAACAGTCTTCAAGGCAATTATCTCTGGGGCCAG 768
QY 201 ASPROCYSAIAIETHARGLYSPROGLYVALTYRTHRLYSVALCYLSYSTYRVALASP 220

DB 769 GATCCGTGTGCATACCCGGAAGCCGTGTCTACACGAGAAAGTCTCAAAATATGTGAC 828
QY 221 TRPILEGINGLUETHRMETLYSASNSN 229
DB 829 TGGATCCAGAGACGATGAGAACAT 855

RESULT 5
US-10-140-018-505
Sequence 505, Application US/10140018
Publication No. US20030138885A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Flvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C158
CURRENT APPLICATION NUMBER: US/10/140,018
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 505
LENGTH: 1204
TYPE: DNA
ORGANISM: Homo Sapien
US-10-140-018-505

Alignment Scores:
Pred. No.: 1,236-134 Length: 1204
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-856-320a-2_COPY_54_282 (1-229) x US-10-140-018-505 (1-1204)

QY 1 ILEIETLYSGLYPHGLUCYSYSPROHISERGINPROTRPGINLAALALEUPHEGLU 20
DB 169 ATCATCAAGGGGTTGAGTGCAGAGCTCCAGCCCTGGCAGGAGCCCTGTTCCAG 228
QY 21 LYSTHARGLEULEUCYSGLYALATHRLEULEALAPROATGTRPLEULEUTHRALA 40
DB 229 AAGAGCGGCTACTCTGTGGGCGAGCTCATCGCCCGCAATGCTCTCGACAGCAGC 288
QY 41 HISCYSEULYSPROATGYRILEVALHISLEUGLYGNHISASINLEUGLINYSGLUGLU 60
DB 289 CACGTGCTCAAGCCCGCTACATAGTTCACCTGGGGCGAGCAACCTCCAGAGAGAGAG 348
QY 61 GLYCSGLUGINTHARGTRHIALATHRGLUSERPHEPROHISPROGLYPHEASNASNSER 80
DB 349 GGCTGTGAGCAGACCCGCGAGCCACTGAGTCTTCCGCCACCCGCTTCAACACAGC 408
QY 81 LEUPROASNLYSASPHISARGASNASPILLEMETLEUVALYSEMETALASERPROVALSER 100
DB 409 CTCCCAACAAAGACACCCGCAATGACATGCTGTGAAGATGGCATCGCGAGTCTCC 468
QY 101 ILEHTRPALAVALARGPROLEUTHRLEUTHRLEUSERSERARGCYVALTHRALAGLYTHRSER 120

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Db      469 ATACCTGGGCTGTGGACCCCTCACCCCTCTCTCACGCTGTGTCTACTGCTGGCACCAGC 528
QY      121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
      |||
Db      529 TGCCCTATTTCGCGCTGGGCGACAGCTCCAGCCCGAGTTACGCGCTCTCACACCTTG 588
QY      141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsn 160
      |||
Db      589 CGATGGGCGCAACATCACCATCATTTAGACACAGAAAGTGTAGAACCGCTCCCGCGGCAC 648
QY      161 IleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly 180
      |||
Db      649 ATACACAGACACCATGTGCTGTCCAGCGTCCAGAAAGGGGCAAGACTCTCTCCAGCGT 708
QY      181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
      |||
Db      709 GACTCCGGGGCCCTGTGCTGTAAACCACTCTTCAAGCAATTATCTCTGGGGCCAG 768
QY      201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220
      |||
Db      769 GATCCGCTGTCGATCACCCCAAGCCGTGTCTACAGAAAGTCTGCAAAATATGTGGAC 828
QY      221 TrpIleGlnGlnIuThrMetLysAsnAsn 229
      |||
Db      829 TGGATCCAGGAGACGATGAAGAACAAAT 855

RESULT 6
US-10-140-021-505
; Sequence 505, Application US/10140021
; Publication No. US2003013886A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C167
; CURRENT APPLICATION NUMBER: US/10/140,021
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-021-505

Alignment Scores:
Pred. No.:      1,23e-134      Length:      1204
Score:          1258.00      Matches:      229
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     100.00%      Indels:      0
DB:              12          Gaps:          0

US-09-856-320a-2_COPY_54_282 (1-229) x US-10-140-021-505 (1-1204)
QY      1 IleIleLysGlyIleGlyGlyCysLysProHisSerGlnProTrpGlnIleAlaLeuPheGln 20
      |||

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Db      169 ATCATCAAGGGGTTCGAGTGCAGCAAGCTCACTCCAGCCCTGGCAGGACGCCCTGTTCAG 228
QY      21 LysThrArgLeuLeuGlyCysGlyAlaThrLeuIleAlaProArgTrpLeuThrAlaAla 40
      |||
Db      229 AAGACGGCGCTACTCTGTGGGGGAGCGCTATATGCCCCCGAGATGGCTCTCGACAGCACC 288
QY      41 HisCysLeuLysProArgTyrIleValHisLeuGlnGlnHisAsnLeuGlnLysGlnGln 60
      |||
Db      289 CACTGCGCTCAAGCCCGCTCATATGATTCACCTGGGGGAGCACAACCTCCAGAAAGAGAG 348
QY      61 GlyCysGlnGlnIuThrArgThrAlaThrGlnLysSerPheProHisProGlyPheAsnAsnSer 80
      |||
Db      349 GCGCTGTAGAGAGACCGCGAGACGCACTGATCTCTCCCGACCCGCGCTTCAACCAACAG 408
QY      81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
      |||
Db      409 CTCGCCACACAAACACACCGCATATGACATATCTGTGTGAAGTGGCARTGCCAGTCTCC 468
QY      101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
      |||
Db      469 ATACCTGGGCTGTGGACCCCTCACCCCTCTCTCACAGCTGTCTACACTGCTGGCACCAG 528
QY      121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
      |||
Db      529 TGCCCTATTTCGCGCTGGGCGACAGCTCCAGCCCGAGTTACGCGCTCTCACACCTTG 588
QY      141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsn 160
      |||
Db      589 CGATGGGCGCAACATCACCATCATTTAGACACAGAAAGTGTAGAAAGCGCTTACCCCGCAC 648
QY      161 IleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly 180
      |||
Db      649 ATCACAGACACCATGTGCTGTCCAGCGTCCAGAAAGGGGCAAGACTCTCTCCAGCGGT 708
QY      181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
      |||
Db      709 GACTCCGGGGCCCTGTGCTGTAAACCACTCTTCAAGCAATTATCTCTGGGGCCAG 768
QY      201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220
      |||
Db      769 GATCCGCTGTCGATCACCCCAAGCCGTGTCTACAGAAAGTCTGCAAAATATGTGGAC 828
QY      221 TrpIleGlnGlnIuThrMetLysAsnAsn 229
      |||
Db      829 TGGATCCAGGAGACGATGAAGAACAAAT 855

RESULT 7
US-10-140-274-505
; Sequence 505, Application US/10140274
; Publication No. US2003014367A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C161
; CURRENT APPLICATION NUMBER: US/10/140,274
; CURRENT FILING DATE: 2002-05-06

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Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 505
 ; LENGTH: 1204
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-140-274-505

Alignment Scores:
 Pred. No.: 1,236-134 Length: 1204
 Score: 1258.00 Matches: 229
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-09-856-320a-2_copy_54_282 (1-229) x US-10-140-274-505 (1-1204)

Qy 1 llellelysglyphneglucyslyspromisserginprotrpglnalaleupheglu 20
 Db 169 ATCATCAAGGGGTTGAGTGCAGAGCTCCAGCCCTGGCAGGAGCCCTGTTCCAG 228
 Qy 21 lysthrargleuleucysglyalathrleullealaproargtrpleuethralaia 40
 Db 229 AAGAGCGCGCTACTCTGTGGGGCAGCGCTCATCGCCCAATGGCTCTGTACAGCAGCC 288
 Qy 41 Hiscysleuysproargtyrillevalhisleuglylnhisasnleuglnlysglu 60
 Db 289 CACTGCCCTCAAGCCCCCTACATAGTTCACCTGGGGCAGCAACCTCCAGAGAGAGAG 348
 Qy 61 glycsygluglnthrarqthralthrleugluserpheprohissprogllypheasnanser 80
 Db 349 GCGTGTGAGCAGCCCGGAGCAGCACTGATCTTCCGCCCAAGGCTTCAACAGCAGC 408
 Qy 81 leuproasnlysaaphisargasnaspillemetleuvalysmetalaaserprovalser 100
 Db 409 CTCCCAACAAAGACACCCGCAATGACATCATGCTGGGAAGATGGCATCCGCACTGCC 468
 Qy 101 llethrtpralavalarqproleuthrleuserserargcysvalthrilaaglythrser 120
 Db 469 ATCACAGTGGCGTGTGGCAGCCCTCAGCTCCAGCTGTCAGTGTGGCAGCAGC 528
 Qy 121 cystleuileserglytrpglyserthrserserproglinleuaglleuprohisthrleu 140
 Db 529 TGCCATATTTCCGGCTGGGGCAGCAGCTCCAGCCCTGACCTGCTCCACAGCTTGG 588
 Qy 141 argcysalaasnillethrilleleuglnhislyscysgluasnalatyrproglyasn 160
 Db 589 CGATGCGCCACATCACCATCATTTGAGCAGCAGAAAGTGTGAAGACGCTTACCCGGCAGC 648
 Qy 161 llethraspthrmctvalcysalaservaleinglnuglylylsaspserscysglnly 180
 Db 649 ATCACAGACACCATGAGTGTGGCCAGCGCTGCAGAGAGGGGGCAGAGACTCTGCCAGGCT 708
 Qy 181 asperglyglyproleuvalcysasnnglnserleuglnlyllelesertrpglyln 200
 Db 709 GACTCCGGGGGCGCTGTGGTGTGTACACAGCTCTTCAAGGCAATATCTCTGGGGCCAG 768
 Qy 201 asprrocysalailethrarqthrlyspromisserginprotrpglnalaleupheglu 220
 Db 769 GATCGCGTGTGAGTGCAGCAGCAGAAAGCTGTGTACAGAAAGTGTGCAATATGTGGAC 828
 Qy 221 trpilleglnlunthrmctlysasnasn 229
 Db 829 TGGATCCAGAGAGAGATGAAGACAAT 855

RESULT 8
 US-10-140-471-505
 ; Sequence 505, Application US/10140471
 ; Publication No. US2003013887A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen

APPLICANT: DeForge, Laura
 APPLICANT: Desnoyers, Luc
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Sherwood, Steven
 APPLICANT: Smith, Victoria
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3330R1C13
 CURRENT APPLICATION NUMBER: US/10/140,471
 PRIOR APPLICATION: 2002-05-06
 PRIOR APPLICATION: 2002-05-06
 NUMBER OF SEQ ID NOS: 550
 SEQ ID NO 505
 LENGTH: 1204
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-10-140-471-505

Alignment Scores:
 Pred. No.: 1,236-134 Length: 1204
 Score: 1258.00 Matches: 229
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-09-856-320a-2_copy_54_282 (1-229) x US-10-140-471-505 (1-1204)

Qy 1 llellelysglyphneglucyslyspromisserginprotrpglnalaleupheglu 20
 Db 169 ATCATCAAGGGGTTGAGTGCAGAGCTCCAGCCCTGGCAGGAGCCCTGTTCCAG 228
 Qy 21 lysthrargleuleucysglyalathrleullealaproargtrpleuethralaia 40
 Db 229 AAGAGCGCGCTACTCTGTGGGGCAGCGCTCATCGCCCAATGGCTCTGTACAGCAGC 288
 Qy 41 Hiscysleuysproargtyrillevalhisleuglylnhisasnleuglnlysglu 60
 Db 289 CACTGCCCTCAAGCCCCCTACATAGTTCACCTGGGGCAGCAACCTCCAGAGAGAGAG 348
 Qy 61 glycsygluglnthrarqthralthrleugluserpheprohissprogllypheasnanser 80
 Db 349 GCGTGTGAGCAGCCCGGAGCAGCACTGATCTTCCGCCCAAGGCTTCAACAGCAGC 408
 Qy 81 leuproasnlysaaphisargasnaspillemetleuvalysmetalaaserprovalser 100
 Db 409 CTCCCAACAAAGACACCCGCAATGACATCATGCTGGGAAGATGGCATCCGCACTGCC 468
 Qy 101 llethrtpralavalarqproleuthrleuserserargcysvalthrilaaglythrser 120
 Db 469 ATCACAGTGGCGTGTGGCAGCCCTCAGCTCCAGCTGTCAGTGTGGCAGCAGC 528
 Qy 121 cystleuileserglytrpglyserthrserserproglinleuaglleuprohisthrleu 140
 Db 529 TGCCATATTTCCGGCTGGGGCAGCAGCTCCAGCCCTGACCTGCTCCACAGCTTGG 588
 Qy 141 argcysalaasnillethrilleleuglnhislyscysgluasnalatyrproglyasn 160
 Db 589 CGATGCGCCACATCACCATCATTTGAGCAGCAGAAAGTGTGAAGACGCTTACCCGGCAGC 648
 Qy 161 llethraspthrmctvalcysalaservaleinglnuglylylsaspserscysglnly 180
 Db 649 ATCACAGACACCATGAGTGTGGCCAGCGTGCAGAGAGGGGGCAGAGACTCTGCCAGGCT 708

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OY 181 AspSerGlyProLeuValCysAsnGlnSerLeuGlnIleIleSerTrpGlyGln 200
DB 709 GACTCCGGGGGCCCTCTGGTGTCAAGCAGCTCTTCAAGCAGCTATATCTCTGGGGCCAG 768
OY 201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220
DB 769 GATCCGGGTGCGATCAACCCGAAAGCCGTGTCTACAGAAAGTGTGCAATAATGTGGAC 828
OY 221 TrpIleGlnIuThrMetLysAsnAsn 229
DB 829 TGGATCCAGGAGACGATGAAGAACAAAT 855

RESULT 9
US-10-140-807-505
; Sequence 505, Application US/10140807
; Publication No. US20030134354A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C174
; CURRENT APPLICATION NUMBER: US/10/140,807
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Saplen
US-10-140-807-505

Alignment Scores:
Pred. No.: 1,23e-134 Length: 1204
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-856-320a-2_copy_54_282 (1-229) x US-10-140-807-505 (1-1204)
OY 1 IleIleIleGlyheGlyCysLysProHisSerGlnProTrpGlnAlaIleAsnheGlu 20
DB 169 ATCATCAAGGGGTTCGAGTCAAGCCCTCACTCCAGCCCTGGAGGAGGAGCCGTGTGAG 228
OY 21 LysThrArgLeuLeuGlyAlaThrIleAlaProArgTrpLeuLeuThrAlaAla 40
DB 229 AAGACGGGCTACTGTGTGGGGGAGCGCTCATGCCCCCGAATGGCTCTCGAAGCAGCC 288
OY 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60
DB 289 CACTGCGCTCAAGCCCGGCTACATAGTTCACCTGGGAGCAGCAACCTCGAAGAGAGAG 348
OY 61 GlyCysGlnGlnIuThrArgThrAlaThrGlnUserPheProHisProGlyPheAsnAsnSer 80
DB 349 GGCTGTGAGCAGACCCGGAGCAGCCACTGAGTCTTCCGCCACCCGGCTTCAACACAGC 408
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OY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
DB 409 CTCGCCCAACAAGACCAACCGCATATGATCATGCTGTGAATGGATGGCCAGTCTCC 468
OY 101 IleThrTrpAlaValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
DB 469 ATCAACCGGGCTGTGGCAGCCCTCACCCCTCTCTCACAGCTGTGTACATGCTGTGGCAGCC 528
OY 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
DB 529 TGGCTCATTTCCGGCTGTGGGAGCAGCAGCTCCAGCCCCAGTAGCCCTGACACTTG 568
OY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsn 160
DB 589 CGATGGCCCAACATACCATCATATGAGCAGCAGAAAGTGTGAGAAGCGCTACCCGGGAC 648
OY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly 180
DB 649 ATCAGACAGACCATGTGTGTGCAGGCTCAGAGAGGGGCAAGGACTCTCCAGGGT 708
OY 181 AspSerGlyProLeuValCysAsnGlnSerLeuGlnIleIleSerTrpGlyGln 200
DB 709 GACTCCGGGGGCCCTCTGGTGTCAAGCAGCTCTTCAAGCAGCTATATCTCTGGGGCCAG 768
OY 201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220
DB 769 GATCCGGGTGCGATCAACCCGAAAGCCGTGTCTACAGAAAGTGTGCAATAATGTGGAC 828
OY 221 TrpIleGlnIuThrMetLysAsnAsn 229
DB 829 TGGATCCAGGAGACGATGAAGAACAAAT 855

RESULT 10
US-10-140-922-505
; Sequence 505, Application US/10140922
; Publication No. US2003013889A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C179
; CURRENT APPLICATION NUMBER: US/10/140,922
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Saplen
US-10-140-922-505

Alignment Scores:
Pred. No.: 1,23e-134 Length: 1204
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-856-320a-2_copy_54_282 (1-229) x US-10-140-924-505 (1-1204)

```
OY 1 llellelysglypbglnucyslyspromhisserginprotrpdlalalaleuphegiu 20
DB 169 atcattcaagggttgagtgcaagcctcactcccaagccctggcagacacccctgttcgag 228
OY 21 lysthrargileuencysglyalathrleuilealproargtrpleuethralaia 40
DB 229 aagacggcgctactgtgtggcgacgctcattcccccagatggcttcttgacacagcc 288
OY 41 hiscysleuylspproargtrylevalhisleuglyglnhisasnleuglnlysglugu 60
DB 289 cactcctccaaacccccggtactacgttcacctgggggacacaaacctcagaaggagag 348
OY 61 glycysgluglnthrargthrleathrghuserpheprohisproglypheasnanser 80
DB 349 ggccttgagcacacccgggacagcactgactcttccccacccggccttcaaacacacg 408
OY 81 leuproasnlyasphhisargasnaspillemleuvallysmetalaserprovalser 100
DB 409 ctcccccaaaagacacccgcaatgacatcattgctgtaaatgagcattggcagctctcc 468
OY 101 lletthrtpalavalargproleuthrleuserserargcysvalthrallgylthrsr 120
DB 469 atcacctggcgctgctgacacccctcactctcctcagcgtgtgctgacagcagc 528
OY 121 cystleuilleserglytrpglyserthrserserproglinleuargleuprohisthrleu 140
DB 529 tgccctcattttccggctgggggacagcgtccacccccagttacgctgctcacccttg 588
OY 141 argcysalaasnillethrillelegluhisglnlyscysgluasnalatyrproglyasn 160
DB 569 cgatcgccgaacatcaccatcatttgacacccagaaagtggagaaagccctaccccgcaac 648
OY 161 lletthrappthmetvalcysalaservalglnuglyglylyaspsersercysglnly 180
DB 649 atcacagacaccatgctgtgtgccagcgtgcagaaagggggacaaagacctgcacaggt 708
OY 181 aspserglyglyproleuvalcysasnnglnserleuglnlylleilesertrpelygin 200
DB 709 gactccggggggccctctgctgtgaacacagctcttcaaggcattatctcggggccag 768
OY 201 aspprocysalaallethrarglysproglyvaltyrthrlyvalcyslystyryalasp 220
DB 769 gatccggtggcgatcaccgaaagccctgtgtctcagaaagctctgcaaaatattgtgac 828
OY 221 trpilleglnluthrmetlysaasn 229
DB 829 tggatccagagacgatgaaagacaat 855
```

RESULT 11

US-10-140-924-505

; Sequence 505, Application US/10140924

; Publication No. US20030134353A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Collin K

; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/140,924
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-140-924-505

Alignment Scores:

Pred. No.:	1,23e-134	Length:	1204
Score:	1258.00	Matches:	229
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-09-856-320a-2_copy_54_282 (1-229) x US-10-140-924-505 (1-1204)

```
OY 1 llellelysglypbglnucyslyspromhisserginprotrpdlalalaleuphegiu 20
DB 169 atcattcaagggttgagtgcaagcctcactcccaagccctggcagacacccctgttcgag 228
OY 21 lysthrargileuencysglyalathrleuilealproargtrpleuethralaia 40
DB 229 aagacggcgctactgtgtggcgacgctcattcccccagatggcttcttgacacagcc 288
OY 41 hiscysleuylspproargtrylevalhisleuglyglnhisasnleuglnlysglugu 60
DB 289 cactcctccaaacccccggtactacgttcacctgggggacacaaacctcagaaggagag 348
OY 61 glycysgluglnthrargthrleathrghuserpheprohisproglypheasnanser 80
DB 349 ggccttgagcacacccgggacagcactgactcttccccacccggccttcaaacacacg 408
OY 81 leuproasnlyasphhisargasnaspillemleuvallysmetalaserprovalser 100
DB 409 ctcccccaaaagacacccgcaatgacatcattgctgtaaatgagcattggcagctctcc 468
OY 101 lletthrtpalavalargproleuthrleuserserargcysvalthrallgylthrsr 120
DB 469 atcacctggcgctgctgacacccctcactctcctcagcgtgtgctgacagcagc 528
OY 121 cystleuilleserglytrpglyserthrserserproglinleuargleuprohisthrleu 140
DB 529 tgccctcattttccggctgggggacagcgtccacccccagttacgctgctcacccttg 588
OY 141 argcysalaasnillethrillelegluhisglnlyscysgluasnalatyrproglyasn 160
DB 569 cgatcgccgaacatcaccatcatttgacacccagaaagtggagaaagccctaccccgcaac 648
OY 161 lletthrappthmetvalcysalaservalglnuglyglylyaspsersercysglnly 180
DB 649 atcacagacaccatgctgtgtgccagcgtgcagaaagggggacaaagacctgcacaggt 708
OY 181 aspserglyglyproleuvalcysasnnglnserleuglnlylleilesertrpelygin 200
DB 709 gactccggggggccctctgctgtgaacacagctcttcaaggcattatctcggggccag 768
OY 201 aspprocysalaallethrarglysproglyvaltyrthrlyvalcyslystyryalasp 220
DB 769 gatccggtggcgatcaccgaaagccctgtgtctcagaaagctctgcaaaatattgtgac 828
OY 221 trpilleglnluthrmetlysaasn 229
DB 829 tggatccagagacgatgaaagacaat 855
```

```
RESULT 12
US-10-140-926-505
; Sequence 505, Application US/10140926
; Publication No. US20030134356A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; FILE REFERENCE: P3330R1C187
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; ACIDS ENCODING THE SAME
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US/10/140,926
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-926-505

Alignment Scores:
Pred. No.: 1,23e-134 Length: 1204
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-856-320a-2_COPY_54_282 (1-229) x US-10-140-926-505 (1-1204)
QY 1 IleIleIleSgIlypHeGluCysLysProHISserGlnProTrrpLlnAlaIaleupheGlu 20
Db 169 ATCATCAAGGGGTTTCAGAGCTCAAGCTCATCTCCAGGCCGCGAGGAGGAGGCTTTCGAG 228
QY 21 LysThrArgLeuLeuGlyGlyAlaIaThrLeuIleAlaIaProArgTrpLeuLeuThrAlaIa 40
Db 229 AAGACCGCGCTACTCTGTGGGGCGAGCGCTCATCGCCCGCCAGATGGCTCTCGACAGAGCC 288
QY 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlu 60
Db 289 CACTGCTCAAGCCCGGCTACATAGTTCACTGGGCGAGCACAACCTCCAGAGAGAGG 348
QY 61 GlyCysGlnGlnIaThrArgThrAlaIaThrGluSerPheProHisProGlyPheAsnAsnSer 80
Db 349 GGCTGTGAGAGACAGCCGAGAGCCACTGAGTCTCTCCCGACCCCGGCTTCAACACAGC 408
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
Db 409 CTCGCCAACAAGACCAACCCCAATGACATCATCTGTGAAATGAGCATCGCACAGTCTCC 468
QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
Db 469 ATACCTGGGGCTGTGGAGCCCTCACCTCTCTCTCAAGCTGTGTCTGTGGACACAGC 528
QY 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
Db 529 TGGCTCATTTCCGGCTGGGGGAGACAGTCCAGCCGCCAGTTACGCTTGCCTCACACCTTGG 568
```

```
QY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaIaIaIaIaIaIa 160
Db 589 CGATGGCCCAACATATCATCATATGAGCAGACAGAGTGTGAGAACGGCTTACCCGGGCAAC 648
QY 161 IleThrAspThrMetValCysAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 180
Db 649 ATCAGACAGACATGAGTGTGTGCGAGGTGCGAGAGAGGGGAGAGACTCTCCAGGGGT 708
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnIleIleIleSerTrpGlyGln 200
Db 709 GACTCCGGGGGCGCCCTCTGGTCTGTACCACTCTCTTACAGGCAATATCTCTGGGGCAG 768
QY 201 AspProCysAlaIaIeThrArgLysProGlyValIaIaIaIaIaIaIaIaIaIaIaIaIa 220
Db 769 GATCCGCTGTCGATCAACCCGAAAGCCGTGTGTCTACAGCAAGAGTGTCAAAATATGTGGAC 828
QY 221 TrpIleGlnGlnThrMetLysAsnAsn 229
Db 829 TGGATCCAGAGAGACGATGAAGAACAT 855

RESULT 13
US-10-141-698-505
; Sequence 505, Application US/10141698
; Publication No. US20030134357A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C206
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US/10/141,698
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-141-698-505

Alignment Scores:
Pred. No.: 1,23e-134 Length: 1204
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-856-320a-2_COPY_54_282 (1-229) x US-10-141-698-505 (1-1204)
QY 1 IleIleIleSgIlypHeGluCysLysProHISserGlnProTrrpLlnAlaIaleupheGlu 20
Db 169 ATCATCAAGGGGTTTCAGAGCTCAAGCTCATCTCCAGGCCGCGAGGAGGAGGCTTTCGAG 228
QY 21 LysThrArgLeuLeuGlyGlyAlaIaThrLeuIleAlaIaProArgTrpLeuLeuThrAlaIa 40
Db 229 AAGACCGCGCTACTCTGTGGGGCGAGCGCTCATCGCCCGCCAGATGGCTCTCGACAGAGCC 288
```

QY 41 H1SCYSLAULYSPROARGTyrTlleValH1SLAUGLYGlnH1SASnLeuGlnInLYSLGlu 60
| | | | |
Db 289 CACTGCCCTCAAGCCCCGCTACATAGTCACTGGGGGACGACCAACCTCAGAAAGAGAG 348
QY 61 GLYCSGLUGlnThrArgThrAlaThrGlnSerPheProH1SProGlyPheAsnAsnSer 80
| | | | |
Db 349 GCGTGTGAGCAGACCCGAGACGCCCTGAGTCTTCCCCACCCGGGCTTCAACCAAGC 408
QY 81 LeuProAsnLYSAspHisArgAsnAspIleMetLeuValLYSMetAlaSerProValSer 100
| | | | |
Db 409 CTCCCAACAAAGAACCCGACCAATGACATGCTGTGAAGATGGATCGGCACTGCC 468
QY 101 IleThrTPALaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
| | | | |
Db 469 ATCACTGGGTGGTGGAGACCCCTCACCTCTCCACCTGTCTACTGTGGCCAGC 528
QY 121 CysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProH1SThrLeu 140
| | | | |
Db 529 TGCCCATTTCCGGGTGGGGGACGACGTCACGCCCTTACGCTTCCCTCACACTTG 588
QY 141 ArgCysAlaAsnIleThrIleIleGlnH1SGLnLYSCysGluAsnAlaTyrProGlyAsn 160
| | | | |
Db 589 CGATCGCCCAACATCACCATTGATGACACCGAAGTGTGAAGAGCGCTACCCGGCAAC 648
QY 161 IleThrAspThrMetValCysAlaSerValGlnGlnLYSLysAspSerCysGlnGly 180
| | | | |
Db 649 ATCAGAGACACCATGTGTGTGCCAGCGTGCAGGAAGGGGCGCAAGACTCTCCAGG 708
QY 181 AspSerGlyLYSProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrPlyGln 200
| | | | |
Db 709 GACTCGGGGGGCCCTGTGTGTGTAACAGTCTCTCAAGGCAATATCTCCGGGGCCAG 768
QY 201 AspProCysAlaIleThrArgLYSProGlyValTyrThrLYSValCysLYSLeTyrValAsp 220
| | | | |
Db 769 GATCCGTGGGATCACCAGAAAGCCGTGTGTCTACAGAAAGTGTGCAAAATATGTGGAC 828
QY 221 TrpIleGlnGlnThrMetLYSAsnAsn 229
| | | | |
Db 829 TGGATCCAGAGACGATGAAGAACAT 855

RESULT 14
US-10-141-702-505
; Sequence 505, Application US/10141702
; Publication No. US20030134358A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria A.
; APPLICANT: Stewart, Daniel
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C208
; CURRENT APPLICATION NUMBER: US/10-141,702
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien

US-10-141-702-505
Alignment Scores:
Pred. No.: 1,23e-134 Length: 1204
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-141-702-505 (1-1204)

QY 1 IleIleLYSGlyPheGlnCysLYSProH1SProGlnAlaAlaLeuPheGln 20
| | | | |
Db 169 ATCATCAAGAGGGGTGGAGTGCAAGGCTCACTCCAGCCCTGGCAGGACCCCTGTTCGAG 228
QY 21 LysThrArgLeuLeuCysGlyValaThrLeuIleAlaProArgTyrLeuThrAlaAla 40
| | | | |
Db 229 AAGACGGGCTACTGTGTGGGGGAGCGTCATCGCCCCAGATGGCTCTCGACACAGCC 288
QY 41 H1SCYSLAULYSPROARGTyrTlleValH1SLAUGLYGlnH1SASnLeuGlnInLYSLGlu 60
| | | | |
Db 289 CACTGCCCTCAAGCCCCGCTACATATTCTACCTGGGGGACGACCAACCTCCAGAAAGAGAG 348
QY 61 GLYCSGLUGlnThrArgThrAlaThrGlnSerPheProH1SProGlyPheAsnAsnSer 80
| | | | |
Db 349 GCGTGTGAGCAGACCCGAGACGCCACTGAGTCTTCCCCACCCGGGCTTCAACCAAGC 408
QY 81 LeuProAsnLYSAspHisArgAsnAspIleMetLeuValLYSMetAlaSerProValSer 100
| | | | |
Db 409 CTCCCAACAAAGAACCCGACCAATGACATCAAGCTGTGAAGATGGATCGGCACTGCC 468
QY 101 IleThrTPALaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
| | | | |
Db 469 ATCACTGGGTGGTGGAGACCCGACCACTGATCTCTCAAGCTGTGTACTGTGGCCAGC 528
QY 121 CysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProH1SThrLeu 140
| | | | |
Db 529 TGCCCATTTCCGGGTGGGGGACGACGTCACCCCTTACGCTTCCCTCACACTTG 588
QY 141 ArgCysAlaAsnIleThrIleIleGlnH1SGLnLYSCysGluAsnAlaTyrProGlyAsn 160
| | | | |
Db 589 CGATCGCCCAACATCACCATTGATGACACCGAAGTGTGAAGAGCGCTACCCGGCAAC 648
QY 161 IleThrAspThrMetValCysAlaSerValGlnGlnLYSLysAspSerCysGlnGly 180
| | | | |
Db 649 ATCAGAGACACCATGTGTGTGCCAGCGTGCAGGAAGGGGCGAAAGACTCTCCAGG 708
QY 181 AspSerGlyLYSProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrPlyGln 200
| | | | |
Db 709 GACTCGGGGGGCCCTGTGTGTGTAACAGTCTCTCAAGGCAATATCTCCGGGGCCAG 768
QY 201 AspProCysAlaIleThrArgLYSProGlyValTyrThrLYSValCysLYSLeTyrValAsp 220
| | | | |
Db 769 GATCCGTGGGATCACCAGAAAGCCGTGTGTCTACAGAAAGTGTGCAAAATATGTGGAC 828
QY 221 TrpIleGlnGlnThrMetLYSAsnAsn 229
| | | | |
Db 829 TGGATCCAGAGACGATGAAGAACAT 855

RESULT 15
US-10-141-704-505
; Sequence 505, Application US/10141704
; Publication No. US20030134359A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C209
CURRENT APPLICATION NUMBER: US/10/141,704
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 505
LENGTH: 1204
TYPE: DNA
ORGANISM: Homo Sapien
US-10-141-704-505

Alignment Scores:

Pred. No.:	1,23e-134	Length:	1204
Score:	1258.00	Matches:	229
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-09-856-320a-2_copy_54_282 (1-229) x US-10-141-704-505 (1-1204)

QY 1 llelelysglypnegiucyslyspnohisserglnprotrpglnalaaleupheglu 20
DB 169 ATCATCAAGGGGTTGAGTGCAGCAAGCCCTCCAGCCCTGGCAGCGCCCTGTTCGAG 228
QY 21 lvsThrargleuencysglylaThrleuilealaproargtrpleuThrAlaAla 40
DB 229 AAGACGGGCTACTCTGTGGGCGACGCTCATCGCCCAAGATGGCTCTGACAGCAGCC 288
QY 41 HiscysleuylsproargtryllevalHisdleuglylnHisaasnleuglnlysglu 60
DB 289 CACTGGCTCAAGCCCGCTACATAGTTCACCTGGGGCAGCACAACCTCCAGAGAGAG 348
QY 61 GlycysgluInThrargThrAlaThrGluSerPhebrohisproglypheasnanser 80
DB 349 GGGTGTAGCAGACCCGAGCAGCCACTGAGTCTTCCCCACCCCGGCTTCAACACAGC 408
QY 81 leuprohisaspHisargasnanserllemetleuValylsMetAlaSerProvalSer 100
DB 409 CTCCTCCAAACCAAGCCACCCCAATGACATGCTGGTGAAGATGGCATGCCAGTCTCC 468
QY 101 lleThrTrpAlaValArgProleuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
DB 469 ATCACTGGGGCTGTGGCAGCCCTCACCTCTCTCACGCTGTGTCACTGCTGGCACCAGC 528
QY 121 CysleuileserglytrpglyserThrSerSerProglInleuArgLeuProhisThrLeu 140
DB 529 TGCCTCATTTCCGGCTGGGCGACAGCTCCAGCCCAAGTTAGCCCTGCCCTCACACCTTG 588
QY 141 ArgCysAlaAsnleThrIleleIleGlnHisdleuglylnsnaAlaTyrProglyAsn 160
DB 589 CGATGGCCCAACATCATTCATTTGACACACAGAAAGTGTAGAAAGCGCTTACCCCGCAC 648
QY 161 lleThrAspThrMetValCysAlaSerValGlnGluGlylylYsAspSerCysGlnGly 180
DB 649 ATCAACAGACACCATGGTGTGTGCCAGGCTCAGAGAGGGGCAAGACTCTTGCAGAGGT 708
QY 181 AspSerGlyGlyProleuValCysAsnGlnSerleuGlnGlylleIleSerTrpGlyGln 200
DB 709 GACTCCGGGGGCGCTGTGTGTGAACCACTCTTCAAGCACTTATCTCTGGGGGCCAG 768
QY 201 AspProCysAlaIleThrArgLysProGlyValTyrThrlyValCysLysTyrValAsp 220

DB 769 GATCGGTGGATCACCCGAAAGCTGGTGTCTACAGAAAGTTCGCAAAATATGTGAC 828
QY 221 TrpIleGlnIleThrMetlysAsnAsn 229
DB 829 TGGATCCAGAGAGCATGAAAGAACAT 855

Search completed: October 15, 2003, 23:04:22
Job time : 258.648 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 15, 2003, 20:58:42 ; Search time 63.636 Seconds
(without alignments)
1588.358 Million cell updates/sec

Title: US-09-856-320A-2_COPY_54_282
Perfect score: 1258
Sequence: 1 IIKGPECKPHSQPMQALFE.....GVYTKVCKYVMDIGETMKN 229

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-O=/cgn2.1/USPTO_SPAOL_P/US09856320/rn1at_15102003.105826.10042/app.query.fasta_1.846
-DB-Issued Patents_NA -OEWTF=fastap -SUFFIT=rm1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdt
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pro -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_MMAP -LARGEOBJECT -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents_NA:*

1: /cgn2.6/ptodata/2/ina/5A.COMB.seq:*
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4: /cgn2.6/ptodata/2/ina/6B.COMB.seq:*
5: /cgn2.6/ptodata/2/ina/PCUUS.COMB.seq:*
6: /cgn2.6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1258	100.0	1192	3	US-08-944-483-8 Sequence 8, Appl1
2	1258	100.0	1292	4	US-09-205-258-189 Sequence 189, App
3	1258	100.0	1314	4	US-09-025-059-2 Sequence 2, Appl1
4	1248	99.2	1146	4	US-09-205-258-247 Sequence 247, App
5	1246	99.0	1166	3	US-08-944-483-7 Sequence 7, Appl1
6	1219.5	96.9	1052	4	US-09-386-642-10 Sequence 10, Appl1
7	1213	96.4	833	2	US-08-790-137-2 Sequence 2, Appl1
8	916.5	72.9	618	4	US-09-280-116-3 Sequence 3, Appl1
9	681	54.1	944	3	US-09-070-526-1 Sequence 1, Appl1
10	673	53.5	994	4	US-09-008-271A-19 Sequence 19, Appl1
11	671.5	53.4	1049	4	US-09-386-642-9 Sequence 9, Appl1
12	644.5	51.2	1570	4	US-09-996-243-308 Sequence 308, App

C	13	634.5	50.4	1364	4	US-09-280-116-20	Sequence 20, Appl1
14	631.5	50.2	1476	2	US-08-824-874-2	Sequence 2, Appl1	
15	631.5	50.2	1476	2	US-09-210-084-2	Sequence 2, Appl1	
16	631.5	50.2	1476	2	US-09-764-762-2	Sequence 2, Appl1	
17	577.5	45.9	711	3	US-08-622-046B-13	Sequence 13, Appl1	
18	577.5	45.9	711	3	US-09-100-264-2	Sequence 2, Appl1	
19	577.5	45.9	711	4	US-08-843-076D-2	Sequence 2, Appl1	
20	577.5	45.9	760	3	US-08-768-859A-7	Sequence 7, Appl1	
21	577.5	45.9	760	3	US-08-767-820A-7	Sequence 7, Appl1	
22	577.5	45.9	766	3	US-08-768-859A-9	Sequence 9, Appl1	
23	577.5	45.9	766	3	US-08-767-820A-9	Sequence 9, Appl1	
24	577.5	45.9	766	3	US-08-622-046B-17	Sequence 17, Appl1	
25	577.5	45.9	766	3	US-09-100-264-6	Sequence 6, Appl1	
26	577.5	45.9	766	4	US-08-843-076D-6	Sequence 6, Appl1	
27	577.5	45.9	822	3	US-09-100-264-8	Sequence 8, Appl1	
28	577.5	45.9	832	3	US-08-768-859A-5	Sequence 5, Appl1	
29	577.5	45.9	832	3	US-08-767-820A-5	Sequence 5, Appl1	
30	577.5	45.9	832	3	US-08-622-046B-15	Sequence 15, Appl1	
31	577.5	45.9	832	4	US-08-843-076D-4	Sequence 4, Appl1	
32	577.5	45.9	1341	4	US-08-983-075D-6	Sequence 6, Appl1	
33	577.5	45.9	1358	4	US-08-983-075D-8	Sequence 8, Appl1	
34	577	45.9	732	1	US-08-361-395-2	Sequence 2, Appl1	
35	577	45.9	897	2	US-08-956-267A-1	Sequence 1, Appl1	
36	574.5	45.7	711	3	US-08-622-046B-2	Sequence 2, Appl1	
37	574.5	45.7	766	3	US-08-622-046B-6	Sequence 6, Appl1	
38	574.5	45.7	832	3	US-08-768-859A-20	Sequence 20, Appl1	
39	574.5	45.7	832	3	US-08-767-820A-20	Sequence 20, Appl1	
40	574.5	45.7	832	3	US-08-622-046B-4	Sequence 4, Appl1	
41	573.5	45.6	760	5	PCR-US95-06157-7	Sequence 7, Appl1	
42	573.5	45.6	766	5	PCR-US95-06157-9	Sequence 9, Appl1	
43	573.5	45.6	832	5	PCR-US95-06157-5	Sequence 5, Appl1	
44	570	45.3	1504	4	US-09-280-116-1	Sequence 1, Appl1	
45	564	44.8	825	3	US-09-120-582-1	Sequence 1, Appl1	

ALIGNMENTS

RESULT 1
US-08-944-483-8
; Sequence 8, Application US/08944483
; Patent No. 6232456

GENERAL INFORMATION:
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1192 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-944-483-8

Alignment Scores:
Pred. NO.: 1.85e-123 Length: 1192
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-856-320a-2_COPY_54_282 (1-229) x US-08-944-483-8 (1-1192)

QY 1 llellelysglypnehlucylsProHisSerGlnProTrpGlnAlaLeuPheGlu 20
DB 170 ATCATCAAGGGGTTGAGTGCAGACCTCCAGCCCTGGCAGGAGCCCTTTCGAG 229
QY 21 LysThrArgLeuLeuGlyAlaThrLeuLeuAlaProArgTrpLeuThrAlaAla 40
DB 230 AAGACGGGGTACTCTGTGGGGCGACGCTCATGCCCCAGATGGCTCTGACGACGAGC 289
QY 41 HisGlyLeuLysProArgTrpLleValHisLeuGlyLinhHisLeuGlnLysGluGlu 60
DB 290 CACTGGCTCAAGCCCGCTACATAGTTCACCTGGGGCAGCACAACCTCCGAAAGAGAG 349
QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyIleAsnAsnSer 80
DB 350 GGCTGTAGAGAGACCGGACAGCAGTCCCTCCGCCACCGGGCTTCAACAAAGC 409
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
DB 410 CTCGCCAACAAGACCCCAATGACATCATGCTGTGAAGATGGCATGCCAGTCTCC 469
QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
DB 470 ATCACTGGGCTGTGCACCCCTCACCCTCTCCACAGCTGTGTCACTGCTGGCACCAGC 529
QY 121 CysLeuLieserGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
DB 530 TGCCTATTCCCGGCTGGGACACGCTCCAGCCCCAGTTAGCCCTGCACACCTTG 589
QY 141 ArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTrpProGlyAsn 160
DB 590 CGATGGCCCAACATCAATCATTTGACACACAGAAAGTGAAGCCCTACCCCGGACAC 649
QY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly 180
DB 650 ATCACAACACCAATGGGTGTGCCAGGTCCAGAAAGGGGCAAGGACTCTCCAGAGGT 709
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
DB 710 GACTCCGGGGGCCCTCTGGTCTGTAACTCTTTCAGAGCATTAATCTCTGGGGCAG 769
QY 201 AspProCysAlaIleThrArgLysProGlyValTrpThrLysValCysLysTrpValAsp 220
DB 770 GATCCGGGTGCGATACACCCGAAAGCCGTGTCTACACGAAAGTCTGCAATATGTGGAC 829
QY 221 TrpIleGlnLuhThrMetLysAsnAsn 229
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DB 830 TGCATCCAGAGACGATGAAGAACAT 856

RESULT 2
US-09-205-258-189
Sequence 189, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
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EARLIER APPLICATION NUMBER: 60/048,896
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EARLIER APPLICATION NUMBER: 60/049,020
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EARLIER APPLICATION NUMBER: 60/048,876
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EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
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EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883

EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
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EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 189
LENGTH: 1292
TYPE: DNA
ORGANISM: Homo sapiens
US-09-205-258-189

Alignment Scores:
Pred. No.: 2,096-123
Score: 1258.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 4
Matches: 1292
Conservative: 229
Mismatch: 0
Indels: 0
Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-205-258-189 (1-1292)

QY 1 llellelysglyphglucyslysbrohisserglnprotrpglnalalaaleupheglu 20
DB 270 ATCATCAAGGGGTTGAGTGCAGAGCTCCAGCCCTGCGAGGAGCCCTGTTCGAG 329
QY 21 lvsThrargleuleucysglyalathrleuleialaProArgTyrpleulethrAlala 40
DB 330 AAGACGGGCTACTCTGTGGGGGAGGCTCATCGCCCGAGTGGCTCTGTACACAGCC 389
QY 41 HiscysleuysProArgTyrIleValHisleuglylnHlsasnlouglInysglu 60
DB 390 CACTGCCCTCAAGCCCCGCTACTACTTCACTCGGGGCGACACCTCCAGAGAGAG 449
QY 61 GlycysgluglnThrArgThrAlaThrGlnSerPheProHlsProGlyPheAsnAsnser 80
DB 450 GGCTGTGAGCAGACCCGGAGACCCAGTGCCTTCCCCACCCGGCTTCAACAGAGC 509
QY 81 leuproAsnlyAspHisArgAsnAspIleMetleuValysMetAlaSerProValser 100
DB 510 CTCCCAACAAAGACACCGCAGATCATGCTGGTGAAGATGGCATCGGCACTTCC 569
QY 101 lIethrTPAlaValArgProleuthrleuSerSerArgCysValThrAlaglythrser 120
DB 570 ATCACTGGGCTGTGCGACCCCTCACTCTCTCTCACTGTGTACTGTGCGACAC 629
QY 121 CysleuileSerGlyTyrPglySerThrSerSerProGlnleuArgleuProHlsThrleu 140
DB 630 TGYCTCATTTCCGGCTGGGGGAGCAGTCCAGCCCCCGATTAGCGCTGCCTCACAC 689
QY 141 ArgCysAlaAsnIleThrIleleuHlsGlnlyscysgluAsnAlaTyrProGlyasn 160
DB 690 CGATCGCCACATCATCATTCATGACCAAGAGTGTGAAGAGCGCTACCCCGGCAAC 749
QY 161 lIethrAspThrMetValCysAlaSerValGlnuglyglylyAspSerCysGlnly 180
DB 750 ATCAAGACACCATGTGTGTGCGCAGCTGCGAGAGAGGGGCGAGAGATCTCTGCGAG 809

QY 181 AspserGlyGlyProleuValCysAsnGlnSerleuglnGlylleIleserTpglyln 200
DB 810 GACTCCGGGGCCCTGTGTCTGTACAGTCTTCAAGGCAATATCTCGGGCCAG 869
QY 201 AspProCysAlaIleThrArgysProGlyValTyrThrlyValCyslystYrValasp 220
DB 870 GATCCGTGTGCGATCACCCGAAAGCCTGTGTCTACAGAAAGTGTCAAAATGTGTGAG 929
QY 221 TrpIleGlnIuThrMetlysAsn 229
DB 930 TGATCCAGAGACGATGAAGAAAT 956

RESULT 3
US-09-025-059-2
Sequence 2, Application US/09025059
Patent No. 6075136
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,059
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0481 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1314 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGWUT10
CLONE: 2723646
US-09-025-059-2

Alignment Scores:
Pred. No.: 2,146-123
Score: 1258.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 3
Length: 1314
Matches: 229
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-025-059-2 (1-1314)

QY 1 llellelysglyphglucyslysbrohisserglnprotrpglnalalaaleupheglu 20
DB 287 ATCATCAAGGGGTTGAGTGCAGAGCTCCAGCCCTGCGAGGAGCCCTGTTCGAG 346

QY 21 LysThrArgLeuLeuGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAla 40
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Db 347 AAGACGGGCTACTCTGTGGGGGACGCTCATCGCCCCAGATGGCTCTGACGACGCC 406
QY 41 HisGlySerLeuGlyProAlaGlyTrpIleValHisLeuGlyGlnHisAsnLeuGlnGlyGlu 60
|||
Db 407 CACTGCTCAAGCCCTCACTACATAGTTCACCTGGGGAGACAACTCCAGAAAGAGAG 466
QY 61 GlySerGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 80
|||
Db 467 GGGGTGAGACGACCCGACGACGACCTGAGTCTCTCCCAACCCCGGCTTCAACAAGCC 526
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
|||
Db 527 CTCCCAACAAGACACCCGCAATGACATCATGCTGTGAAGATGGATGCCCGCAGTCTCC 586
QY 101 IleThrTrpAlaValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
|||
Db 587 ATCACTGGGCTGTGGACCCCTACCTCTCTCAAGCTGTGTCACTGTGGGACACG 646
QY 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
|||
Db 647 TGCTCATTTCCGGCTGGGACGACCTCCAGCCCAAGTTAGCCTGCTGACACCTTG 706
QY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsn 160
|||
Db 707 CGATGCCCAACATCACATCATTCAGACACACAGAAAGTGAAGACGCTACCCCGGAC 766
QY 161 IleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly 180
|||
Db 767 ATCAACACACACATGGGTGTGTGCCAGCGAGAAAGGGGCAAGGACTCTGCAAGGT 826
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
|||
Db 827 GACTCCGGGGGCTCTGGTCTGTGAACCACTCTTCAAGCATATCTCTGGGGCAG 886
QY 201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220
|||
Db 887 GATCCGTTGCGAGACACCCGAAAGCTGTGTCTACAGAAAGTCTCAATATATGTGAC 946
QY 221 TrpIleGlnGlnThrMetLysAsnAsn 229
|||
Db 947 TGAATCCAGAGACGATGAAGAACAT 973

RESULT 4
US-09-205-258-247
Sequence 247, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OR INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
EARLIER FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
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EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
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EARLIER APPLICATION NUMBER: 60/048,895
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EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
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EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
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EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
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EARLIER APPLICATION NUMBER: 60/048,970
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
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EARLIER APPLICATION NUMBER: 60/048,875
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EARLIER APPLICATION NUMBER: 60/048,974
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 247
LENGTH: 1146
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (20)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:

NAME/KEY: SITE
LOCATION: (35)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (36)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (37)
OTHER INFORMATION: n equals a,t,g, or c
US-09-205-258-247

Alignment Scores:
Pred. No.: 1,986-122 Length: 1146
Score: 1248.00 Matches: 227
Percent Similarity: 99.13% Conservative: 0
Best Local Similarity: 99.13% Mismatches: 2
Query Match: 99.21% Indels: 0
Gaps: 0
DB:

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-205-258-247 (1-1146)

QY 1 llellelysglyphgglucyslyspriohisserglnprotrpglnalaleupheglu 20
DB 124 ATCATCAAGGGGTTGAGTGCAGAGCTCCTCCAGCCCTGGCAGGAGCCCTGTTCCAG 183
QY 21 lysthrargleuLeucysglyAlaThrleuilealaproargtrpleuLeuThrala 40
DB 184 AAGAGCGGCTACTCTGTGGGGCGAGCTCATCGCCCAAGATGGCTCTGCAGACAGCC 243
QY 41 HiscysleuLysProargTyrIleValHiscleuglylnHnAsnleuglnLysglu 60
DB 244 CACTGCCCAAGCCCGCTACATAGTTCACCTGGGGCAGCAACCTCCAGAGAGAG 303
QY 61 GlycysgluInthrargThralaThrGlnSerPheProHisProGlyPheAsnanser 80
DB 304 GCGTGTGAGCAGACCCGAGACGCCCTAGTCTTCCCCACCCCGGCTTCAACACAGC 363
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
DB 364 CTCCCAACAAAGACACCGCATGATGATGCGTGGAGATGAGATCGCAGCTGCC 423
QY 101 IleHtrpAlaValArgProleuThrLeuSerSerArgCysValThAlaGlyThrser 120
DB 424 ATCACTGGGCTGTGGCAGCCCTCCTCCTCAGCTGTGCTGCTGGCAGCAGC 483
QY 121 CysleuIleSerGlyTTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrleu 140
DB 484 TGCTCATTTCCGGCTGGGGGAGAGAGTCCAGCCCGCTTACGCTCCCTCAGCCTTG 543
QY 141 ArgCysAlaAsnIleThrIleIleGlnHiscLysCysGlnAsnAlaTyrProGlyAsn 160
DB 544 SGATGCGGCACATCATCATGATGAGCAGCAAGTGTGAGAGCGCTTACCCCGCAGC 603
QY 161 IleHtrpAlaMetValCysAlaSerValGlnGlyGlyLysAspSerCysGlnGly 180
DB 604 ATCAAGAGACACCATGCTGTGCCAGCTGCAGAGAGGGGCGCAAGAGATCTCTGCCAGGGGT 663
QY 181 AsperGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTTrpGlyln 200
DB 664 GACTCCGGGGGCCCTGTGCTGTAAAGTCTTCAAGGCAATATATCTCTGGGGCAG 723
QY 201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220
DB 724 GATCGGTGTGGATCAACCCGAAAGCTGTCTTACAGAAAGTCTGCAAAATATCTGCAC 783
QY 221 TrpIleGlnGlnThrMetLysAsn 229
DB 784 TGGATCCAGAGAGATGAGAGACAT 810
RESULT 5
US-08-944-483-7

Sequence 7, Application US/08944483
Patent No. 6232456
GENERAL INFORMATION:
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLAUS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
NUMBER OF INVENTION: OF THE PROSTATE
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESS: 100 Abbott Park Road
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:

CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183-US-01

TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1166 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-944-483-7

Alignment Scores:

Pred. No.: 3,316-122 Length: 1166
Score: 1246.00 Matches: 227
Percent Similarity: 99.13% Conservative: 0
Best Local Similarity: 99.13% Mismatches: 2
Query Match: 99.05% Indels: 0
Gaps: 0
DB:

US-09-856-320A-2_COPY_54_282 (1-229) x US-08-944-483-7 (1-1166)

QY 1 llellelysglyphgglucyslyspriohisserglnprotrpglnalaleupheglu 20
DB 166 ATCATCAAGGGGTTGAGTGCAGAGCTCCTCCAGCCCTGGCAGGAGCCCTGTTCCAG 225
QY 21 lysthrargleuLeucysglyAlaThrleuilealaproargtrpleuLeuThrala 40
DB 226 AAGAGCGGCTACTCTGTGGGGCGAGCTCATCGCCCAAGATGGCTCTGCAGACAGCC 285
QY 41 HiscysleuLysProargTyrIleValHiscleuglylnHnAsnleuglnLysglu 60
DB 286 CACTGCCCAAGCCCGCTACATAGTTCACCTGGGGCGAGCAACCTCCAGAGAGAGAG 345
QY 61 GlycysgluInthrargThralaThrGlnSerPheProHisProGlyPheAsnanser 80

Db 346 GGGCTGACGACGACCCGACGACGACCTCTCCCGACCCCGGCTTCAACAGC 405
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
Db 406 CTCGCCAACAAGACACCGCAATGATCATGTGTGTAAGATGGATGCGCAGTCTCC 465
QY 101 IleThrTrpAlaValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
Db 466 ATCCACTGCGGCTGTGCGACCCCTCCACCTCTCCACAGCTGTGCATGCTGTGGACACG 525
QY 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
Db 526 TGGCTCATTTCCGGCTGGGAGCAGCTCCAGCCCGAGTACGCTGCTCAACCTTG 585
QY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTrpProGlyAsn 160
Db 586 CGATGGCCCAACATCACCATCATTTGACACAGAAAGTGAAGACGCTACCCGCGAC 645
QY 161 IleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly 180
Db 646 ATCAACACACACATAGTGTGTGCGACGCTGACAGAAAGGGGCAAGGACTCTGCGACAGGT 705
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
Db 706 GACTCCGGGGGCGCTTGGTGTGTGACCAAGTCTCTTAAGGCAATATCTCTGGGGCAG 765
QY 201 AspProCysAlaIleThrArgLysProGlyValTrpThrLysValCysLysTrpValAsp 220
Db 766 GATCCGCTGCGATCAACCCGAAAGCGTGTGTACACGAAAGTCTCAAAATATGTGAC 825
QY 221 TrpIleGlnGlnLysThrMetLysAsnAsn 229
Db 826 TGGATCCAGAGACGATGAAGAACAAAT 852

RESULT 6
US-09-386-642-10
; Sequence 10, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jensen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386, 642
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1052
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-10

Alignment Scores:
Pred. No.: 1,78e-119 Length: 1052
Score: 1219.50 Matches: 223
Percent Similarity: 98.26% Conservative: 3
Best Local Similarity: 96.96% Mismatches: 3
Query Match: 96.94% Indels: 1
Gaps: 1

US-09-856-320a-2_copy_54_282 (1-229) x US-09-386-642-10 (1-1052)

QY 1 IleIleLysGlyPheGlyCys---LysProHisSerGlnProTrpGlnAlaAlaLeuPhe 19
Db 166 ATCGTTGGGGGCTACAACTGTCTAGAAAGCACTCCAGCGCCGAGGAGCGCCGTGTC 225
QY 20 GlnLysThrArgLeuLeuLysGlyAlaThrLeuIleAlaProArgTrpLeuThrAla 39

Db 226 GAGAAAGCGGGCTACTCTGTGGGCGACCCCTATGCGCCCGCAGATGGCTCTGACAGCA 285
QY 40 ALHisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGln 59
Db 286 GCCCACTGCTTCAAGCCCGCTTCAATGTTCACCTGGGGAGACAACTCCGAAAGGAG 345
QY 60 GlnGlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsn 79
Db 346 GAGGGCTGTAGAGACACCGGACAGCACATGAGTCTTCCCGACCCCGGCTTCAACAC 405
QY 80 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 99
Db 406 AGCCTCCCAACAAGACCCACCAATGACATCATGTGTGTAAGATGGCATGCCACAGTC 465
QY 100 SerIleThrTrpAlaValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 119
Db 466 TCCATCACTGGGCTGTGCGACCCCTCACCTTCTCTACAGCTGTGTCACTGTGGCACC 525
QY 120 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 139
Db 526 AGCTGCTCATTTCCGGCTGGGAGCAGCTGCCAGCCCGCAGTACGCTGCTCAACAC 585
QY 140 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTrpProGly 159
Db 586 TTGCGATGCGCAACATCACCATCATTTGACACAGAAAGTGAAGACGCTACCCCGCG 645
QY 160 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 179
Db 646 AACATCACACACACATAGTGTGTGCGACGCTGACAGAAAGGGGCAAGGACTCTCCAG 705
QY 180 GlnAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 199
Db 706 GGTGACTCCGGGGGCGCTTGGTGTGTGTAACCAAGTCTCTTAAGGCAATATCTCTGGGG 765
QY 200 GlnAspProCysAlaIleThrArgLysProGlyValTrpThrLysValCysLysTrpVal 219
Db 766 CAGATTCGCTGTCGATCAACCCGAAAGCGTGTGTACACGAAAGTCTGCAAAATATGTG 825
QY 220 AspTrpIleGlnGlnLysThrMetLysAsnAsn 229
Db 826 GACTGATCCAGAGACGATGAAGAACAAAT 855

RESULT 7
US-08-790-137-2
; Sequence 2, Application US/08790137
; Patent No. 5840871
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL PROSTATE-ASSOCIATED
; TITLE OF INVENTION: KALIKREIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,137
; FILING DATE: Filed Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0195 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 833 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-790-137-2

Alignment Scores:
Pred. No.: 6,09e-119 Length: 833
Score: 1213.00 Matches: 219
Percent Similarity: 97.82% Conservative: 5
Best Local Similarity: 95.63% Mismatches: 5
Query Match: 96.42% Indels: 0
Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x US-08-790-137-2 (1-833)

QY 1 llelelelysglypnehlucyslyspnohisserglnprotpglnalalaleupheclu 20
DB 99 attgtggagcgtgagctgtgagcagcatccagccctggcagcgctctgtacacg 158
QY 21 lysthratgleuleucysglyalathrleulealaproatgtrpleuleuthralala 40
DB 159 aagacggcgcctactctgtggggcagcagtcacatnccccacagatggcttcgacacgacc 218
QY 41 hiscysleulyspnoatgtrylevalhisleuglygnhisasnleuglnlysglu 60
DB 219 cactgacctnagaccggcctacatagttcactggggcagcacaacctcagagagagag 278
QY 61 glycysgluglnthrargthralathrgluserpheprohisproglypheasnanser 80
DB 279 ggctgtgagcagcccgacagccactgagtcctccccacccggcctcaacmacagc 338
QY 81 leuproasnlyspahisargasnaspillemetleuvalylsmetalaserprovalser 100
DB 339 ctccccacacagacacccgacatgacatgctggtagatggcagtcgacgctcc 398
QY 101 llethrtrpalaValargproleuthrleuserserargcysvalthrAlaglythrsr 120
DB 399 atcacctggcgtgagcagccctcaccctcctcagcctgtgtcactgctggcagcagc 458
QY 121 cysleuleserglyttrpglyserthrserserprogluleuargleuprohisthrleu 140
DB 459 tgcctcatattccggcctggcgacagcgtccagccccagcttaccgctccacaccttg 518
QY 141 argcysalaasnillethrillelelgnhisglnlyscysgluasnalatyrproglyasn 160
DB 519 cgatggccgacacatcaccatcatgtgacacagaaagtgtgaaagccttaccggcgac 578
QY 161 llethrspthrmctvalcysalaservaleinglnlyglylyspasercysglnly 180
DB 579 atcacagacacacatgagtggtgacagcggtgacagaaaggggcagaaagactctgcagag 638
QY 181 aspergerglyproleuvalcysasnnglnserleuglnlylleeserttrpglyln 200
DB 639 gacttcgggggcccctgtggtgtgtaaccagtccttcaaggcattatctctggggcgag 698
QY 201 aspprocysalallethrarglysproglyvaltyrthrlysalcyslystyrvalasp 220
DB 699 gatccggtgagatcaccgaaagcctggtgtcttaccagaaagcttgcataatggtgac 758
QY 221 trplleinglnlurhmetlysasasn 229
DB 759 tggatccagagagcagatgaaagacaat 785

RESULT 8

US-09-280-116-3
; Sequence 3, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: trypsin-like serine proteases
US-09-280-116-3

Alignment Scores:
Pred. No.: 7.8e-88 Length: 618
Score: 916.50 Matches: 184
Percent Similarity: 90.78% Conservative: 3
Best Local Similarity: 89.32% Mismatches: 4
Query Match: 72.85% Indels: 16
Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-280-116-3 (1-618)

QY 23 argleuleucysglyalathrleulealapro-argtrpleuleuthralalaleiscy 42
DB 2 cggctactctgtggggcgacac--TCATCGCCTCAGATGGCTCCGACAGCCACCTG 58
QY 42 sleulyspnoatgtrylevalhisleuglygnhisasnleuglnlysgluuglycy 62
DB 59 cctcagcccgctcactagttcactggggcagcacaacctccagaaaggagagcgctg 118
QY 62 sgluglnthrargthralathrgluserpheprohisproglypheasnanserleupr 82
DB 119 tgagcagacccggacagccactgagtcctccccacccggcctcaacmacagcctcc 178
QY 82 obasnlyspahisargasnaspillemetleuvalylsmetalaserproval-serile 102
DB 179 caacaaagacacccgacatgacatgctggtagatggcagtcgacgctccacatca 238
QY 102 htrpalaValargproleuthrleuserserargcysvalthrAlaglythrserysl 122
DB 239 cctggcgtgagcagccctcaccctcctcagcctgtgtcactgctggcagcagcctcc 298
QY 122 euileserglyttrpglyserthrserserprogluleuargleuprohisthrleuargc 142
DB 299 tcatttccggcgtggcgacagcagctccagcccgacttaccgctccacaccttgagat 358
QY 142 ysalaasnillethrillelelgnhisglnlyscysgluasnalatyrproglyasnile 162
DB 359 gccgacacatcaccatcatgtgacacagaaagtgtgaaagccttaccggcgacatca 418
QY 162 hrspthrmctvalcysalaservaleinglnlyglylyspasercysglnlyasp 182
DB 419 cagacacacatgagtggtgacagcggtgacagaaaggggcagaaagactctgcagag 471
QY 182 erglyglyproleuvalcysasnnglnserleuglnlylleeserttrpglylnasp 201
DB 472 -----gtrcttcc-AAAGGATATATCTCCCTGGGGGCCAGGAC 507
QY 202 -Procysalallethrarglysproglyvaltyrthrlysalcyslystyrvalasp 221
DB 508 tccgtgtgagatcaccgaaagcctggtgtcttaccagaaagcttgcataatggtgac 567
QY 221 pilleinglnl 224
DB 568 gatccagagaa 577

RESULT 9
US-09-070-526-1
Sequence 1, Application US/09070526
Patent No. 6100059
GENERAL INFORMATION:
APPLICANT: SOUTHAN, CHRISTOPHER
APPLICANT: CLINKENBEARD, HELEN
APPLICANT: BURGESS, NICOLA
TITLE OF INVENTION: No. 6100059e1 Compounds
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,526
FILING DATE: 30-APR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9711952.3
FILING DATE: 9-JUN-1997
APPLICATION NUMBER: EP 97309646.4
FILING DATE: 1-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-30353
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 944 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-070-526-1
Alignment Scores:
Pred. No.: 1.07e-62 Length: 944
Score: 681.00 Matches: 116
Percent Similarity: 70.54% Conservative: 42
Best Local Similarity: 51.79% Mismatches: 64
Query Match: 54.13% Indels: 2
DB: 3 Gaps: 2
US-09-856-320a-2_COPY_54_282 (1-229) x US-09-070-526-1 (1-944)
QY 1 llellelysglypcheucyslyspromisserglnprotrpplnlaaleupheglu 20
Db 201 gtctctgggggtatgatgacacccacccattccgacgcttgacgagccgctttccag 260
QY 21 lvsfthargleuencysgalyalathrleuilealaproargtrpleuethrleuilaia 40
Db 261 gccacagcaatctgctggcggtgctctgttagtgagcgaactgggcttctacagctgcc 320
QY 41 hiscysleuylproargtrrlllevalhislenglycglinhissnleuglnlysglu 60
Db 321 caactgaaaaaacgaaatgacacgtagccctgggagacacgacctacgaataaagat 380
QY 61 glycysgluglnthrargthralathrgluserphaprophihisproglypheasna 80
Db 381 ggccacagacgaagaataatctctgtgcttccatccacacccctgctatpaaagcagc 440

QY 81 leuproasnllyspahisargasnaspillemetleuvallysmetalaaserprovalser 100
Db 441 ---gattgtgagagcaccacacacatgattcttcttgaactgggtgacacgagatcc 497
QY 101 llethtrpalaivalargproleuthrleuserSerArgcysvalthrallaglythrser 120
Db 498 ctgggggtccaaatgaaagcccatgacgctggcagatcattgacccacgctggcagaaag 557
QY 121 cysleuileserglytrpglyserthrSerSerProglInleuargleuprophisrhrleu 140
Db 558 tgcacccgtctcagcctggcactgacacagtcacacagaaattttctgacactctc 617
QY 141 argcysalasnlethrillellegluhislglcysgluasnalartrproglyasn 160
Db 618 aactgtcagaaagtaaaatctttcccaagaaagatgtagatcttaccggggcag 677
QY 161 llethrasphrmetvalcysalaserValglnglgllylysaspserysgllyngly 180
Db 678 atcacagatggcattgctgtgacagcagcagcagcagcagcagcagcagcagcagcagc 734
QY 181 aspserglylproleuvalcysaanglnserleuglnglylletlesertrpglyln 200
Db 735 gattctggagagcccccctgctgtgacgctcctcagcagcagcagcagcagcagcagcagc 794
QY 201 aspsercysalathrarglysproglyvaltyrthrlysalcyslystyryvalasp 220
Db 795 gacccctgtggagagctgcacaaacctgggcttatcacaacatctggccctacgagac 854
QY 221 trpilleglngu 224
Db 855 tggatcagaag 866
RESULT 10
US-09-008-271a-19
Sequence 19, Application US/09008271A
Patent No. 6203979
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Yue, Henry
Hillman, Jennifer L.
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Purya
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271A
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 19:


```

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 994 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: COINNOT27
; CLONE: 1798496
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 19 :
US-09-008-271A-19

Alignment Scores:
Pred. No.: 8, 1e-62 Length: 994
Score: 673.00 Matches: 115
Percent Similarity: 70.09% Conservative: 42
Best Local Similarity: 51.34% Mismatches: 65
Query Match: 53.50% Indels: 2
DB: 3 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-008-271A-19 (1-994)

QY 1 llelelsglypnehlucyslysProHisSerGlnProTPrGlnAlaAlaLeuPheGlu 20
DB 251 GTGCTGGGGGTCATGAGTGGCAACCCCATTCGACGCTTGGCAGCGGCTGTGCCAG 310
QY 21 LysThrArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
DB 311 GGCACGCAACTACTCTGTGGCGTGTCTGTAGGTGGCAACTGGGCTTACACAGCTGCC 370
QY 41 HisCysLeuLysProArgTyrLleValHisLeuGlnHisAsnLeuGlnLysGlu 60
DB 371 CACGTGTAACCAACGAAATATACACAGTACGCTGGGAGACACAGCTTACACAGCAGC 430
QY 61 GlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 80
DB 431 GCGCCAGACGAAGAAATACATCCGTGGTTCATCCACACCCCTGTACACAGCAGC 490
QY 81 LeuProAsnLysAspHisArgAsnAspLleMetLeuValLysMetAlaSerProValSer 100
DB 491 --GATGTGGAGGACCCACMACCATGATCTGTTCACACTGCTGACAGGACATCC 547
QY 101 lleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
DB 548 CTGGGGTCCCAAGGAAAGCCATCAGCTGGCAGATCATTCACCCAGCCCTGGCCAGAG 607
QY 121 CysLeuLysSerGlyTPrGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
DB 608 TGCACCGTCTCAGGCTGGGCGACCTGTCCACAGTCCCGAGAGAAATTTCCGTGACACTGTC 667
QY 141 ArgCysAlaAsnLleThrLleIleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsn 160
DB 668 AACTGTGCAGAGTAAATCTTTCCCGAGAAAGTGTGAGATGCTTACCCGGGGCAG 727
QY 161 lleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly 180
DB 728 ATCACAAGATGGCAGTGTCTGTGCGACGACGACGAAAGGGCT---GACACCTGCCAGGGC 784
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyLleIleSerTPrGlyGln 200
DB 785 GATTCGTGAGGCGCCCTGTGTGTGATGTGTCACCTCAGGGCATTACATCTGGGGGCTCA 844
QY 201 AspProCysAlaLleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220
DB 845 GACCCCTGTGGAGAGTCCGACAAACCTGGGCTTATACCAACATCTGCCGCTACCTGAC 904
QY 221 TrpIleGlnLys 224
DB 905 TGTGATCAAGAAG 916

RESULT 11
US-09-386-642-9
; Sequence 9, Application US/09386642
; Patent No. 6420157
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;
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jensen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 9
; LENGTH: 1049
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-9

Alignment Scores:
Pred. No.: 1, 26e-61 Length: 1049
Score: 671.50 Matches: 116
Percent Similarity: 70.22% Conservative: 42
Best Local Similarity: 51.56% Mismatches: 64
Query Match: 53.38% Indels: 3
DB: 4 Gaps: 3

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-386-642-9 (1-1049)
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QY 1 llelelsglypnehlucys---LysProHisSerGlnProTPrGlnAlaAlaLeuPhe 19
DB 166 ATGTTTGGGCTTACACATCTGTAGGAGTGGCAACTGGGCTTACACAGCTGTGTC 225
QY 20 GluLysThrArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 39
DB 226 CAGGGCCAGCAACTACTCTGTGGCGTGTCTGTAGGTGGCAACTGGGCTTACACAGCT 285
QY 40 AlaHisCysLeuLysProArgTyrLleValHisLeuGlnHisAsnLeuGlnLysGlu 59
DB 286 GCCCACTGTAAACCAACGAAATATACACAGTACGCTGGGAGACACACAGCTTACAGAAATAA 345
QY 60 GluLysCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsn 79
DB 346 GATGGCCAGACGAAGAAATACCTGTGGTTCATCCACACACCCCTGTACAAACAGC 405
QY 80 SerLeuProAsnLysAspHisArgAsnAspLleMetLeuValLysMetAlaSerProVal 99
DB 406 AGC---GATGTGGAGGACACACACATGATCTGTTCACACTGCTGACCCAGGCA 462
QY 100 SerlleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 119
DB 463 TCCCTGGGGTCCAAAGTGAAGCCATCAGCTGGGAGATCATGTGACCCAGCTGGCCAG 522
QY 120 SerCysLeuLysSerGlyTPrGlySerThrSerSerProGlnLeuArgLeuProHisThr 139
DB 523 AAGTGCACCGTCTCAGGCTGGGCGACCTGTCCACAGTCCCGAGAGAAATTTCCGTGACACT 582
QY 140 LeuArgCysAlaAsnLleThrLleIleGlnHisGlnLysCysGlnAsnAlaTyrProGly 159
DB 583 CTCAACGTGTGAGAGTAAATCTTTCCCGAGAAAGTGTGAGATGCTTACCCGGGG 642
QY 160 AsnLleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 179
DB 643 CAGATCACAGATGGCATGTCTGTGCGACGACGACGAAAGGGCT---GACACCTGCCAG 699
QY 180 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyLleIleSerTPrGly 199
DB 700 GCGCATTCGTGAGGCGCCCTGTGTGTGATGTGTCACCTCAGGGCATTACATCTGGGGC 759
QY 200 GlnAspProCysAlaLleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 219
DB 760 TCAGACCCCTGTGGAGAGTCCGACAAACCTGGGCTTATACCAACATCTGCCGCTACCTG 819
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OY 220 AsptriplecIngu 224
Db 820 GACTGGATCAAGAG 834

RESULT 12
US-09-996-243-308
Sequence 308, Application US/09996243
Patent No. 6478825

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijaviri, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C13
CURRENT APPLICATION NUMBER: US/09/996,243
CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
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PRIOR FILING DATE: 1998-06-04
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PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
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PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22

PRIOR APPLICATION NUMBER: 60/090254
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 PRIOR APPLICATION NUMBER: 60/090349
 PRIOR FILING DATE: 1998-06-23
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 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091544
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091626
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.: 1.64e-58 Length: 1570
 Score: 644.50 Matches: 117
 Percent Similarity: 67.97% Conservative: 40
 Best Local Similarity: 50.65% Mismatches: 67
 Query Match: 51.23% Indels: 7
 Gaps: 4

US-09-856-320a-2_COPY_54_282 (1-229) x US-09-996-243-308 (1-1570)

QY 1 IletlelysglyPhneglucylsProHisserlinProtrpglnAlaAa---Leuphe 19
 ||||| ||| :||| |||:||||| ||||| |||

Db 552 ATCATCAATGATCCGACTGCGATATGCACACCCAGCCGTGGCAGCCGCGTGTCTGA 611
 QY 20 GluylsthrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThrAla 39
 Db 612 AGCCCAACACAGCTTACTGCGGGCGGCTGTGGCATCCACATGCTGCTCAGCCG 671
 QY 40 AlaHisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLys 58
 Db 672 GCCCACTCAGAGAAAGATTTCAGAGTCCGCTCGGCCACTACTCCCTGCACACAGT 731
 QY 59 GluGluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsn 78
 Db 732 TATGAACTGGGAGCATATGTTCCAGGGGGTCAATATCCACCCCTGCTATCC 791
 QY 79 AsnSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerPro 98
 Db 792 -----CACCGCGCCACTCTAACGACCTCATGCTCATTAACCTGAACGAAGA 839
 QY 99 ValSerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGly 118
 Db 840 ATTCGTCCCACTAAGATGTGACACCATCAACGCTCTCATTTGTCCTGCTGCG 899
 QY 119 ThrSerCysLeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHis 138
 Db 900 ACAAGTCTGTGTCTGGCTGGGGAACAACCAAGATCCCAAGTGCCTTCCCTAAG 959
 QY 139 ThrLeuArgCysAlaAsnIleThrIleLeuGlnHisGlnLysCysGlnAsnAlaLeuPro 158
 Db 960 GTCTCCCACTGTCTGAATATACGCTGCTGAAGTCAAGAAAGTGGAGAGATCTACCG 1019
 QY 159 GlyAsnIleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCys 178
 Db 1020 AGACAGATAGATGACACCATGTTCTGCGCGGT---GACAAAGCGTAGAGACTCGTC 1076
 QY 179 GlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleLeuSerTrp 198
 Db 1077 CAGGTGATCTGGGGGCTGTGTGTGCATGTGCTCCGACAGGAGCTGTGTCGCG 1136
 QY 199 GlyGlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyr 218
 Db 1137 GGAGTTACCTTGTGGCGGCCGCCACACAGACCGGGTGTCTACAGAACCTGTGCAATTC 1196
 QY 219 ValAspTrpIleGlnGluThrMetLysAsnAsn 229
 Db 1197 ACCAAGTGTATCCAGAAACCATCCAGGCCAAC 1229

RESULT 13

US-09-280-116-20/C
 ; Sequence 20, Application US/09280116A
 ; Patent No. 6331427
 ; GENERAL INFORMATION:
 ; APPLICANT: Robison, Keith E.
 ; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
 ; FILE REFERENCE: 5800-24, 035800/176965
 ; CURRENT APPLICATION NUMBER: US/09/280,116A
 ; CURRENT FILING DATE: 1999-03-26
 ; NUMBER OF SEQ ID NOS: 268
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 20
 ; LENGTH: 1364
 ; TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: trypsin-like serine proteases

NAME/KEY: misc_feature

LOCATION: (1)..(1364)

OTHER INFORMATION: n = a, t, c, or g

US-09-280-116-20

Alignment Scores:

Pred. No.: 1.51e-57 Length: 1364
 Score: 634.50 Matches: 123

Percent Similarity: 64.82% Conservative: 41
 Best Local Similarity: 48.62% Mismatches: 60
 Query Match: 50.44% Indels: 29
 DB: 4 Gaps: 3

US-09-856-320a-2_copy_54_282 (1-229) x US-09-280-116-20 (1-1364)

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QY      4 GlyPheLeuLysLysProHisSerGlnProTyrGlnAlaAlaLeuPheGluLysThrArg 23
      |||::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      828 GGCTACACCTGCTCCCTCCACTCCACCTCGGAGGCTCCCTACTAGTGAAGGCGG 769

QY      24 LeuLeuGlyGlyAlaThr-LeuIleAlaProArgTyrPheLeuThrAlaIleHisCysLe 43
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      768 CTACTCTGTGGGGAGATCTCTGGTCCACCCCAATGGCTCTCTGCTCCGACCTGTCT 709

QY      43 uLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluLysCysG1 63
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      708 AAAGGAGGCGCTCAAGATTACTAGGCAAGCAAGCCCTTAGGGGCTGTGAAGCTGTGCA 649

QY      63 uGlnThrArgTyrAlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAs 83
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      648 GCAGGTGAGGGAAGTTGTCCACTTATCCCTGAAATACCAGGAAGCCCAACCA 589

QY      83 nLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTr 103
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      588 CCGAACACACNACCATCATCATCTGTGGAGCTGACAGTCCCGGTCCAGCTCACAGG 529

QY      103 palValAlaArgProLeuThrLeuSer---SerArgCysValThrAlaGlyThrSerCysLe 122
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      528 CTACATCCAAACCCCTGCTCCCTCCCAACCAACCCGCTAACCCCTGGCACACACTGTGC 469

QY      122 uLysSerGlyTyrGlySerThrSerSerProGln-----LeuArg 135
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      468 GGCTGTGGCTGGGGACACACACACCCCGAGGTATGACCCACACAGTGTGCTGAG 409

QY      135 g-----le 136
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      408 GCGCCATAGAGAGTGGCGGGAACAGGGGACAGATGGAGAGAGTGTGATGATATT 349

QY      136 uProHis-ThrLeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnA 156
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      348 ACCCCAAACCTCATATGTCGCAACATCCACTGCTCAGATGAGAGAGTGTGCTGCTCAAG 289

QY      156 latYrProGlnAsnIleThrAspThrMetValCysAlaSerValGlnGluGlyLysA 176
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      288 TCTACCCGAGGAAGATCATGACACATGTTGTGTGCGGACACAAAGAGGCTGGCAAG 229

QY      176 spSerCysGlnGlyAspSerGlyLysProLeuValCysAsnGlnSerLeuGlnGlyIle 196
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      228 ACTCCTGTGAGGCTGACTCTGGGGGCCCCCTGTCTGTAAACAAACCTGTATGGCATCG 169

QY      196 leSerTyrPheGlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValC 216
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      168 TCTCTGGGAGAGACTTCCCATGTGGGCAACCTGACCGGCTGTGTCTAACACCCGTGTCT 109

QY      216 yslYsTyrValAspTyrPheGlnGluThrMetLys 227
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      108 CAAGATACGCTGTGTGATCCGTGAACAATCCGA 74

RESULT 14
US-08-824-874-2
; Sequence 2, Application US/08824874
; Patent No. 5962300
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA

```

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; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,874
; FILING DATE: Filed Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1476 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KERN0702
; CLONE: 820694
; US-08-824-874-2

Alignment Scores:
Pred. No.: 3,53e-57 Length: 1476
Score: 631.50 Matches: 117
Percent Similarity: 67.67% Conservative: 40
Best Local Similarity: 50.43% Mismatches: 67
Query Match: 50.20% Indels: 8
DB: 2 Gaps: 4

US-09-856-320a-2_copy_54_282 (1-229) x US-08-824-874-2 (1-1476)

QY      1 IleIleLysGlyPheGluCysLysProHisSerGlnProTyrGlnAlaAla---LeuArg 19
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      475 ATCATCAATGAGACCCAGCTGCGATATGACACCCAGCTGGGCGGAGCGGCTGTGCT 534

QY      19 eGluLysThrArgLeuGlyAlaThrIleIleAlaProArgTyrPheLeuThrAl 39
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DB      535 AAGGCCCAACCACTTACTGCGGGCGGCTGTGTGTCATCCACAGTGTGCTCACGGC 594

QY      39 alaHisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLys-- 58
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      595 CGCCCACTGAGAGAAAGATTTCAGAGTCGCTCGGCACTACTCCCTGCACCACT 654

QY      59 -GluGluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAs 78
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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QY      78 naAsnSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerPr 98
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DB      715 C-----CACCTGGCCACTTCTAACGACCTCATGCTCATTAACCTGAACAGAG 762

QY      98 oValSerIleThrTyrPheValaArgProLeuThrLeuSerSerArgCysValThrAlaG1 118
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      763 AATTCCTCCACATAAAGATGTAGACCATCAACGCTCTCTCATATGTCCCTGTGCTGG 822

QY      118 yThrSerCysLeuIleSerGlyTyrPheLysThrSerSerProGlnLeuArgLeuProH1 138
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      823 GACAAAGTCTGTGTCTCGGCTGGGGAACCAAGACCCCAAGTGCATCTCCCTTA 882

QY      138 sThrLeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrPr 158
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      883 GGCTCTCCAGTGTGTAATATCAGCTGTGTAAGTGAAGAAAGTGGAGATGCTTACCC 942

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QY 158 oGlyAsnIleThrAspThrMetValCysAlaSerValGlnGluGlyGlyAspSerCys 178
 DB 943 GAGACAGATGATGACACCATGTCTGCCCGGT---GACAAAGCAGTAGAGACTCCG 999
 QY 178 sGlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTr 198
 DB 1000 CCAGGATGATCTGGGGGCGCTGTGCTGCATAGCTCCCTGCAGGGAGCTGCTCCG 1059
 QY 198 pGlyGlnAspProCysAlaIleThrArgGlySerProGlyValIleThrIleValCysLysTr 218
 DB 1060 GGGAGATTACCTTTGTGCCCGGCCCAACAGACCGGGGTGTCTACAGCAACTCTGCAAGTT 1119
 QY 218 rValAspTrpIleGlnGluThrMetLysAsn 229
 DB 1120 CACCAAGTGATCCAGAAACCATCCAGGCCAAC 1153

RESULT 15

US-09-210-084-2
 ; Sequence 2, Application US/09210084
 ; Patent No. 6197511
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Lal, Preeti
 ; TITLE OF INVENTION: NOVEL KALLIKREIN
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/210,084
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/824,874
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0252 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1476 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: KERANOT02
 ; CLONE: 820694
 ; US-09-210-084-2

Alignment Scores:
 Pred. No.: 3.53e-57 Length: 1476
 Score: 631.50 Matches: 117
 Percent Similarity: 67.67% Conservative: 40
 Best Local Similarity: 50.43% Mismatches: 67
 Query Match: 50.20% Indels: 8
 DB: 3 Gaps: 4

US-09-856-320a-2_COPY_54_282 (1-229) x US-09-210-084-2 (1-1476)

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 QY 19 eGluLysThrArgLeuLeuCysGlyAlaIleThrIleValHisLeuGlnHisAsnLeuGln 39
 DB 535 AAGGCCCAACAGCTCTTACTGCGGGGGGTGTGTGTCATCCACAGTGGCTCTCAAGGC 594
 QY 39 AlaHisCysLeuLysProArgTrpIleValHisLeuGlnHisAsnLeuGln 58
 DB 595 CGCCCACTCAGAGAAAGTTTCAGAGTCCGCTCGGCCACTACTCCCTCAGCAAGT 654
 QY 59 -GluGluGlyCysGluGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAs 78
 DB 655 TTATGATCTGGGAGAGATGTCTCAGGGGGTCAATCCATCCACCCAGCTGGCTACTG 714
 QY 78 nasnSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValIleMetAlaSerP 98
 DB 715 C-----CACCTGGCCACTCTACAGCACTCATGCTCATCAACCTGACAGAG 762
 QY 98 oValSerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaG 118
 DB 763 AATTGTCCTCACTAAGATGTGACAGCCATCAAGCTCTCTCATTTGCTCTGCTG 822
 QY 118 yThrSerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProH 138
 DB 823 GACAAAGTCTTGCTGGCTGGGGGACAAAGACCCCAAGTCCACTCTCCCTTA 882
 QY 138 sThrLeuArgCysAlaAsnIleThrIleIleLeuHisGlnLysCysGlnAsnAlaTrp 158
 DB 883 GGTCTCCAGTCTTGAATATCAGCGTGTAACTCAGAAAGTGTGAGATGCTTACCC 942
 QY 158 oGlyAsnIleThrAspThrMetValCysAlaSerValGlnGluGlyGlyAspSerCys 178
 DB 943 GAGACAGATGATGACACCATGTCTGCCCGGT---GACAAAGCAGTAGAGACTCCG 999
 QY 178 sGlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTr 198
 DB 1000 CCAGGATGATCTGGGGGCGCTGTGCTGCATAGCTCCCTGCAGGGAGCTGCTCCG 1059
 QY 198 pGlyGlnAspProCysAlaIleThrArgLysProGlyValIleThrIleValCysLysTr 218
 DB 1060 GGGAGATTACCTTTGTGCCCGGCCCAACAGACCGGGGTGTCTACAGCAACTCTGCAAGTT 1119
 QY 218 rValAspTrpIleGlnGluThrMetLysAsn 229
 DB 1120 CACCAAGTGATCCAGAAACCATCCAGGCCAAC 1153

Search completed: October 15, 2003, 21:09:06
 Job time : 69.636 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OK protein - protein search, using sw model

Run on: October 15, 2003, 20:58:02 ; Search time 20.6145 Seconds
(without alignments)
1789.927 Million cell updates/sec

Title: US-09-856-320a-2_COPY_54_282

Perfect score: 1258
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Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubppaa/PCF_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep:*
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- 15: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
- 16: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
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- 18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1258	100.0	250	11	US-09-946-374-170
2	1258	100.0	250	12	US-10-015-387a-1170
3	1258	100.0	250	12	US-10-137-870-506
4	1258	100.0	250	12	US-10-140-018-506
5	1258	100.0	250	12	US-10-140-021-506
6	1258	100.0	250	12	US-10-140-274-506
7	1258	100.0	250	12	US-10-140-471-506
8	1258	100.0	250	12	US-10-140-807-506
9	1258	100.0	250	12	US-10-140-822-506
10	1258	100.0	250	12	US-10-140-924-506
11	1258	100.0	250	12	US-10-140-926-506
12	1258	100.0	250	12	US-10-141-698-506
13	1258	100.0	250	12	US-10-141-702-506
14	1258	100.0	250	12	US-10-141-704-506
15	1258	100.0	250	12	US-10-142-421-506

16	1258	100.0	250	12	US-10-142-432-506
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19	1258	100.0	250	12	US-10-144-994-506
20	1258	100.0	250	12	US-10-145-628-506
21	1258	100.0	250	12	US-10-145-631-506
22	1258	100.0	250	12	US-10-145-633-506
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26	1258	100.0	250	12	US-10-145-826-506
27	1258	100.0	250	12	US-10-145-870-506
28	1258	100.0	250	12	US-10-145-876-506
29	1258	100.0	250	12	US-10-145-959-506
30	1258	100.0	250	12	US-10-146-724-506
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43	1258	100.0	250	12	US-10-158-783-506
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45	1258	100.0	250	12	US-10-006-130A-170

ALIGNMENTS

RESULT 1
US-09-946-374-170
; Sequence 170, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fond, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paonli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PICI
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750

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2	PRIOR APPLICATION NUMBER: 60/098803
3	PRIOR FILING DATE: 1998-09-02
4	PRIOR APPLICATION NUMBER: 60/098822
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6	PRIOR APPLICATION NUMBER: 60/098843
7	PRIOR FILING DATE: 1998-09-02
8	PRIOR APPLICATION NUMBER: 60/099536
9	PRIOR FILING DATE: 1998-09-02
10	PRIOR APPLICATION NUMBER: 60/099569
11	PRIOR FILING DATE: 1998-09-09
12	PRIOR APPLICATION NUMBER: 60/099598
13	PRIOR FILING DATE: 1998-09-09
14	PRIOR APPLICATION NUMBER: 60/099602
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36	PRIOR APPLICATION NUMBER: 60/100663
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PRIOR APPLICATION NUMBER:	60/102965
PRIOR FILING DATE:	1998-10-02
PRIOR APPLICATION NUMBER:	60/103258
PRIOR FILING DATE:	1998-10-06
PRIOR APPLICATION NUMBER:	60/103314
PRIOR FILING DATE:	1998-10-07
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PRIOR FILING DATE:	1998-10-07
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PRIOR FILING DATE:	1998-10-08
PRIOR APPLICATION NUMBER:	60/104257
PRIOR FILING DATE:	1998-10-08

PRIOR FILING DATE: 1998-10-14
PRIOR APPLICATION NUMBER: 60/104987
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105000
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PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105807

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Best Local Similarity 100.0%; Pred. No. 1.3e-118;
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DB 142 CLISGWSTSSPOLRPLPTLRCANTTIEHOKCENAYPGNTIDTWVCASVQEGKDSGCG 201
QY 181 DSGGPLVCNOSLOGIISWGQDPCAITRKPGYTYTKYCKYVDWIOETMKN 229
DB 202 DSGGPLVCNOSLOGIISWGQDPCAITRKPGYTYTKYCKYVDWIOETMKN 250

RESULT 2
US-10-015-387A-170
Sequence 170, Application US/10015387A
Publication No. US20030135034A1

GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C54
CURRENT APPLICATION NUMBER: US/10/015,387A
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION REMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 170
LENGTH: 250
TYPE: PRT
ORGANISM: Homo sapiens
US-10-015-387A-170

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Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 142 CLISGWSTSSPOLRPLPTLRCANTTIEHOKCENAYPGNTIDTWVCASVQEGKDSGCG 201
QY 181 DSGGPLVCNOSLOGIISWGQDPCAITRKPGYTYTKYCKYVDWIOETMKN 229
DB 202 DSGGPLVCNOSLOGIISWGQDPCAITRKPGYTYTKYCKYVDWIOETMKN 250

RESULT 3
US-10-137-870-506
Sequence 506, Application US/10137870
Publication No. US20030138883A1

GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C155
CURRENT APPLICATION NUMBER: US/10/137,870
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION REMOVED - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 506
LENGTH: 250
TYPE: PRT
ORGANISM: Homo Sapien
US-10-137-870-506

Query Match 100.0%; Score 1258; DB 12; Length 250;

Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGECKPHSOPWQMALEFETRLICGATLLAPRMLTAAHCKRRTYVHLGQHNLOKEE 60
DB 22 IIKGECKPHSOPWQMALEFETRLICGATLLAPRMLTAAHCKRRTYVHLGQHNLOKEE 81
QY 61 GCEOTRTATESPFBPGFNNSLPNKDRNDIMLVKASPVSTWAVRPLTSSRCVTAGTS 120
DB 82 GCEOTRTATESPFBPGFNNSLPNKDRNDIMLVKASPVSTWAVRPLTSSRCVTAGTS 141
QY 121 CLISGWSTSSPOLRPLPTLRCANTTIEHOKCENAYPGNTIDTWVCASVQEGKDSGCG 180
DB 142 CLISGWSTSSPOLRPLPTLRCANTTIEHOKCENAYPGNTIDTWVCASVQEGKDSGCG 201
QY 181 DSGGPLVCNOSLOGIISWGQDPCAITRKPGYTYTKYCKYVDWIOETMKN 229
DB 202 DSGGPLVCNOSLOGIISWGQDPCAITRKPGYTYTKYCKYVDWIOETMKN 250

```
Db      202 DSGGPLVNCNOSLOGIISWGDPCATITRKPGVYTKVCKYVDWIOETMKN 250

RESULT 4
US-10-140-018-506
; Sequence 506, Application US/10140018
; Publication No. US20030138885A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C158
; CURRENT APPLICATION NUMBER: US/10/140,018
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-018-506

Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IIKGFCKRPHSQWQALFEKTRLLCGATLIAPRWMLTFAHCLKPRYIVHLGQHNLOKBE 60
        |||
Db      22 IIKGFCKRPHSQWQALFEKTRLLCGATLIAPRWMLTFAHCLKPRYIVHLGQHNLOKBE 81
        |||
QY      61 GCEQRTATSEFPHPGFNNSLPKDHNDIMLVKASPSITVAVRPLTSSRCYTAGTS 120
        |||
Db      82 GCEQRTATSEFPHPGFNNSLPKDHNDIMLVKASPSITVAVRPLTSSRCYTAGTS 141
        |||
QY      121 CLISGWGSTSSPOLRLPHTLRKANITIIHOKCENAYPGNITDTMVCASVQEGKDSGCG 180
        |||
Db      142 CLISGWGSTSSPOLRLPHTLRKANITIIHOKCENAYPGNITDTMVCASVQEGKDSGCG 201
        |||
QY      181 DSGGPLVNCNOSLOGIISWGDPCATITRKPGVYTKVCKYVDWIOETMKN 229
        |||
Db      202 DSGGPLVNCNOSLOGIISWGDPCATITRKPGVYTKVCKYVDWIOETMKN 250

RESULT 5
US-10-140-021-506
; Sequence 506, Application US/10140021
; Publication No. US20030138886A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C161
; CURRENT APPLICATION NUMBER: US/10/140,021
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-021-506

Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IIKGFCKRPHSQWQALFEKTRLLCGATLIAPRWMLTFAHCLKPRYIVHLGQHNLOKBE 60
        |||
Db      22 IIKGFCKRPHSQWQALFEKTRLLCGATLIAPRWMLTFAHCLKPRYIVHLGQHNLOKBE 81
        |||
QY      61 GCEQRTATSEFPHPGFNNSLPKDHNDIMLVKASPSITVAVRPLTSSRCYTAGTS 120
        |||
Db      82 GCEQRTATSEFPHPGFNNSLPKDHNDIMLVKASPSITVAVRPLTSSRCYTAGTS 141
        |||
QY      121 CLISGWGSTSSPOLRLPHTLRKANITIIHOKCENAYPGNITDTMVCASVQEGKDSGCG 180
        |||
Db      142 CLISGWGSTSSPOLRLPHTLRKANITIIHOKCENAYPGNITDTMVCASVQEGKDSGCG 201
        |||
QY      181 DSGGPLVNCNOSLOGIISWGDPCATITRKPGVYTKVCKYVDWIOETMKN 229
        |||
Db      202 DSGGPLVNCNOSLOGIISWGDPCATITRKPGVYTKVCKYVDWIOETMKN 250

RESULT 6
US-10-140-274-506
; Sequence 506, Application US/10140274
; Publication No. US20030143674A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C161
; CURRENT APPLICATION NUMBER: US/10/140,274
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-274-506

Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IIKGFCKRPHSQWQALFEKTRLLCGATLIAPRWMLTFAHCLKPRYIVHLGQHNLOKBE 60
        |||
Db      22 IIKGFCKRPHSQWQALFEKTRLLCGATLIAPRWMLTFAHCLKPRYIVHLGQHNLOKBE 81
        |||
QY      61 GCEQRTATSEFPHPGFNNSLPKDHNDIMLVKASPSITVAVRPLTSSRCYTAGTS 120
        |||
Db      82 GCEQRTATSEFPHPGFNNSLPKDHNDIMLVKASPSITVAVRPLTSSRCYTAGTS 141
        |||
QY      121 CLISGWGSTSSPOLRLPHTLRKANITIIHOKCENAYPGNITDTMVCASVQEGKDSGCG 180
        |||
Db      142 CLISGWGSTSSPOLRLPHTLRKANITIIHOKCENAYPGNITDTMVCASVQEGKDSGCG 201
        |||
QY      181 DSGGPLVNCNOSLOGIISWGDPCATITRKPGVYTKVCKYVDWIOETMKN 229
        |||
Db      202 DSGGPLVNCNOSLOGIISWGDPCATITRKPGVYTKVCKYVDWIOETMKN 250
```

```
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-274-506

Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFCKPHSQPQWALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 60
   |||
DB 22 IIKGFCKPHSQPQWALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 81
   |||

QY 61 GCEQTRTATESPFPHGFNNSLPNKDHRNDIMLVKMASPVSTTMAVRPLTSSRCVTAGTS 120
   |||
DB 82 GCEQTRTATESPFPHGFNNSLPNKDHRNDIMLVKMASPVSTTMAVRPLTSSRCVTAGTS 141
   |||

QY 121 CLISGSGTSSPOLRPLPTLRCANITTEHOKCENAYGNTTDMVWCAVDEGKDSGCG 180
   |||
DB 142 CLISGSGTSSPOLRPLPTLRCANITTEHOKCENAYGNTTDMVWCAVDEGKDSGCG 201
   |||

QY 181 DSGGPLVNCNOSLQGIISWGDPCCATRRKPGYTTKVCCKVDMIOETMKN 229
   |||
DB 202 DSGGPLVNCNOSLQGIISWGDPCCATRRKPGYTTKVCCKVDMIOETMKN 250
   |||

RESULT 7
US-10-140-471-506
; Sequence 506, Application US/10140471
; Publication No. US20030138887A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C163
; CURRENT APPLICATION NUMBER: US/10/140,471
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-471-506

Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFCKPHSQPQWALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 60
   |||
DB 22 IIKGFCKPHSQPQWALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 81
   |||

QY 61 GCEQTRTATESPFPHGFNNSLPNKDHRNDIMLVKMASPVSTTMAVRPLTSSRCVTAGTS 120
   |||
DB 82 GCEQTRTATESPFPHGFNNSLPNKDHRNDIMLVKMASPVSTTMAVRPLTSSRCVTAGTS 141
   |||

QY 121 CLISGSGTSSPOLRPLPTLRCANITTEHOKCENAYGNTTDMVWCAVDEGKDSGCG 180
   |||
DB 142 CLISGSGTSSPOLRPLPTLRCANITTEHOKCENAYGNTTDMVWCAVDEGKDSGCG 201
   |||

QY 181 DSGGPLVNCNOSLQGIISWGDPCCATRRKPGYTTKVCCKVDMIOETMKN 229
   |||
DB 202 DSGGPLVNCNOSLQGIISWGDPCCATRRKPGYTTKVCCKVDMIOETMKN 250
   |||
```

```
DB 142 CLISGSGTSSPOLRPLPTLRCANITTEHOKCENAYGNTTDMVWCAVDEGKDSGCG 201
   |||

QY 181 DSGGPLVNCNOSLQGIISWGDPCCATRRKPGYTTKVCCKVDMIOETMKN 229
   |||
DB 202 DSGGPLVNCNOSLQGIISWGDPCCATRRKPGYTTKVCCKVDMIOETMKN 250
   |||

RESULT 8
US-10-140-807-506
; Sequence 506, Application US/10140807
; Publication No. US20030134354A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C174
; CURRENT APPLICATION NUMBER: US/10/140,807
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-807-506

Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFCKPHSQPQWALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 60
   |||
DB 22 IIKGFCKPHSQPQWALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 81
   |||

QY 61 GCEQTRTATESPFPHGFNNSLPNKDHRNDIMLVKMASPVSTTMAVRPLTSSRCVTAGTS 120
   |||
DB 82 GCEQTRTATESPFPHGFNNSLPNKDHRNDIMLVKMASPVSTTMAVRPLTSSRCVTAGTS 141
   |||

QY 121 CLISGSGTSSPOLRPLPTLRCANITTEHOKCENAYGNTTDMVWCAVDEGKDSGCG 180
   |||
DB 142 CLISGSGTSSPOLRPLPTLRCANITTEHOKCENAYGNTTDMVWCAVDEGKDSGCG 201
   |||

QY 181 DSGGPLVNCNOSLQGIISWGDPCCATRRKPGYTTKVCCKVDMIOETMKN 229
   |||
DB 202 DSGGPLVNCNOSLQGIISWGDPCCATRRKPGYTTKVCCKVDMIOETMKN 250
   |||

RESULT 9
US-10-140-922-506
; Sequence 506, Application US/10140922
; Publication No. US20030138889A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
```

```
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C179
CURRENT APPLICATION NUMBER: US/10/140,922
CURRENT FILING DATE: 2002-05-07
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 506
LENGTH: 250
TYPE: PRT
ORGANISM: Homo Saplen
US-10-140-922-506
```

```
Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 IIRGFCKRHSQWQALFEKTRILCGATLIARWMLTAHCKPRIVYHVGHNLOKEE 60
DB 22 IIRGFCKRHSQWQALFEKTRILCGATLIARWMLTAHCKPRIVYHVGHNLOKEE 81
QY 61 GCEQTRATSEFPHPGFNNSLPNKDHNDIMLVKMASPVSIYAVRPLTSSRCVYAGTS 120
DB 82 GCEQTRATSEFPHPGFNNSLPNKDHNDIMLVKMASPVSIYAVRPLTSSRCVYAGTS 141
QY 121 CLISWGSTSSPOLRLPHTLRCANITIIHQKCNAPGNITDTMVCASVQEGKDSGCG 180
DB 142 CLISWGSTSSPOLRLPHTLRCANITIIHQKCNAPGNITDTMVCASVQEGKDSGCG 201
QY 181 DSGGPLVCNOSLOGIISWGDDPCATIRKPGVYTRKCKYVDWIDETMKN 229
DB 202 DSGGPLVCNOSLOGIISWGDDPCATIRKPGVYTRKCKYVDWIDETMKN 250
```

RESULT 10

```
US-10-140-924-506
Sequence 506, Application US/10140924
Publication No. US20030134355A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C177
CURRENT APPLICATION NUMBER: US/10/140,924
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```
CURRENT FILING DATE: 2002-05-07
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 506
LENGTH: 250
TYPE: PRT
ORGANISM: Homo Saplen
US-10-140-924-506
```

```
Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 IIRGFCKRHSQWQALFEKTRILCGATLIARWMLTAHCKPRIVYHVGHNLOKEE 60
DB 22 IIRGFCKRHSQWQALFEKTRILCGATLIARWMLTAHCKPRIVYHVGHNLOKEE 81
QY 61 GCEQTRATSEFPHPGFNNSLPNKDHNDIMLVKMASPVSIYAVRPLTSSRCVYAGTS 120
DB 82 GCEQTRATSEFPHPGFNNSLPNKDHNDIMLVKMASPVSIYAVRPLTSSRCVYAGTS 141
QY 121 CLISWGSTSSPOLRLPHTLRCANITIIHQKCNAPGNITDTMVCASVQEGKDSGCG 180
DB 142 CLISWGSTSSPOLRLPHTLRCANITIIHQKCNAPGNITDTMVCASVQEGKDSGCG 201
QY 181 DSGGPLVCNOSLOGIISWGDDPCATIRKPGVYTRKCKYVDWIDETMKN 229
DB 202 DSGGPLVCNOSLOGIISWGDDPCATIRKPGVYTRKCKYVDWIDETMKN 250
```

RESULT 11

```
US-10-140-926-506
Sequence 506, Application US/10140926
Publication No. US20030134356A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C187
CURRENT APPLICATION NUMBER: US/10/140,926
CURRENT FILING DATE: 2002-05-07
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 506
LENGTH: 250
TYPE: PRT
ORGANISM: Homo Saplen
US-10-140-926-506
```

```
Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 IIRGFCKRHSQWQALFEKTRILCGATLIARWMLTAHCKPRIVYHVGHNLOKEE 60
DB 22 IIRGFCKRHSQWQALFEKTRILCGATLIARWMLTAHCKPRIVYHVGHNLOKEE 81
```

```
QY 61 GCEQRTATSESPHGFNNSLPNKRNDIMLVKMASPVSTWAVRPLTSSRCTYAGTS 120
    |||||||
DB 82 GCEQRTATSESPHGFNNSLPNKRNDIMLVKMASPVSTWAVRPLTSSRCTYAGTS 141
QY 121 CLISGWSSTSPQRLPHTLRCANITITIEHOKCENAYPGNTIDTMVCAVSGGKDSGCG 180
    |||||||
DB 142 CLISGWSSTSPQRLPHTLRCANITITIEHOKCENAYPGNTIDTMVCAVSGGKDSGCG 201
QY 181 DSGGPLVCNOSLOGIISWGODPCAITRRPGVYTKVKYVDWIOETMKN 229
    |||||||
DB 202 DSGGPLVCNOSLOGIISWGODPCAITRRPGVYTKVKYVDWIOETMKN 250
```

RESULT 12

```
US-10-141-698-506
; Sequence 506, Application US/10141698
; Publication No. US20030134357A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C206
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION REMOVED - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-141-698-506
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Query Match 100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 IIRGECRPHSQPMAALFEKTRLLCGATLAPRMLTFAHCLKRPYVHIGOHNLQKEE 60
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DB 22 IIRGECRPHSQPMAALFEKTRLLCGATLAPRMLTFAHCLKRPYVHIGOHNLQKEE 81
QY 61 GCEQRTATSESPHGFNNSLPNKRNDIMLVKMASPVSTWAVRPLTSSRCTYAGTS 120
    |||||||
DB 82 GCEQRTATSESPHGFNNSLPNKRNDIMLVKMASPVSTWAVRPLTSSRCTYAGTS 141
QY 121 CLISGWSSTSPQRLPHTLRCANITITIEHOKCENAYPGNTIDTMVCAVSGGKDSGCG 180
    |||||||
DB 142 CLISGWSSTSPQRLPHTLRCANITITIEHOKCENAYPGNTIDTMVCAVSGGKDSGCG 201
QY 181 DSGGPLVCNOSLOGIISWGODPCAITRRPGVYTKVKYVDWIOETMKN 229
    |||||||
DB 202 DSGGPLVCNOSLOGIISWGODPCAITRRPGVYTKVKYVDWIOETMKN 250
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RESULT 13

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US-10-141-702-506
; Sequence 506, Application US/10141702
; Publication No. US20030134358A1
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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C208
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION REMOVED - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-141-702-506
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Query Match 100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 IIRGECRPHSQPMAALFEKTRLLCGATLAPRMLTFAHCLKRPYVHIGOHNLQKEE 60
    |||||||
DB 22 IIRGECRPHSQPMAALFEKTRLLCGATLAPRMLTFAHCLKRPYVHIGOHNLQKEE 81
QY 61 GCEQRTATSESPHGFNNSLPNKRNDIMLVKMASPVSTWAVRPLTSSRCTYAGTS 120
    |||||||
DB 82 GCEQRTATSESPHGFNNSLPNKRNDIMLVKMASPVSTWAVRPLTSSRCTYAGTS 141
QY 121 CLISGWSSTSPQRLPHTLRCANITITIEHOKCENAYPGNTIDTMVCAVSGGKDSGCG 180
    |||||||
DB 142 CLISGWSSTSPQRLPHTLRCANITITIEHOKCENAYPGNTIDTMVCAVSGGKDSGCG 201
QY 181 DSGGPLVCNOSLOGIISWGODPCAITRRPGVYTKVKYVDWIOETMKN 229
    |||||||
DB 202 DSGGPLVCNOSLOGIISWGODPCAITRRPGVYTKVKYVDWIOETMKN 250
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RESULT 14

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US-10-141-704-506
; Sequence 506, Application US/10141704
; Publication No. US20030134359A1
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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
```

APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C209
CURRENT APPLICATION NUMBER: US/10/141,704
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 350
SEQ ID NO 506
LENGTH: 250
TYPE: PRT
ORGANISM: Homo Sapien
US-10-141-704-506

Query Match 100.0%; Score 1258; DB 12; length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIGFECKPHSQWQAALFEKTRILCGATLIAPRWLLTAHCLKPRYIVHGGHNLQKEE 60
DB 22 IIGFECKPHSQWQAALFEKTRILCGATLIAPRWLLTAHCLKPRYIVHGGHNLQKEE 81
QY 61 GCEQTRATSEFPHPGFNNSLPNKDHNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 120
DB 82 GCEQTRATSEFPHPGFNNSLPNKDHNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 141
QY 121 CLISGWSSTSSPOLRLPHTLRCAANTITIEHOKCENAVPGNITDPMWCASVQEGKDSGCG 180
DB 142 CLISGWSSTSSPOLRLPHTLRCAANTITIEHOKCENAVPGNITDPMWCASVQEGKDSGCG 201
QY 181 DSGGPLVCNQSLOGIISWGDDPCAITRKPGVYTRKCKYVDWIOETMKN 229
DB 202 DSGGPLVCNQSLOGIISWGDDPCAITRKPGVYTRKCKYVDWIOETMKN 250

RESULT 15

US-10-142-421-506
Sequence 506, Application US/10142421
Publication No. US20030134360A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C218
CURRENT APPLICATION NUMBER: US/10/142,421
CURRENT FILING DATE: 2002-05-09
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 506
LENGTH: 250
TYPE: PRT
ORGANISM: Homo Sapien
US-10-142-421-506

Query Match 100.0%; Score 1258; DB 12; length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIGFECKPHSQWQAALFEKTRILCGATLIAPRWLLTAHCLKPRYIVHGGHNLQKEE 60
DB 22 IIGFECKPHSQWQAALFEKTRILCGATLIAPRWLLTAHCLKPRYIVHGGHNLQKEE 81
QY 61 GCEQTRATSEFPHPGFNNSLPNKDHNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 120
DB 82 GCEQTRATSEFPHPGFNNSLPNKDHNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 141
QY 121 CLISGWSSTSSPOLRLPHTLRCAANTITIEHOKCENAVPGNITDPMWCASVQEGKDSGCG 180
DB 142 CLISGWSSTSSPOLRLPHTLRCAANTITIEHOKCENAVPGNITDPMWCASVQEGKDSGCG 201
QY 181 DSGGPLVCNQSLOGIISWGDDPCAITRKPGVYTRKCKYVDWIOETMKN 229
DB 202 DSGGPLVCNQSLOGIISWGDDPCAITRKPGVYTRKCKYVDWIOETMKN 250

Search completed: October 15, 2003, 21:06:23
Job time : 21.6145 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2003, 20:55:12 ; Search time 12.9961 Seconds
(without alignments)
745.546 Million cell updates/sec

Title: US-09-856-320a-2_COPY_54_282

Perfect score: 1258
Sequence: 1 IIKGECKPHSQPMQALFE.....GVYTKCKYVDMIOETMKN 229

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
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6: /cgn2_6/ptodata/2/1aa/Backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1258	100.0	250	4	US-09-205-258-427 Sequence 427, App
2	1258	100.0	282	3	US-09-025-059-1 Sequence 1, Appl
3	1227	97.5	248	4	US-08-944-483-24 Sequence 24, Appl
4	1219.5	96.9	289	4	US-09-386-642-14 Sequence 14, Appl
5	684	54.4	260	3	US-09-025-059-3 Sequence 3, Appl
6	681	54.1	260	3	US-09-070-526-2 Sequence 2, Appl
7	673	53.5	260	3	US-09-008-271A-7 Sequence 7, Appl
8	671.5	53.4	288	4	US-09-386-642-13 Sequence 13, Appl
9	651	51.7	228	4	US-09-203-258-1150 Sequence 1150, Ap
10	651	51.7	246	4	US-09-205-258-1149 Sequence 1149, Ap
11	644.5	51.2	293	4	US-09-996-243-309 Sequence 309, App
12	597.5	47.5	268	2	US-08-824-874-1 Sequence 1, Appl
13	597.5	47.5	268	2	US-08-210-084-1 Sequence 1, Appl
14	597.5	47.5	268	4	US-09-764-762-1 Sequence 1, Appl
15	591.5	47.0	263	2	US-08-790-137-4 Sequence 4, Appl
16	591.5	47.0	263	2	US-08-824-874-5 Sequence 5, Appl
17	591.5	47.0	263	2	US-08-807-151-5 Sequence 5, Appl
18	591.5	47.0	263	3	US-09-210-084-5 Sequence 5, Appl
19	591.5	47.0	263	4	US-09-478-957-5 Sequence 5, Appl
20	591.5	47.0	263	4	US-09-764-762-5 Sequence 5, Appl
21	587	46.7	246	2	US-08-978-404B-44 Sequence 44, Appl
22	578	45.9	232	2	US-08-978-404B-45 Sequence 45, Appl
23	577.5	45.9	237	3	US-08-768-859A-16 Sequence 16, Appl
24	577.5	45.9	237	3	US-08-767-820A-16 Sequence 16, Appl
25	577.5	45.9	237	3	US-08-622-046B-12 Sequence 12, Appl
26	577.5	45.9	237	3	US-08-944-483-37 Sequence 37, Appl
27	577.5	45.9	237	3	US-09-100-264-1 Sequence 1, Appl

28	577.5	45.9	237	4	US-08-843-076D-1 Sequence 1, Appl
29	577.5	45.9	238	3	US-08-768-859A-8 Sequence 8, Appl
30	577.5	45.9	238	3	US-08-767-820A-8 Sequence 8, Appl
31	577.5	45.9	244	3	US-08-768-859A-10 Sequence 10, Appl
32	577.5	45.9	244	3	US-08-767-820A-10 Sequence 10, Appl
33	577.5	45.9	244	3	US-08-622-046B-16 Sequence 16, Appl
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35	577.5	45.9	244	4	US-08-843-076D-5 Sequence 5, Appl
36	577.5	45.9	261	3	US-08-768-859A-6 Sequence 6, Appl
37	577.5	45.9	261	3	US-08-622-046B-14 Sequence 6, Appl
38	577.5	45.9	261	3	US-09-100-264-7 Sequence 7, Appl
39	577.5	45.9	261	3	US-08-983-075D-7 Sequence 7, Appl
40	577.5	45.9	261	4	US-08-843-076D-3 Sequence 3, Appl
41	577.5	45.9	261	4	US-08-278-091-7 Sequence 7, Appl
42	577	45.9	228	1	US-08-483-859-7 Sequence 7, Appl
43	577	45.9	228	1	US-08-472-173-7 Sequence 7, Appl
44	577	45.9	228	1	US-08-483-859-7 Sequence 7, Appl
45	577	45.9	228	2	US-08-487-167-7 Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-205-258-427
; Sequence 427, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06

9
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; EARLIER APPLICATION NUMBER: 60/049, 019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049, 373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049, 374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070, 923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092, 921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094, 657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 427
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-427

Query Match      100.0%; Score 1258; DB 4; Length 250;
Best Local Similarity 100.0%; Pred. No. 9, 6e-126;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IINGFECKPHSOPWQALFEKTRILCGATLIAPRWLLTAHCLKPRYIVHLGQHNLOKEE 60
DB 22 IINGFECKPHSOPWQALFEKTRILCGATLIAPRWLLTAHCLKPRYIVHLGQHNLOKEE 81
QY 61 GCQOTRATSEFPHGPNNSLPKNDHNDIMLVKMA SPVITWAVRPLTSSRCVYAGTS 120
DB 82 GCQOTRATSEFPHGPNNSLPKNDHNDIMLVKMA SPVITWAVRPLTSSRCVYAGTS 141
QY 121 CLISGSGSTSSPOLRLPHILRCANITIIIEHOKCENAYPGNITDTMVCASVQEGGKDSGCG 180
DB 142 CLISGSGSTSSPOLRLPHILRCANITIIIEHOKCENAYPGNITDTMVCASVQEGGKDSGCG 201
QY 181 DSGGPLVNCNSLOGIISWGDDPCATIRKPGVYTKVKCYVWIOETMKN 229
DB 202 DSGGPLVNCNSLOGIISWGDDPCATIRKPGVYTKVKCYVWIOETMKN 250

RESULT 2
US-09-025-059-1
; Sequence 1, Application US/09025059
; Patent No. 6075136
```

```

; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025, 059
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0481 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 282 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGTUT10
; CLONE: 2723646
US-09-025-059-1

Query Match      100.0%; Score 1258; DB 3; Length 282;
Best Local Similarity 100.0%; Pred. No. 1, 1e-125;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IINGFECKPHSOPWQALFEKTRILCGATLIAPRWLLTAHCLKPRYIVHLGQHNLOKEE 60
DB 54 IINGFECKPHSOPWQALFEKTRILCGATLIAPRWLLTAHCLKPRYIVHLGQHNLOKEE 113
QY 61 GCQOTRATSEFPHGPNNSLPKNDHNDIMLVKMA SPVITWAVRPLTSSRCVYAGTS 120
DB 114 GCQOTRATSEFPHGPNNSLPKNDHNDIMLVKMA SPVITWAVRPLTSSRCVYAGTS 173
QY 121 CLISGSGSTSSPOLRLPHILRCANITIIIEHOKCENAYPGNITDTMVCASVQEGGKDSGCG 180
DB 174 CLISGSGSTSSPOLRLPHILRCANITIIIEHOKCENAYPGNITDTMVCASVQEGGKDSGCG 233
QY 181 DSGGPLVNCNSLOGIISWGDDPCATIRKPGVYTKVKCYVWIOETMKN 229
DB 234 DSGGPLVNCNSLOGIISWGDDPCATIRKPGVYTKVKCYVWIOETMKN 282

RESULT 3
US-08-944-483-24
; Sequence 24, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
```


APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
TITLE OF INVENTION: OF THE PROSTATE
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183 .US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6232456e
US-08-944-483-24

Query Match 97.5%; Score 1227; DB 3; Length 248;
Best Local Similarity 99.1%; Pred. No. 1.9e-122;
Matches 227; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 IIKGFEC-PHSQPMQALFEKTRILCGATLLAPRWLTAAHCLKPRYIVHIGQHNLOKEE 60
DB 22 IIKGFEC-PHSQPMQALF-KTRILCGATLLAPRWLTAAHCLKPRYIVHIGQHNLOKEE 79
QY 61 GCEQTRATESFPHGFNNSLPNKDRNDIMLVKASPVSTMAVRPLTSSRCVTAGT 120
DB 80 GCEQTRATESFPHGFNNSLPNKDRNDIMLVKASPVSTMAVRPLTSSRCVTAGT 139
QY 121 CLISGWSSTSPQRLPRTLTCANITTEHOKCENAYPGNTIDTWVCASVOEGKDSQCG 180
DB 140 CLISGWSSTSPQRLPRTLTCANITTEHOKCENAYPGNTIDTWVCASVOEGKDSQCG 199
QY 181 DSGGPLVNCOSLOGIISWGODPCAITRRPGYTVCKYVDMIOETMKN 229
DB 200 DSGGPLVNCOSLOGIISWGODPCAITRRPGYTVCKYVDMIOETMKN 248

RESULT 4
US-09-386-642-14
Sequence 14, Application US/09386642
Patent No. 6420157
GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Q1, Jensen

APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 289
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-14

Query Match 96.9%; Score 1219.5; DB 4; Length 289;
Best Local Similarity 97.0%; Pred. No. 1.5e-121;
Matches 223; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 IIKGFEC-PHSQPMQALFEKTRILCGATLLAPRWLTAAHCLKPRYIVHIGQHNLOKEE 59
DB 52 IYGVNCLKHSQPMQALFEKTRILCGATLLAPRWLTAAHCLKPRYIVHIGQHNLOKEE 111
QY 60 ECEQTRATESFPHGFNNSLPNKDRNDIMLVKASPVSTMAVRPLTSSRCVTAGT 119
DB 112 ECEQTRATESFPHGFNNSLPNKDRNDIMLVKASPVSTMAVRPLTSSRCVTAGT 171
QY 120 SCLISGWSSTSPQRLPRTLTCANITTEHOKCENAYPGNTIDTWVCASVOEGKDSQCG 179
DB 172 SCLISGWSSTSPQRLPRTLTCANITTEHOKCENAYPGNTIDTWVCASVOEGKDSQCG 231
QY 180 DSGGPLVNCOSLOGIISWGODPCAITRRPGYTVCKYVDMIOETMKN 229
DB 232 DSGGPLVNCOSLOGIISWGODPCAITRRPGYTVCKYVDMIOETMKN 281

RESULT 5
US-09-025-059-3
Sequence 3, Application US/09025059
Patent No. 6075136
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,059
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0481 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166

TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Genbank
; CLONE: 1020091
US-09-025-059-3

Query Match 54.4%; Score 684; DB 3; Length 260;
Best Local Similarity 53.1%; Pred. No. 1e-64;
Matches 121; Conservative 35; Mismatches 70; Indels 2; Gaps 2;

QY 1 IINGFECKPHSQWQALFEKTRLLCGATLIAPRWLITAAHCKPRITYVHLGQHNLOKEE 60
DB 33 ILEGRCEIPHSQWQALFEKTRLLCGATLIAPRWLITAAHCKPRITYVHLGQHNLOKEE 92
QY 61 GCEOTRATESPFPHPGNNSLPNKDRNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 120
DB 93 QPEDEIQVAOSIHPHCYNNSP-EDHSHDMLIRLQNSANLGDVKFVQLANLCPKVGOK 151
QY 121 CLISGWSSTSPQLRLPHTLRCAITITIEHOKCENAYPGNITDTMVCASVOEGKSDSCG 180
DB 152 CIIISGWSCTVSPQENFPNTLNCALVKIYSONKCEKATPGKITEGVCAG-SSNGADTCOG 210
QY 181 DSGGPLVNCNLSLOGIISWGDPICATIRKPGVYTRKVCYVWIOETMKN 228
DB 211 DSGGPLVCDGLQGITSMGSDPCGKPEKPGVYTRKICRYTWIKKTMDN 258

RESULT 6
US-09-070-526-2
; Sequence 2, Application US/09070526
; Patent No. 6100059
; GENERAL INFORMATION:
; APPLICANT: SOUTHAN, CHRISTOPHER
; APPLICANT: CLINKENBEARD, HELEN
; APPLICANT: BURGESS, NICOLA
; TITLE OF INVENTION: No. 6100059e1 Compounds
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATHER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,526
; FILING DATE: 30-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9711952.3
; FILING DATE: 9-JUN-1997
; APPLICATION NUMBER: EP 97309646.4
; FILING DATE: 1-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-30353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-070-526-2

Query Match 54.1%; Score 681; DB 3; Length 260;
Best Local Similarity 51.8%; Pred. No. 2.2e-64;
Matches 116; Conservative 42; Mismatches 64; Indels 2; Gaps 2;

QY 1 IINGFECKPHSQWQALFEKTRLLCGATLIAPRWLITAAHCKPRITYVHLGQHNLOKEE 60
DB 33 ILEGRCEIPHSQWQALFEKTRLLCGATLIAPRWLITAAHCKPRITYVHLGQHNLOKEE 92
QY 61 GCEOTRATESPFPHPGNNSLPNKDRNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 120
DB 93 GPEDEIPVOSIHPHCYNNSS-DVEDHNDIMLQLRQASLSGKVRPISLADHCTPGOK 151
QY 121 CLISGWSSTSPQLRLPHTLRCAITITIEHOKCENAYPGNITDTMVCASVOEGKSDSCG 180
DB 152 CIIISGWSCTVSPQENFPNTLNCALVKIYSONKCEKATPGKITEGVCAG-SSNGADTCOG 210
QY 181 DSGGPLVNCNLSLOGIISWGDPICATIRKPGVYTRKVCYVWIOE 224
DB 211 DSGGPLVCDGLQGITSMGSDPCGKPEKPGVYTRKICRYTWIKKTMDN 254

RESULT 7
US-09-008-271A-7
; Sequence 7, Application US/09008271A
; Patent No. 6203979
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Yue, Henry
; Guegler, Karl J.
; Corley, Neil C.
; Tang, Tom Y.
; Shah, Purvi
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,271A
; FILING DATE: 16-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohan-Peterson, Sheela
; REGISTRATION NUMBER: 41,201
; REFERENCE/DOCKET NUMBER: PF-0458 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; STRANDEDNESS: single


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1 EARLIER APPLICATION NUMBER: 60/048,971
2 EARLIER FILING DATE: 1997-06-06
3 EARLIER APPLICATION NUMBER: 60/048,964
4 EARLIER FILING DATE: 1997-06-06
5 EARLIER APPLICATION NUMBER: 60/048,882
6 EARLIER FILING DATE: 1997-06-06
7 EARLIER APPLICATION NUMBER: 60/048,899
8 EARLIER FILING DATE: 1997-06-06
9 EARLIER APPLICATION NUMBER: 60/048,893
10 EARLIER FILING DATE: 1997-06-06
11 EARLIER APPLICATION NUMBER: 60/048,900
12 EARLIER FILING DATE: 1997-06-06
13 EARLIER APPLICATION NUMBER: 60/048,901
14 EARLIER FILING DATE: 1997-06-06
15 EARLIER APPLICATION NUMBER: 60/048,892
16 EARLIER FILING DATE: 1997-06-06
17 EARLIER APPLICATION NUMBER: 60/048,915
18 EARLIER FILING DATE: 1997-06-06
19 EARLIER APPLICATION NUMBER: 60/049,019
20 EARLIER FILING DATE: 1997-06-06
21 EARLIER APPLICATION NUMBER: 60/048,970
22 EARLIER FILING DATE: 1997-06-06
23 EARLIER APPLICATION NUMBER: 60/048,972
24 EARLIER FILING DATE: 1997-06-06
25 EARLIER APPLICATION NUMBER: 60/048,916
26 EARLIER FILING DATE: 1997-06-06
27 EARLIER APPLICATION NUMBER: 60/049,373
28 EARLIER FILING DATE: 1997-06-06
29 EARLIER APPLICATION NUMBER: 60/048,875
30 EARLIER FILING DATE: 1997-06-06
31 EARLIER APPLICATION NUMBER: 60/049,374
32 EARLIER FILING DATE: 1997-06-06
33 EARLIER APPLICATION NUMBER: 60/048,917
34 EARLIER FILING DATE: 1997-06-06
35 EARLIER APPLICATION NUMBER: 60/048,949
36 EARLIER FILING DATE: 1997-06-06
37 EARLIER APPLICATION NUMBER: 60/048,974
38 EARLIER FILING DATE: 1997-06-06
39 EARLIER APPLICATION NUMBER: 60/048,883
40 EARLIER FILING DATE: 1997-06-06
41 EARLIER APPLICATION NUMBER: 60/048,897
42 EARLIER FILING DATE: 1997-06-06
43 EARLIER APPLICATION NUMBER: 60/048,898
44 EARLIER FILING DATE: 1997-06-06
45 EARLIER APPLICATION NUMBER: 60/048,962
46 EARLIER FILING DATE: 1997-06-06
47 EARLIER APPLICATION NUMBER: 60/048,963
48 EARLIER FILING DATE: 1997-06-06
49 EARLIER APPLICATION NUMBER: 60/048,877
50 EARLIER FILING DATE: 1997-06-06
51 EARLIER APPLICATION NUMBER: 60/048,878
52 EARLIER FILING DATE: 1997-06-06
53 EARLIER APPLICATION NUMBER: 60/070,923
54 EARLIER FILING DATE: 1997-12-18
55 EARLIER APPLICATION NUMBER: 60/092,921
56 EARLIER FILING DATE: 1998-07-15
57 EARLIER APPLICATION NUMBER: 60/094,657
58 EARLIER FILING DATE: 1998-07-30
59 NUMBER OF SEQ ID NOS: 1237
60 SOFTWARE: PatentIn Ver. 2.0
61 SEQ ID NO 1149
62 LENGTH: 246
63 TYPE: PRT
64 ORGANISM: Homo sapiens
65 US-09-205-258-1149
66
67 Query Match 51.7%; Score 651; DB 4; Length 246;
68 Best Local Similarity 91.7%; Pred. No. 3,1e-61;
69 Matches 121; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
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61 1 IIRGECKPHSQMOALFEXTRLIGATLIAPRMULTAHCCLKPRYIVHIGONHTOREE 60
62 IIRGECKPHSQMOALFEXTRLIGATLIAPRMULTAHCCLKPRYIVHIGONHTOREE 81

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QY 61 GCEQRTATRESPPHGFNNSLPNKDRNDIMLVKMASPVSTWAVRPLTSLSRCTACTS 120
DB 82 GCEQRTATESPPHGFNNSLPNKDRNDIMLVKMASPVSTWAVRPLTSLSRCTACTS 141
QY 121 CLISGMSGSSP 132
DB 142 CSFPAGARPD 153

RESULT 11
US-09-996-243-309
Sequence 309, Application US/09996243
Patent No. 64/8825
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC13
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US/09/996,243
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
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PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021

PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
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PRIOR FILING DATE: 1998-06-19

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2	PRIOR FILING DATE: 1998-06-19
3	PRIOR APPLICATION NUMBER: 60/090246
4	PRIOR FILING DATE: 1998-06-22
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34	PRIOR FILING DATE: 1998-06-25
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36	PRIOR FILING DATE: 1998-06-25
37	PRIOR APPLICATION NUMBER: 60/090690
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39	PRIOR APPLICATION NUMBER: 60/090694
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41	PRIOR APPLICATION NUMBER: 60/090695
42	PRIOR FILING DATE: 1998-06-25
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44	PRIOR FILING DATE: 1998-06-25
45	PRIOR APPLICATION NUMBER: 60/090862
46	PRIOR FILING DATE: 1998-06-26
47	PRIOR APPLICATION NUMBER: 60/090863
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58	PRIOR FILING DATE: 1998-07-02
59	PRIOR APPLICATION NUMBER: 60/091633
60	PRIOR FILING DATE: 1998-07-02
61	PRIOR APPLICATION NUMBER: 60/091978
62	PRIOR FILING DATE: 1998-07-07
63	PRIOR APPLICATION NUMBER: 60/091982
64	PRIOR FILING DATE: 1998-07-07
65	PRIOR APPLICATION NUMBER: 60/092182
66	PRIOR FILING DATE: 1998-07-09

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D6 67 IINGSDODNHTQWQAAALLRPNOLYCGAVLHPQWMLTAACHCKKVFVRALGHYSLSPV 126
QY 59 EEECEQTRATSEFPHPGPNNSLPKMDHRNDIMLYKMASPVSTWAVRPLTLLSRCTYAG 118
D6 127 YESGQOMFOGYSKIPHPGYS---HPGSHNDMLIKLRIRRPKIDVPIVSSHCPGSA 182
QY 119 TSLILGMSGSTSPQRLRPHLTRCANTITILIEQCKENAYPGNITDITWACSVQEGCSDC 178
D6 183 TKLVSQWGTGTPKPOVHPKFLVQCLNTISVLSQKCEDAYPRQIDITMFCAG-DKAGRSDC 241
QY 179 QGSGGPELVNOSLQGIISMGODPALTTRKPPVYKVCAYKYUDMIOETMKNK 229
D6 242 QGSGGPELVNOSLQGIYSWGDYPCARRPRREVYTNLCKFTKMLQETIOAN 292

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US-08-824-874-1
Sequence 1, Application US/08824874
Patent No. 5962300
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874 *
FILING DATE: Filed Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KERANOT02
CLONE: 820694
US-08-824-874-1

47.5%; Score 597.5; DB 2; Length 268;
Best Local Similarity 49.1%; Pred No. 1,7e-55;
Matches 110; Conservative 39; Mismatches 68; Indels 7; Gaps 4

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109 FGVGKSLIPDGS---HGHSNDMLTKLRRLRPDKVIRPIVWSHCPSACTKCLVSG 164
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us-09-856-320a-2_copy_54_282.ra

9; Gaps 2;

IKDVMMANN 262